

Daniel G. Brown

Curriculum Vitae

July 1, 2016

David R. Cheriton School of Computer Science
University of Waterloo
200 University Ave. West
Waterloo, Ontario N2L 3G1, Canada
email: dan.brown@uwaterloo.ca
voice: +1-519-888-4567x36278
web: www.cs.uwaterloo.ca/~browndg

Education

- Ph.D., Computer Science, Cornell University, 2000
Algorithmic methods in genetic mapping
Supervisor: David B. Shmoys
- M.S., Computer Science, Cornell University, 1999
- S.B., Mathematics with Computer Science, Massachusetts Institute of Technology, 1995

Professional Employment

- Professor of computer science, University of Waterloo, 2016-present
 - Director of undergraduate studies, July 2016-present
 - Adjunct professor of biology, 2016-present
- Associate professor of computer science, University of Waterloo, 2007-2016
 - Director of undergraduate studies, July 2013-December 2014
 - Associate (vice) director of School, July 2011-June 2013
 - Director of first-year studies, July 2006-June 2009
 - Adjunct associate professor of biology, 2011-2016
- Assistant professor of computer science, University of Waterloo, 2000-2007
- Visiting assistant professor of computer science, University of California, Davis, 2006
- Research scientist, Massachusetts Institute of Technology/Whitehead Institute Center for Genome Research (now Broad Institute), 2000-2001
- Undergraduate researcher, Charles Stark Draper Laboratory, 1994-1995
- Software development intern, Microsoft, summers 1992-1994

Publications

Book edited

2014

- D.G. Brown and B. Morgenstern (eds.). *Algorithms in Bioinformatics*. Proceedings volume for 2014 Workshop on Algorithms in Bioinformatics. Lecture Notes in Bioinformatics, volume 8701, Springer.

Journal articles

Under review

- C. Lamb, D.G. Brown, C.L.A. Clarke. A taxonomy of generative poetry techniques. Under review at *Journal of Mathematics and the Arts*.
- C. Lamb, D.G. Brown, C.L.A. Clarke. Evaluating computational creativity: theory and practice. Under review at *ACM Computing Surveys*.
- D.G. Brown, M. Stange, K.A. Harrigan. Do low-income Ontario residents buy the most scratch tickets? A demographic analysis. Under review at *Journal of Gambling Issues*.
- D.G. Brown, M. Owen. Mean and variance of phylogenetic trees. Under review at *Systematic Biology*.

To appear

- M. Stange, D.G. Brown, K.A. Harrigan, M.J. Dixon. Built-in bad luck: evidence of near-miss outcomes by design in scratch cards. To appear in *Journal of Gambling Studies*.

2017

- K.R. Barton, Y. Yazdani, N. Ayer, S. Kalvapalle, S. Brown, J. Stapleton, D.G. Brown, K.A. Harrigan. The effect of losses disguised as wins and near misses in electronic gaming machines: A Systematic Review. *Journal of Gambling Studies*. Published online 18 April 2017, 20 pages.

2015

- K. Harrigan, D.G. Brown, V. MacLaren. Gamble while you gamble: electronic games in Ontario Charitable Gaming Centres. *International Journal of Mental Health and Addiction* **13**(6): 740-750.
- E. Marinier, D.G. Brown, B. McConkey. Pollux: platform-independent error correction of single and mixed genomes. *BMC Bioinformatics* **16**:10, 2015.

2014

- K. Harrigan, M. Dixon, D.G. Brown. Modern multi-line slot machine games: The effect of lines wagered on winners, losers, bonuses, and losses disguised as wins. *Journal of Gambling Studies* **31**(2): 423-439, 2014.
- K. Harrigan, V. MacLaren, D.G. Brown, M. Dixon, C. Livingstone. Games of chance or masters of illusion: multiline slots design may promote cognitive distortions. *International Gambling Studies* **14**(2): 301-317, 2014.
- M. Ackerman, D.G. Brown, D. Loker. Effects of rooting via outgroups on ingroup topology in phylogeny. *International Journal of Bioinformatics Research and Applications* **10**(4/5): 426-446, 2014 (special issue on selected papers from ICCABS 2012).

2013

- Brown D.G., J. Truszkowski. Fast error-tolerant quartet phylogeny algorithms. *Theoretical Computer Science* **483**: 104-114, 2013 (special issue on selected papers from CPM 2011).
- D. Dexter, D.G. Brown. Fast half-sibling population reconstruction: theory and algorithms. *Algorithms for Molecular Biology* **8**: 20, 2013 (Special issue on selected papers from WABI 2012), 12 pages.

2012

- J. Truszkowski, Y. Hao, D.G. Brown. Towards a practical $O(n \log n)$ phylogeny algorithm. *Algorithms in Molecular Biology* **7**:32, 2012 (Special issue for best papers from WABI 2011), 10 pages.

- A.P. Masella, A.K. Bartram, J. Truszkowski, D.G. Brown, J.D. Neufeld. PANDAseq: PAired-eND assembler for Illumina sequences. *BMC Bioinformatics* **13**:31, 2012, 7 pages.
- 2011
- A.K. Hudek, D.G. Brown. FEAST: sensitive alignment with multiple rates of evolution. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* **8**:697-709, 2011.
 - J. Truszkowski, D.G. Brown. More accurate recombination prediction in HIV-1 using a robust decoding algorithm for HMMs. *BMC Bioinformatics* **12**: 168, 2011, 11 pages.
 - H. Hirjee, D.G. Brown. Using automated rhyme detection to characterize rhyming style in rap music. *Empirical Musicology Review* **5**(4): 121-145, 2011.
- 2010
- D.G. Brown, D. Golod. Decoding HMMs using the k best paths: algorithms and applications. *BMC Bioinformatics* **11**(Suppl 1): S28, 2010. Special issue for proceedings of Asia-Pacific Bioinformatics Conference (APBC) 2010.
 - D.G. Brown, J. Truszkowski. New decoding algorithms for hidden Markov models using distance measures on state paths. *BMC Bioinformatics* **11**(Suppl 1): S40, 2010. Special issue for proceedings of Asia-Pacific Bioinformatics Conference (APBC) 2010.
- 2009
- *Schistosoma japonica* Genome Sequence and Functional Analysis Consortium. The *Schistosoma japonicum* genome reveals features of host-parasite interplay. *Nature* **460**: 345-352, 2009.
 - D.G. Brown, D. Golod. A tutorial of techniques for improving standard hidden Markov model algorithms. *Journal of Bioinformatics and Computational Biology* **7**: 737-754, 2009.
 - B. Brejova, T. Vinar, Y. Chen, S. Wang, G. Zhao, D.G. Brown, M. Li, Y. Zhou. Finding genes in *Schistosoma japonicum*: annotating novel genomes with help of extrinsic evidence. *Nucleic Acids Research* **37**: e52, 2009.
- 2007
- B. Brejova, D.G. Brown, T. Vinar. The most probable annotation problem in HMMs and its application to bioinformatics. *Journal of Computing and System Sciences*, **73** (7): 1060-1077, 2007.
- 2006
- D.G. Brown, I.M. Harrower. Integer programming approaches to haplotype inference by pure parsimony. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **3**(2):141-154. 2006
 - J. Xu, D.G. Brown, M. Li, B. Ma. Optimizing multiple spaced seeds for homology search. *Journal of Computational Biology*. **13**(7): 1355-1368, 2006.
 - E.W. Xu, P. Kearney, D.G. Brown. The use of functional domains to improve transmembrane protein topology prediction. *Journal of Bioinformatics and Computational Biology* **4**:109-113, 2006 (Special issue for the best papers of the 2005 Asia-Pacific Bioinformatics Conference).
- 2005
- A.K. Hudek and D.G. Brown. Ancestral sequence alignment under optimal conditions. *BMC Bioinformatics* **6**:273, 2005.
 - B. Brejova, D.G. Brown, M. Li, T. Vinar. ExonHunter: a comprehensive approach to gene finding. *Bioinformatics* **21**(S1):i57-i65, 2005 (Proceedings of Intelligent Systems in Molecular Biology 2005).

- D.G. Brown. Multiple seeds for protein alignment. *IEEE/ACM Transactions on Bioinformatics and Computational Biology* **2**: 29-38, 2005 (Special issue for the best papers of the 2004 Workshop on Algorithms in Bioinformatics).
- B. Brejova, D.G. Brown, T. Vinar. Vector seeds: an extension to spaced seeds. *Journal of Computer and System Sciences* **70**: 364-380, 2005.

2004

- D.G. Brown, M. Li, B. Ma. A tutorial of recent developments in the seeding of local alignment. *Journal of Bioinformatics and Computational Biology* **2**(4):819-842, 2004.
- B. Brejova, D.G. Brown, T. Vinar. Optimal spaced seeds for homologous coding regions. *Journal of Bioinformatics and Computational Biology* **1**(4): 595-610, 2004.

2002

- Mouse Genome Sequencing Consortium. Initial sequencing and comparative analysis of the mouse genome. *Nature* **420**: 520-562, 2002.

2001

- International Human Genome Sequencing Consortium. Initial sequencing and analysis of the human genome. *Nature* **409**: 860-921, 2001. (Member of genome analysis group)

2000

- T.J. Vision, D.G. Brown, S.D. Tanksley. The origins of genomic duplications in *Arabidopsis*. *Science* **290**: 2114-2117, 2000.
- T.J. Vision, D.G. Brown, D.B. Shmoys, R.T. Durrett, and S.D. Tanksley. Selective mapping: A strategy for optimizing the construction of linkage map. *Genetics* **155**: 407-420, 2000.

Conference proceedings

2017

- D. Bountouridis, D.G. Brown, H.V. Koops, F. Wiering, R.C. Veltkamp. Melody retrieval and classification using biologically-inspired techniques. *Proceedings of the 2016 International Conference on Evolutionary and Biologically Inspired Music and Art (EVOMUSART)*, 49-64.
- D. Bountouridis, F. Wiering, D.G. Brown, R.C. Veltkamp. Towards polyphony reconstruction using multidimensional multiple sequence alignment. *Proceedings of EVOMUSART 2017*, 33-48.
- C.E. Lamb, D.G. Brown and C.L.A. Clarke. Incorporating novelty, meaning, reaction and craft into computational poetry: a negative experimental result. *Proceedings of the 2017 International Conference on Computational Creativity (ICCC)*.

2016

- C.E. Lamb, D.G. Brown and C.L.A. Clarke. A taxonomy of generative poetry techniques. *Proceedings of Bridges 2016*, 195-202.
- C.E. Lamb, D.G. Brown and C.L.A. Clarke. Evaluating digital poetry: insights from the CAT. *Proceedings of ICC 2016*.

2015

- C.E. Lamb, D.G. Brown and C.L.A. Clarke. Human competence in creativity evaluation. *Proceedings of ICC 2015*, 102-109.
- C.E. Lamb, D.G. Brown and C.L.A. Clarke. Can human assistance improve a computational poet? *Proceedings of Bridges 2015*, 37-44.

- A. Singhi and D.G. Brown. Can song lyrics predict hits? *Proceedings of the 2015 Conference on Computer Music and Multidisciplinary Research (CMMR)*, 457-472.
- 2014
- D.G. Brown and A. Singhi. On experiential, textual and cultural components to music mood. *Proceedings of the 2014 International Society for Music Information Retrieval Conference (ISMIR)*, 1-6.
 - D.G. Brown and A. Singhi. Are lyrics and poetry all that different? *Proceedings of ISMIR 2014*, 471-476.
- 2013
- D.G. Brown and J. Truszkowski. LSHPlace: Fast phylogenetic placement using locality-sensitive hashing. *Proceedings of the 2013 Pacific Symposium in Biocomputing (PSB)*, 310-319.
- 2012
- B. Martin, D.G. Brown, P. Hanna, P. Ferraro. BLAST for audio sequences alignment: a fast scalable cover identification tool. *Proceedings of ISMIR 2012*.
 - D.G. Brown and D. Dexter. Combinatorial approaches to half-sibling reconstruction. *Proceedings of the 2012 Workshop on Algorithms in Bioinformatics (WABI)*, 44-56.
 - D.G. Brown, J. Truszkowski, Fast phylogeny algorithms using locality-sensitive hashing. *Proceedings of WABI 2012*, 14-29.
 - M. Ackerman, D.G. Brown, D. Loker. Effects of rooting via outgroups on ingroup topology in phylogeny. *Proceedings of the International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2012)*, 7 pages.
- 2011
- D.G. Brown, J. Truszkowski. Toward a practical $O(n \log n)$ quartet phylogeny algorithm. *Proceedings of WABI 2011*, 14-25.
 - D.G. Brown, J. Truszkowski. Fast error-tolerant quartet phylogeny algorithms. *Proceedings of the 2011 Symposium on Combinatorial Pattern Matching (CPM)*, 147-161.
- 2010
- D.G. Brown, T. Berger-Wolf. Discovering kinship through small subsets. *Proceedings of WABI 2010*, 111-123.
 - H. Hirjee, D.G. Brown. Solving misheard lyric search queries using a probabilistic model of speech sounds. *Proceedings of ISMIR 2010*, 147-152. Best Student Paper Award.
- 2009
- H. Hirjee, D.G. Brown. Automatic detection of internal and imperfect rhymes in rap music lyrics. *Proceedings of ISMIR 2009*, 711-716.
 - C. Boucher, D.G. Brown. Detecting motifs in a large data set: applying probabilistic insights to motif finding. *Proceedings of Bioinformatics and Computational Biology (BiCOB 2009)*, 139-150.
- 2008
- C. Boucher, D.G. Brown, S. Durocher. On the structure of small motif recognition instances. *Proceedings of String Processing and Information Retrieval (SPIRE) 2008*, 269-281.
- 2007

- D. Gusfield, Y. Frid, D.G. Brown: Integer programming formulations and computations solving phylogenetic and population genetic problems with missing or genotypic data. *Proceedings of the 2007 Conference on Computing and Combinatorics (COCOON)*, 51-64.
- C. Boucher, D.G. Brown, P. Church: A graph clustering approach to weak motif recognition. *Proceedings of WABI 2007*, 149-160.

2006

- B. Brejova, D.G. Brown, I.M. Harrower, T. Vinar. New bounds for motif finding in strong instances. *Proceedings of CPM 2006*, 94-105.
- D.G. Brown, I.M. Harrower. Toward an algebraic understanding of haplotype inference by pure parsimony. *Proceedings of the 2006 Computational Systems Bioinformatics Conference (CSB)*, 211-222.

2005

- B. Brejova, D.G. Brown, I.M. Harrower, A. Lopez-Ortiz, T. Vinar. Sharper upper and lower bounds for Consensus-Pattern. *Proceedings of CPM 2005*, 1-10.
- E.W. Xu, D.G. Brown, P. Kearney. The use of functional domains to improve transmembrane protein topology prediction. *Proceedings of APBC 2005*, 105-116.

2004

- D.G. Brown. Multiple vector seeds for protein alignment. *Proceedings of WABI 2004*, 170-181.
- D.G. Brown, I.M. Harrower. A new integer programming formulation for the pure parsimony problem in haplotype analysis. *Proceedings of WABI 2004*, 254-265.
- D.G. Brown, A.K. Hudek. New algorithms for multiple DNA sequence alignment. *Proceedings of WABI 2004*, 314-325
- B. Brejova, D.G. Brown, T. Vinar. The most probable labeling problem in HMMs and its applications to bioinformatics. *Proceedings of WABI 2004*, 426-437.
- J. Xu, D.G. Brown, M. Li, B. Ma. Optimizing multiple spaced seeds for homology search. *Proceedings of CPM 2004*, 47-58.

2003

- B. Brejova, D.G. Brown, T. Vinar. Optimal DNA signal recognition models with a fixed amount of intrasignal dependency. *Proceedings of WABI 2003*, 78-94.
- B. Brejova, D.G. Brown, T. Vinar. Vector seeds: an extension to spaced seeds allows substantial improvements in sensitivity and specificity. *Proceedings of WABI 2003*, 39-54.
- B. Brejova, D.G. Brown, T. Vinar. Optimal spaced seeds for hidden Markov models, with applications to homologous coding regions. *Proceedings of CPM 2003*, 42-54.

2001

- D.G. Brown. A probabilistic analysis of a greedy algorithm arising from computational biology. *Proceedings of the 2001 ACM/SIAM Symposium on Discrete Algorithms (SODA)*, pp 208, 206 (misprinted in proceedings).

2000

- D.G. Brown, T.J. Vision, S.D. Tanksley. Selective mapping: a discrete optimization approach to selecting a population subset for use in a high-density genetic mapping project. *Proceedings of SODA 2000*, 419-428.

Book chapters

2008

- B. Brejova, D.G. Brown, T. Vinar. Advances in hidden Markov models for sequence annotation. In *Bioinformatics Algorithms: Techniques and Applications*. J. Wiley and Sons, 2008; I. Mandoiu and A. Zelikovsky, eds.
 - D.G. Brown. A survey of seeding for sequence alignments. In *Bioinformatics Algorithms: Techniques and Applications*. J. Wiley and Sons, 2008; I. Mandoiu and A. Zelikovsky, eds.
- 2007
- D.G. Brown. A survey of sequence alignment. In *Computational Genomics: Current methods*. Horizon Press, 2007; N. Stojanovic, ed., pp. 95-120.
- 2004
- D.G. Brown, B. Ma, M. Li. Homology search methods. In *The Practical Bioinformatician*, ed: L. Wong. Singapore: World Scientific, 2004, 217-244.
- 2000
- T.J. Vision, D.G. Brown. Genome archaeology: Detecting ancient polyploidy in contemporary genomes. In *Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment and the Evolution of Gene Families*, eds. D. Sankoff and J.H. Nadeau, Amsterdam: Kluwer Academic Press, 2000, 479-491.

Tutorials

2016

- D.G. Brown, J. van Balen, E. Hein. Why hip-hop is interesting. 3-hour tutorial at ISMIR 2016.

Invited abstracts

2011

- D.G. Brown. Fast and theoretically strong algorithms for kinship discovery. *Proceedings of the International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2011)*, 5, 2011.

Software

2014

- D.G. Brown and A. Singhi. Hit Finder: finding hits using lyric features. Presented as a late-breaking demo at ISMIR 2014.

2010

- H. Hirjee and D.G. Brown. Rhyme Analyzer: An analysis tool for Rap Lyrics. Presented as a late-breaking demo at ISMIR 2010.

2002

- D.G. Brown. SNPSelect v 2.0, software for high-throughput multiplexing of SNPs into panels for mass spectroscopy.

1999

- D.G. Brown and T.J. Vision. MapPop: software for choosing mapping samples from genetic populations and placing new markers onto genetic maps, with T.J. Vision. (Also technical report CCOP-99-10 from Cornell University.)

Technical reports

2012

- D.G. Brown, J. Truszkowski. Fast reconstruction of phylogenetic trees using locally-sensitive hashing. arXiv:1111.0379, November 2011, revised May 2012.
- 2010
- F. Faghih, D.G. Brown. Answer set programming or hypercleaning: where does the magic lie in solving maximum quartet consistency? Technical Report CS-2010-20, School of Computer Science, University of Waterloo, November 2010.
- 2005
- D.G. Brown, I.M. Harrower. Towards an understanding of haplotype inference by pure parsimony. Technical Report CS-2005-027, School of Computer Science, University of Waterloo, September 2005.
 - D.G. Brown, I.M. Harrower. A new formulation for haplotype inference by pure parsimony. Technical Report CS-2005-004, School of Computer Science, University of Waterloo, March 2005.
- 2004
- B. Brejova, D.G. Brown, M. Li, T. Vinar. ExonHunter: A comprehensive approach to gene Finding. Technical Report CS-2004-57, School of Computer Science, University of Waterloo, October 2004.
- 2002
- B. Brejova, D.G. Brown. Optimal spaced seeds for finding homologous coding regions. Technical Report CS-2002-40. School of Computer Science, University of Waterloo. October 2002.
- 1999
- D.G. Brown, T.J. Vision. A computationally novel way to place new markers onto genetic maps. Cornell University Technical Report CCOP-99-9.

Non-refereed publications

- 2016
- C. Larche, M. Stange, K.A. Harrigan, D.G. Brown, M.J. Dixon. Evidence Exchange: the current state of skill-based gambling in North America. Report prepared for Gambling Research Exchange Ontario, October 2016, 50 pages.
- 2015
- D. Brown and C. Cotton. Comments on the paper by Kuznekoff and Kasumovic. *PLOS ONE*.
- 2014
- D. Brown and K. Harrigan, How slots trick gamblers into losing more than they know. Article for *The Conversation*, November 2014
 - D. Brown and K. Harrigan, Ontario makes gambling sexy. Article in *The Spin*, newsletter published by Centre for Addiction and Mental Health, 2014.
- 2010
- D.G. Brown. How I wasted too long finding a concentration inequality for sums of geometric variables. Published on my own webpage, November 2010. (Cited at least 6 times!)

Awards and honours

2015

- Cheriton Research Fellowship (internal, 3 years)
- 2013
- Outstanding Performance Award, University of Waterloo
- 2010
- Best Student Paper award (with student co-author H. Hirjee), International Society for Music Information Retrieval conference
- 2009
- Outstanding Performance Award, University of Waterloo
- 2006
- Early Researcher Award, Province of Ontario
- 1996
- NSF Graduate Research Fellowship (3 years)
- 1995
- Cornell University Sage Graduate Fellowship
 - Phi Beta Kappa, Massachusetts Institute of Technology

Research grants

- 2017
- Investigating quilting maker communities to inform gender inclusiveness in hackathons and game jams in STEM fields. HeForShe gender equity research grant, \$10,000 (PI: M. Hancock), submitted
- 2016
- Skill-based gambling games: an Evidence Exchange. Gambling Research and Exchange Ontario (GREO), C\$10,000 with K. Harrigan and M. Dixon
 - Analysis of words: algorithms for biological sequences, music and texts. NSERC, 2016-2021, C\$18,000/year
- 2015
- The University of Waterloo Gambling Research Lab KTE Knowledge Hub, GREO, C\$275,000. 2015-2018, with K. Harrigan and M. Dixon; multiple grants over the years
 - Rapid assessment evaluation of losses disguised as wins and weighted reels to inform best practice for responsible gambling, GREO, C\$25,000. 2015-2016, with K. Harrigan and J. Stapleton
- 2014
- Classification of slot machines in Ontario: Providing relevant information to players, Ontario Problem Gambling Research Centre, C\$75,000, co-PI with K. Harrigan
- 2010
- Theory and applications of sequence analysis, NSERC, 2010-2016, C\$34,000/year
 - Computer server for bioinformatics research, NSERC research tools and instruments grant, 2010, with B. Ma (PI) and M. Li, C\$63,793
- 2009
- Evolutionary analysis and bioinformatics algorithms, Joint Waterloo/McMaster bioinformatics initiative, 2009-2010, with B. Golding (McMaster University), C\$22,500
- 2007
- Early researcher award, Province of Ontario. 2007-2012, C\$28,000/year
- 2005

- Knowledge discovery in biological sequences, NSERC, 2005-2010, C\$26,000/year
- 2002
- Revealing telencephalic evolution through comparative functional analysis of gene regulatory regions, Human Frontier Science Program, with P. Blader (PI, Universiti Paul Sabatier, Tolouse, France), E. Jarvis (Duke University) and C. Schuurmans (University of Calgary), 2002-2006, US\$1,000,000
- 2001
- Algorithmic methods in computational genomics, NSERC, 2001-2005, C\$22,000/year
 - Computing Infrastructure: A collaborative computing environment for research in mathematical and computer sciences, Canada Foundation for Innovation, with 5 other new professors (PI: G. Baranoski), 2001-2006, C\$730,000

Invited talks and conference presentations

- 2017
- Challenges Associated with Diversity in STEM. Panel discussion at EQUALS (Equity and Quality in Academic Life in STEM) conference, Waterloo, May 2017
 - EGMs - Hazards, Potency, and Harm Reduction. Alberta Gambling Research Institute conference, Banff Centre, April 2017, jointly given with Kevin Harrigan (Drama and Speech Communications)
 - Disentangling the EGM dilemma. International Think Tank on Gambling Research, Policy and Practice, Banff Centre, April 2017, jointly given with Kevin Harrigan (Drama and Speech Communications)
 - Classification of slot machines in Ontario: providing relevant information to players. New Horizons in Problem Gambling, British Columbia Lottery Commission, Vancouver, February 2017, jointly given with Melissa Sleightholm (OLG) and Kevin Harrigan (Drama and Speech Communications)
 - Fast algorithms for phylogenetic reconstruction of aligned sequences. Banff International Research Station conference, February 2017
- 2015
- What's wrong with a recent paper about sexism in video games? Gender and Equity Scholarship Series, University of Waterloo, December 2015, jointly given with Cecilia Cotton (Statistics)
 - Do better lyrics make a hit? Complexity of rhymes in music lyrics. Department of Electrical and Computer Engineering, University of Rochester, May 2015
 - Fast algorithms for phylogenetic reconstruction of aligned sequences. Bioinformatics cluster, University of Rochester, May 2015
 - Fast algorithms for phylogenetic reconstruction of aligned sequences. Department of Mathematics and Computer Science, Lehman College, City University of New York, May 2015
 - Do better lyrics make a hit? Complexity of rhymes in music lyrics. Center for Data Science, New York University, May 2015
 - Multiple alignments in biology and music. Computer Science Department, University of Utrecht, the Netherlands, March 2015
 - The Rhyme Analyzer and its use in textual analysis. International workshop on the Structure of Verse, Leiden, the Netherlands, March 2015

2014

- Using locality-sensitive hashing to speed up tree estimation and phylogenetic placement, Canadian Mathematical Society meeting, Hamilton, Ontario, December 2014
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Computer Science, Lakehead University, April 2014

2013

- Using locality-sensitive hashing to speed up tree estimation and phylogenetic placement, Symposium and Workshop on New Methods for Phylogenomics and Metagenomics, University of Texas, February 2013

2012

- Fast algorithms for phylogeny, Workshop on Combinatorial Algorithms in Bioinformatics, Koper, Slovenia (keynote), September 2012
- Fast algorithms for phylogeny, SIAM Discrete Mathematics meeting, Halifax, June 2012
- Fast quartet phylogeny algorithms, Université Lyon, January 2012
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Laboratoire Bordelais de Recherche en Informatique, Université de Bordeaux, January 2012

2011

- Fast phylogeny algorithms: theory and practice, Department of Biology, University of Waterloo, June 2011
- Discovering kinship through small subsets, Invited lecture at 1st IEEE International Conference on Computational Advances in Bio- and Medical Sciences, Orlando, February 2011
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Computer Science, Iowa State University, November 2011
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Computer Science, University of New Brunswick, September 2011

2010

- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Musicology and Informatics, Indiana University, November 2010
- Discovering kinship through small subsets, Workshop on Algorithms in Bioinformatics, Liverpool, England, September 2010
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Département d'informatique et de recherche opérationnelle, Université de Montréal, April 2010
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Univerzita Komenského, Bratislava, Slovakia, March 2010
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Georg Augustus Universität, Göttingen, Germany, March 2010
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Computer Science, University of Victoria, February 2010

2009

- Two new ways to decode HMMs: many paths, or robust decoding, Department of Computer Science, University of Illinois at Chicago, December 2009
- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Electrical Engineering and Computer Science, Northwestern University, December 2009

- From DNA to Jay-Z: Automatic detection of rhymes in rap music lyrics, Department of Computer Science, University of Illinois at Chicago, November 2009
- Two new ways to decode HMMs: many paths, or robust decoding, Department of Statistics, University of Guelph, November 2009
- Two new ways to decode HMMs: many paths, or robust decoding, INFORMS annual meeting, October 2009

2008

- Mathematical structure and optimization approaches to haplotyping problems, DIMACS Workshop on Computational Issues in Genetic Epidemiology, August 2008

2007

- New techniques and uses for hidden Markov models, European Molecular Biology Laboratory, October 2007
- Strong motifs are easy to find, Department of Computer Science, University of Haifa, Israel, May 2007
- Computing with haplotypes: A mathematical perspective, Department of Computer Science, University of Alberta, April 2007
- Why is bioinformatics easier in practice than in theory? Department of Computer Science, Dartmouth College, January 2007

2006

- Computing with haplotypes: an introduction, Algorithms in Bioinformatics Symposium, Independent University of Moscow, July 2006
- New bounds on motif finding in strong instances, Combinatorial Pattern Matching Symposium, Jeju Island, July 2006
- Why is bioinformatics easier in practice than in theory? Department of Computer Science, University of California, Davis, June 2006
- An algebraic understanding of haplotype inference, Department of Mathematics, University of California, Davis, May 2006
- An algebraic understanding of haplotype inference, Department of Bioinformatics, Boston University, April 2006
- A computational introduction to haplotype inference, Department of Bioinformatics, Georg-August Universität, Göttingen, Germany, April 2006
- Incorporating external information into gene prediction, Laboratoire d'Informatique Fondamentale de Lille, France, April 2006
- A computational introduction to haplotype inference, Department of Bioinformatics, Universität Bielefeld, Germany, April 2006
- An introduction to haplotype inference problems, Google Research, March 2006 (available via Google Video)
- Adventures in sequence alignment, Department of Computer Science, Colorado State University Computer Science Department, March 2006
- Adventures in sequence alignment, University of Colorado Bioinformatics Supergroup, February 2006

2005

- Incorporating external information into the prediction of genes. Department of Computer Science, McMaster University, September 2005.

- ExonHunter: New ideas in eukaryotic gene finding. Bioinformatics Developer's Lecture Series, University of Toronto, April 2005.

2004

- New tricks and tips in sequence alignment, Department of Computer Science, Wayne State University, February 2004
- Multiple vector seeds for protein alignment, Workshop on Algorithms in Bioinformatics, Bergen, Norway, September 2004
- New algorithms for haplotype inference, The Hospital for Sick Children, Toronto, February 2004

Student supervision and teaching

Completed PhD students

2013

- Jakub Truszkowski. *Fast algorithms for large-scale phylogenetic reconstruction*. Currently post-doctoral fellow at Cambridge University and European Bioinformatics Institute, UK.

2010

- Alexander K. Hudek. *Improvements in the accuracy of pairwise sequence alignment*. Currently co-founder and CTO, Kira Systems, Toronto.

2005

- Bronislava Brejova. *Evidence combination in hidden Markov models for gene prediction*. Award for outstanding achievement in graduate studies (Co-supervised with Ming Li). Currently Assistant Professor at Comenius University in Bratislava, Slovakia.
- Tomas Vinar. *Enhancements to hidden Markov models for gene finding and other biological applications* (Co-supervised with Ming Li). Currently Associate Professor at Comenius University in Bratislava, Slovakia.

Completed Masters of Mathematics (MMath) thesis students

2015

- Abhishek Singhi. *Lyrics Matter*. Current position: software developer, SAP

2014

- Eric Marinier. *Error Correction of Second-Generation Sequencing Reads* (Co-supervised with Brendan McConkey). Current position: bioinformatics programmer, National Microbiology Laboratory.

2012

- Dan Dexter. *Reconstruction of half-sibling population structures*. Current position: software developer at TripAdvisor.

2010

- Hussein Hirjee. *Rhyme, rhythm, and rhubarb: Using probabilistic methods to analyze hip hop, poetry, and misheard lyrics*. Currently a medical student at University of Western Ontario.

2009

- Daniil Golod. *The k-best paths in hidden Markov models: algorithms and applications to transmembrane protein topology recognition*. Current position: software developer at SAP.

2005

- Sriram Darbha. *Pair seeds for RNA alignment* (Co-supervised with Ming Li). Current position: manager at BlackBerry.
- Ian Harrower. *Haplotype inference using pure parsimony*. Current position: engineer at Google.

2004

- Alexander Hudek. *New anchoring techniques for global multiple alignment of genomic sequences*. Proceeded to PhD.
- Jiang Liu. *A combinatorial approach for motif discovery in unaligned DNA sequences*. Current position: researcher with US Food and Drug Administration.
- Emily Xu. *The use of functional domains to improve transmembrane protein topology prediction* (informal supervision).

Completed MMath essay student

2017

- Elmi Eflöv. *DBMS as a bioinformatics application platform*. Current position: software developer at SAP.

2004

- Fengkai Zhang. *Incorporating spaced seeds into PSI-BLAST search*. Current position: tenured member of research staff, National Institutes of Health.

Current PhD students

- Carolyn Lamb (since September 2013)

Current MMath students

- Jonathan Perrie (jointly supervised with Peter van Beek, since Fall 2016)

External thesis examiner

- PhD thesis: Yufeng Wu (University of California Davis, 2007), Denise Mak (Boston University, 2008), Duong Doan (University of New Brunswick, 2011), Nilgun Donmez (University of Toronto, 2012), Nanyang Technical University of Singapore (candidate name confidential, 2013), Stephanie König (Universität Greifswald, 2017)
- Master's thesis: Michal Nánási (Univerzita Komenského, Bratislava, Slovakia, 2010), Andre Masella (Wilfrid Laurier University, 2010)

Internal thesis examiner / committee member

- PhD: Jinbo Xu (2004), Francisco Zaragosa-Martinez (2004), Daming Yao (did not complete), Linli Xu (2007), Narad Rampersad (2007), Joe Mikhael (Philosophy, 2007), Carlos Hoppen (Combinatorics and Optimization, 2007), Tyrell Russell (2010), Richard Jang (2012), Margareta Ackerman (2012), Omar Khan (2013), Greg Vey (Biology, 2014, dissertation not accepted), Eddie Ma (Biology, did not complete), Gary Au (Combinatorics and Optimization, 2014), Lin He (2014), Jazmin Romero (2015), Matthew Hrycyszyn (Biology, 2015), Trevor Bekolay (2016), Owen Woody (Biology), Vanessa Borges (Biology), Janet Lorv (Biology)
- MMath thesis reader for: Joanne McKinley (2002), Derek Phillips (2003), Keith Ellul (2003), Peter Olsar (2004), Luke Tanur (2005), Xuefeng Cui (2006), Nika Haghtalab (2013)

Undergraduate and exchange students

2011

- Yanqi Hao, NSERC Undergraduate Student Researcher, May-August.
- Michal Nánási. Exchange student from Univerzita Komenského, Bratislava, Slovakia, February-August.

2008

- Hussein Hirjee, NSERC Undergraduate Student Researcher, May-August

2007

- Daniil Golod, NSERC Undergraduate Student Researcher, May-August

2004

- Wolfgang Gehrlach, Exchange student from Universität Bielefeld: research project, September-December
- Sam Leung, Undergraduate research co-op student, September-December
- Mike DiBernardo, Undergraduate Research Assistant, May-December

2003

- Ian Harrower, NSERC Undergraduate Student Researcher, May-August
- Alexandru Ausch. Undergraduate research student, May-August

2002

- Henning Stehr. Exchange student from Technische Universität Hamburg-Harburg: May-August

Teaching

Course developer

- Introduction to computer science 2. Second computer science course for non-majors in the Faculty of Mathematics. Course developer and initial coordinator. First offering Winter 2009
- Biological sequence analysis. Capstone sequence analysis course for bioinformatics undergraduates. Course developer and initial coordinator. First offering Fall 2003

Course instructor: undergraduate

- Introduction to computer science 2. Winter 2009, 2 sections (180 students)
- Introduction to functional programming. Fall 2006, 90 students; fall 2007, 90 students
- Algorithms. Winter 2002: 1 section, 90 students
- Theory of computation. Spring 2003: 2 sections, 170 students; fall 2005: 1 section, 60 students; spring 2010: 1 section, 40 students; fall 2010: 1 section, 60 students, spring 2013: 1 section, 50 students
- Biological sequence analysis. Fall 2003: 17 students; fall 2004: 40 students; winter 2005: 12 students; fall 2005: 40 students; fall 2006: 30 students; fall 2007: 30 students; spring 2014: 7 students; winter 2016: 9 students

Course instructor: graduate

- Markov chains, mixing times, and concentration inequalities. Spring 2011. 6 students.
- Computational phylogenetics. Spring 2010: 11 students, Fall 2010, 3 students (reading course)

- Genome-scale sequence analysis. Winter 2005: 6 students
- Biological sequence analysis. Winter 2003: 20 students
- Comparative genomics. Spring 2002: 6 students
- Proteomics. Winter 2002: 1 student (reading course)

Guest lecturer

- Human genetics: 2002-2007, annual guest lectures about Human and Mouse Genome Projects
- Philosophy of art: 2015-2016, annual guest lecture about computational creativity
- Bioinformatics tools: 2016, guest lecture about hidden Markov models

Professional service

External

Journal editor

- Associate Editor, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2008-present

Conference program chair

- Workshop on Algorithms in Bioinformatics, 2014 (co-chair with B. Morgenstern)

Workshop program chair

- Computational Creativity and Social Justice Workshop, 2017 (co-chair with G. Smith, A. Sullivan)

Conference program committee member

- Intelligent Systems in Molecular Biology 2014-2016
- Workshop on Algorithms in Bioinformatics 2008, 2009, 2011-2015
- Conference on Computing and Combinatorics 2008
- International Symposium on Bioinformatics Research and Applications 2007-2014
- International Workshop on Bioinformatics Research and Applications 2006
- IEEE International Conference on Bioinformatics and Biomedicine 2007-2017
- Biotechnology and Bioinformatics Symposium 2007, 2008
- Computational Biology and Genome Informatics 2003
- International Conference on Cognitive Informatics 2004, 2005
- IEEE International Conference on Computational Advances in Bio and Medical Science 2011-2014
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine, 2012
- Bioinformatics and Computational Biology, 2015-2017
- Algorithms in Computational Biology, 2015
- Asia-Pacific Bioinformatics Conference, 2015-2018
- SIAM Discrete Mathematics Annual Meeting: minsymposium organizer, 2012
- Great Lakes Bioinformatics Conference, 2016-2017
- International Conference on Computational Creativity, 2017

Referee

- Journals:
 - Biology: *Nature*, *Genome Research*, *Nucleic Acids Research*, *Human Genetics*
 - Computer Science: *Journal of Artificial Intelligence Research*, *SIAM Journal on Discrete Mathematics*, *SIAM Journal on Computing*, *Information Science*, *Neural Computation*, *Journal of Discrete Algorithms*, *Informatica*
 - Operations Research: *Operations Research*, *INFORMS Journal on Computing*, *Mathematical Programming*, *Management Science*
 - Bioinformatics: *Bioinformatics*, *BMC Bioinformatics*, *Journal of Bioinformatics and Computational Biology*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *IEEE Transactions on Nanobioscience*, *Algorithms in Molecular Biology*, *Journal of Computational Biology*, *Journal of Bioinformatics and Sequence Analysis*, *BMC Research Notes*, *Computational and Structural Biology*
 - Audio processing: *IEEE Transactions on Audio, Speech and Language Processing*
 - Gambling: *International Gambling Studies*
- Conferences:
 - Theory: SODA, FOCS, IPCO, CPM, ESA, SWAT, WEA, CIAA, COCOON, IC3
 - Bioinformatics: PSB, WABI, ISMB, RECOMB, ISBRA, IWBRA, BIBM, BIOT, CBGI, ICGI, ICCABS, ACM-BCB
 - Creativity and art: ICCA, Bridges
 - Other: High-Performance Scientific Computing, Canadian Conference on Electrical and Computer Engineering
- Grant review panels: Government of British Columbia (2011), US National Science Foundation (2013)
- Grants: Human Frontier Science Program, NSERC, Government of Switzerland, Government of Québec, City University of Hong Kong, Leverhulme Trust
- Books: numerous textbook proposals and chapters for J. Wiley and Sons, Jones and Bartlett, Cambridge University Press, Pearson
- Tenure review: 2 cases in 2010, 1 in 2012, 1 in 2016

Internal

University of Waterloo

- Provost selection committee, 2013-2014 and 2017
- Registrar selection committee, 2017
- Faculty relations committee, 2016-present
- Presidential faculty roundtables, 2016-2017
- Provost's advisory committee on diversity / Diversity advisory committee, 2013-2014, 2016
- Sexual violence policy drafting committee (resource), 2016
- Council of Ontario Universities Academic Colleague, February 2013-June 2014, alternate for September 2012-January 2013
- Senate, 2008-2014
 - Executive committee 2012-2014
 - Finance committee, 2008-2011
- LGBTQQ advisory committee, 2011-2014

- University bioinformatics committee, 2001-2003

Faculty Association of the University of Waterloo

- Treasurer, July 2016-present
 - Includes serving on the Association's board, executive, and as a FAUW representative to the faculty relations committee
- Chair of general meetings, 2012-2014
- Status of women and equity committee, 2010- 2014, January-June 2016, May 2017-present

Faculty of Mathematics

- Online Advising Tools (OAT) management board, July 2013-December 2014, July 2016-present (chair, July 2017-present)
- Faculty committee on student appeals, September 2015-present
- Undergraduate affairs committee, July 2013-December 2014, July 2016-present
- Software engineering curriculum committee and governing board, July 2013-December 2014, July 2016-present
- Faculty council admin committee, July 2011-June 2013
- Research advisory committee, 2010-2013
- Valedictorian selection committee, 2009
- Computational mathematics undergraduate committee, 2008-2009
- Faculty representative council, 2007-2009
- Committee to replace Math Faculty General degree, 2007-2008
- Dean's advisory council, July 2006-2009
- Undergraduate awards committee, 2005-2009
- Presenter, J.W. Graham Seminar and Imperial Oil Seminar (week-long seminar for high-school girls interested in computer science from across Canada), 2002-present
- Presenter, Canadian Computing Competition second stage (week-long training camp for Canada's team to the International Olympiad of Informatics), 2004, 2010, 2011
- Marker, Centre for Education in Mathematics and Computing contests, 2013-2016
- Focus group for Excellence Canada, 2016

David R. Cheriton School of Computer Science

Administrative roles

- Director of undergraduate studies, July 2013-December 2014, July 2016-present
 - Includes chairing undergraduate academic plans committee, membership on other School committees including performance review and lecturer hiring, as well as staff management.
 - School administration fundraising liaison, July 2013-June 2014
- Associate (vice) director of school, July 2011-June 2013
 - Included chairing space, TA assignment, Lecturer hiring and peer teaching evaluation committees, membership on numerous other School committees, including performance review, as well as staff management. Member of Faculty council admin committee *ex officio*.
 - School administration fundraising liaison
- Director of first-year studies, July 2006-June 2009

- Included membership on Dean's advisory council, and other policy-making and Faculty advisory groups

Other School service

- MC for 50th-anniversary alumni event, 2017
- School council acting chair, winter 2016
- Tenure and promotion committee, 2010-2011, 2011-2012
- Committee to select new director of School, 2009
- Outreach committee, 2008-2013 (founding chair, 2008-2009)
- Undergraduate academic plans committee, July 2006-June 2009, July 2011-December 2014 (chair, July 2013-December 2014), January 2016-present (chair, July 2016-present)
- Undergraduate recruiting committee, 2006-2009, 2011-2013
- Advisory committee, 2002-2004
- Graduate committee, 2001-2002
- Faculty advisor, bioinformatics undergraduate club
- Ad hoc committee on the design of the new undergraduate degree, 2001-2002

Other departments and faculties

- Internal reviewer, Music department program review, 2013
- Arts faculty Canada Research Chair in digital media search committee: 2012
- Focus group on HR information system, 2012
- Strategic planning group, Waterloo Stratford campus, 2012
- Biology department faculty search committee: 2011-2012

Community

- Mennonite Coalition for Refugee Support: board member, December 2015-present
- Mennonite Central Committee Ontario: fundraising data analysis volunteer, 1 day/week, 2015
- Friends (Quakers) for LGBTQ Concerns: ministry and counsel committee, 2003-2006 (co-clerk, 2005-2006)