Michael Brudno

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Associate Professor and Canada Research Chair in Computational Biology,
  University of Toronto (2011-present)
- Department of Computer Science
- Banting and Best Department of Medical Research
- Donnelly Centre for Cellular and Biomolecular Research
- Centre for the Analysis of Genome Evolution and Function

Adjunct Scientist, *The Hospital for Sick Children*, Toronto (2009-present)
- Genetics and Genome Biology Division
- The Centre for Applied Genomics (TCAG; Scientific Management Board Member)

Education

Stanford University
Ph.D. in Computer Science, September 2004.
  Thesis Title: Algorithms for Comparison of DNA Sequences
  Thesis Supervisor: Serafim Batzoglou
M.S. in Computer Science, March 2003.

University of California, Berkeley
A.B. degree with High Honors, May 2000.
Double major in Computer Science (Honors Thesis) and History

Previous Positions

University of Toronto
Assistant Professor, 2006-2011

Massachusetts Institute of Technology
Visiting Scientist, CSAIL 9-12/2005
Host: Bonnie Berger

University of California, Berkeley
Postdoctoral Fellow, Computer Science Division 9/2004 – 9/2005.
Supervisor: Gene Myers

GosNIIGenetika, Moscow, Russia
Visiting Fellow, Scientific Center for Biotechnology 9/2003 – 12/2003
Host: Mikhail Gelfand

Perlegen Sciences, Inc.
Scientific Programmer. 10/2000 – 5/2001
Supervisor: Kelly A. Frazer

Lawrence Berkeley National Laboratory
Undergraduate Researcher; Scientific Programmer. 02/1999 – 9/2000; 5/2001 – 12/2001
Supervisor: Inna Dubchak

Awards & Honors

- Alfred P. Sloan Research Fellow 2010-2012
- Ontario Early Researcher Award (ERA) 2009-2014
- European Conference in Computer Systems (Eurosys) Best Paper Award 2009
- Canada Research Chair (CRC) in Computational Biology 2006-2011; 2011-2016
- Intelligent Systems in Molecular Biology (ISMB) Best Paper Award 2004
- National Science Foundation (NSF) Graduate Fellow 2002-2004
- Stanford University School of Engineering Graduate Fellowship 2000-2001
- Samuel Silver Prize for Achievement in Engineering and Humanities, UC Berkeley 2000

Research Awards (12 Awards totalling ~ $11.5 Million)

- University of Toronto Connaught Startup Award
  January 2006, 1 year (PI) CAD$10,000

- National Science and Engineering Research Council (NSERC) Discovery Grant
  April 2006, 5 years (PI) CAD$180,000

- Canada Foundation for Innovation – Canada Research Chair Equipment Grant (CFI-CRC)
  March 2006, 1 year (PI) CAD$204,000

- National Institutes of Health (NIH, USA) R01 Grant
  Sept. 2007, 3 years (Co-PI; PI: Inna Dubchak, LBNL) USD$588,000
  University of Toronto Subcontract USD$210,000

- National Science and Engineering Research Council (NSERC) Strategic Grant
  February 2008, 2 years (Co-PI; PI: Eyal de Lara) CAD$192,000

- Research Grant from Platform Computing
  April 2008 (Joint with Eyal de Lara) CAD$40,000

- Canada Institute for Health Research (CIHR) Catalyst Grant
  October 2008, 3 years (PI; Co-PI: Steve Scherer) CAD$300,000

- Research Grant from Applied Biosystems, Inc
  November 2008 (PI) USD$50,000

- Mathematics of Information Technology and Complex Systems (MITACS) Seed Grant
  February 2009, 2 year (PI) CAD$80,000

- Ontario Early Research Award (ERA)
  March 2009, 5 years CAD$100,000

- Sloan Research Fellowship,
  February 2010, 2 years USD$50,000

- Ontario Research Fund Genomes to Life (ORF-GL2) Grant
  April 2010, 5 years (Co-PI; PIs: Steven Scherer & Peter Szatmari) CAD$9,700,000
  My subcontract: CAD$250,000

- Canadian Genetics of Paediatric Disorders (FORGE) Consortium
  April 2011, 2 years (Member of Steering Committee & Informatics Lead). CAD $2,000,000
  My subcontract: CAD $250,000

Scholarly Work Summary

Career Publication Count	
Scholarly Books (authored)	0
Scholarly Books (edited)	0
Chapters in Books	2
Papers in refereed journals	36
Papers in refereed conferences	13
Major invited contributions	0
Other publications	4

Refereed Publications

Papers where I am a corresponding or senior author are noted with a *, trainees supervised by me are in **bold.** Conference publications that directly appear in a journal are listed only with journal papers. Citations are according to Google Scholar, as of October 21, 2010.

Journal Papers

1. Dralyuk I, Brudno M, Gelfand M, Zorn M, Dubchak I. ASDB: database of alternatively spliced genes. *Nucleic Acids Res.* **28**:296-7. 2000 [Cited by 57]
2. Dubchak I, Brudno M, Pachter LS, Loots GG, Mayor C, Rubin EM, Frazer K. Active conservation of noncoding sequences revealed by 3-way species comparisons. *Genome Res.* **10**:1304-6. 2000 [Cited by 267]
3. Mayor C, Brudno M, Schwartz JR, Poliakov A, Rubin EM, Frazer K, Pachter LS, Dubchak I VISTA: Visualizing global DNA sequence alignments of arbitrary length. *Bioinformatics,* **16**:1046-1047. 2000 [Cited by 515]
4. Brudno M, Gelfand MS, Spengler S, Zorn M, Dubchak I, Conboy JG Computational analysis of candidate intron regulatory elements for tissue-specific alternative pre-mRNA splicing. *Nucleic Acids Res.* **29**:2338-48 2001 [Cited by 93]
5. Brudno M, **Do CB,** Cooper GM, **Kim MF**, Davydov E, Green ED, Sidow A, Batzoglou S. LAGAN and Multi-LAGAN: Efficient tools for large-scale multiple alignment of genomic DNA. *Genome Res.* 13:721-731, 2003. [Cited by 635]
6. Cooper GM, Brudno M, Green ED, Batzoglou S, Sidow A. Quantitative estimates of sequence divergence for comparative analyses of mammalian genomes. *Genome Res.* **13**:813-820, 2003. [Cited by 77]
7. Brudno M, **Malde S**, Poliakov A, **Do CB**, Couronne O, Dubchak I, Batzoglou S. Glocal alignment: finding rearrangements during alignment. *Special Issue on the Proceedings of the ISMB 2003, Bioinformatics* **19**:54i-62i, 2003. [Cited by 139]
8. Taher L, Rinner O, Garg S, Sczyrba A, Brudno M, Batzoglou S, Morgenstern B. AgenDA: homology-based gene prediction. *Bioinformatics* **19**:1575-1577, 2003. [Cited by 22]
9. Brudno M, Chapman M, Göttgens B, Batzoglou S, Morgenstern B. Fast and sensitive multiple alignment of large genomic sequences. *BMC Bioinf.* **4**:66, 2003. [Cited by 162]
10. Shah N, Couronne O, Pennacchio LA, Brudno M, Batzoglou S, Joy S, Bethel W, Rubin EM, Hamann B, Dubchak I. Phylo-VISTA: an interactive visualization tool for multiple DNA sequence alignments. *Bioinformatics* **20**: 636-643, 2004. [Cited by 44]
11. Rat Genome Sequencing Project Consortium. Genome sequence of the Brown Norway Rat yields insights into mammalian evolution. *Nature* **428**:493–521, 2004. [Cited by 673]
12. Brudno M, Steinkamp R, Morgenstern B. The CHAOS/DIALIGN WWW server for multiple sequence alignment. *Nucleic Acids Res*earch **32**:W41 – W44, 2004.

13. Cooper GM, Brudno M, Stone ES, Dubchak I, Batzoglou S, Sidow A. Characterization of evolutionary rates and constraints in three mammalian genomes. *Genome Res.* **14**:539–48, 2004. [Cited by 99]

14. Brudno M, Poliakov A, Salamov A, Cooper GM, Sidow A, Rubin EM, Solovyev V, Batzoglou S, Dubchak I. Automated whole-genome multiple alignment of Rat, Mouse, and Human. *Genome Res.* **14**:685–692, 2004. [Cited by 76]

15. The ENCODE Consortium. The ENCODE (ENCylopedia Of DNA Elements) Project. *Science*, **306:** 636–640, 2004. [Cited by 33]

16. Do CB, Mahabhashyam M, Brudno M, Batzoglou S. ProbCons: Probabilistic consistency-based multiple alignment of amino acid sequences. *Genome Res.* **15:** 330–340, 2005 [Cited by 39]

17. Kovaleva G, Bazykin G, Brudno M, Gelfand M. Comparative genomics of transcriptional regulation in yeasts and its application to identification of a candidate alpha-isopropylmalate transporter. *Journal of Bioinformatics and Comput. Biology* **4**:981-998, 2006 [Cited by 4]

18. Small KS, Brudno M, Hill MM, Sidow A. Extreme genomic variation in a natural population. *Proc Natl Acad Sci USA* **104**:5698-703. 2007. [Cited by 30]

19. Small KS, Brudno M, Hill MM, Sidow A. A haplome alignment and reference sequence of the highly polymorphic Ciona savignyi genome. *Genom Biol.* **8**:R41 2007 [Cited by 17]

20. Brudno M, Poliakov A, Minovitsky S, Ratnere I, Dubchak I. Multiple whole genome alignments and novel biomedical applications at the VISTA postal. *Nucleic Acids Research* 35:W669-74 2007 [Cited by 16]

21. Bazykin GA, Kondrashov FA, Brudno M, Poliakov A, Dubchak I, Kondrashov AS. Extensive parallelism in protein evolution. *Biology Direct*. **2**:20 2007 [Cited by 9]

22. ***Lee S**, **Cheran E**, Brudno M. A Robust Framework for Detecting Structural Variations in a Genome. *Proceedings of the 16th Annual International Conference on Intelligent Systems in Molecular Biology (ISMB); Bioinformatics* **24**:i59-i67, 2008 [Cited by 28]

23. ***Donmez N**, Bazykin G, Brudno M, Kondrashov A. Polymorphism due to multiple amino acid substitutions at a codon site within Ciona savignyi. *Genetics*, **181**:685–90 2009 [Cited by 3]

24. *Dubchak I, Poliakov A, Kislyuk A, Brudno M**.** Multiple Whole Genome alignment without a Reference Sequence. *Genome Res*. **19**:682-689 2009 [Cited by 9]

25. Chan ET, Quon GT, Chua G, Babak T, Trochesset M, Zirngibl RA, Aubin J, Ratcliffe M, Wilde A, Brudno M, Morris QD, Hughes TR. Conservation of core gene expression invertebrate tissues. *Journal of Biology,* **8**:33 2009 [Cited by 15]

26. ***Rumble SM**, Lacroute P, **Dalca AV**, **Fiume M**, Sidow A, Brudno M. SHRiMP: Accurate Mapping of Short Color-space Reads. *PLoS Computational Biology,* **5**:5 2009 [Cited by 56]

27. ***Medvedev P**, Brudno M. Maximum Likelihood Genome Assembly. *Journal of Computational Biology* **16**:1101-1116 2009. [Cited by 4]

28. ***Lee S**, Hormozdiari F, Alkan C, Brudno M. MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions *Nature Methods.* **6**:473-474 2009 [Cited by 16]

29. ***Medvedev P, Stanciu M,** Brudno M. Computational methods for discovering structural variation with next generation sequencing. *Nat. Meth.,* **6**:S13–20 2009 (Review). [Cited by 26]

30. ***Dalca A,** Brudno M. Genome Variation Discovery with High Throughput Sequencing Data. *Briefings in Bioinformatics,* **11**:3-14 2010 (Review). [Cited by 9]

31. Costanzo M and 52 others. The Genetic Landscape of a Cell. Science **327**:425–431 2010 [Cited by 43]

32. ***Dalca, A, Rumble SM,** Levy S, Brudno M. VARiD: A Variation Detection Framework for Colorspace and Letterspace platforms. *Proceedings of the 18th Conference on Intelligent Systems in Molecular Biology (ISMB); Bioinformatics* **26**:i343-i349 2010

33. *__Fiume M, Williams V, Brook A__, Brudno M. Savant: Genome Browser for High Throughput Sequencing Data. *Bioinformatics* __26__:1938-1944 2010 [Cited by 1]
34. *__Medvedev P, Fiume M, Dzamba M, Smith T__, Brudno M. Detecting Copy Number Variation with Mated Short Reads. *Genome Research* __20__:1613-1622 2010
35. *__Lagar-Cavilla A__, __Whitney JA__, Scannel A, Bryant R, Patchin P, __Rumble SM__, de Lara E, Brudno M, Satyanarayanan, M. SnowFlock: Virtual Machine Cloning as a First Class Cloud Primitive. *ACM Transactions on Computer Systems* (Accepted) 2011
36. __*David M, Dzamba M, Lister D,__ Ilie L, Brudno M. Shrimp2: Sensitive Yet Practical Short Read Mapping. *Bioinformatics*, in press 2011.

Conference & Workshop Papers

1. Brudno M, Morgenstern, B. Fast and sensitive alignment of large genomic sequences. *Proc. of the IEEE Computer Society Bioinformatics Conf. (CSB 2002)*.[Cited by 162]
2. Do CB, Brudno M, Batzoglou S. ProbCons: Probabilistic consistency-based multiple alignment of amino acid sequences. *Proceedings of the Nineteenth National Conference on Artificial Intelligence (AAAI)* 2004. [Cited by 39]
3. __Sundararajan M__, Brudno M, Small K, Sidow A, Batzoglou S. Chaining algorithms for alignment of draft sequence. *Proceedings of the Fourth Workshop on Algorithms in Bioinformatics (WABI)* 2004. [Cited by 12]
4. __*Medvedev P__, Georgiou K, Myers EW, Brudno M. Computability and equivalence of models for genome assembly. *Proceedings of the Eighth Workshop on Algorithms in Bioinformatics (WABI)*, 2007 [Cited by 15]
5. *__Dalca AV__, Brudno M. FRESCO: Flexible Alignment with Rectangle Scoring Schemes. *Proceedings of the Pacific Symposium on Biocomputing (PSB)* 2008
6. __*Medvedev P__, Brudno M. Ab initio Whole Genome Shotgun Assembly with Mated Short Reads. *Proc. of the 12th Research in Computational Biology Conference (RECOMB)* 2008 [Cited by 12]
7. __*Yanovsky V__, __Rumble S__, Brudno M. Read Mapping Algorithms for Single Molecule Sequencing Data. *Proceedings of the Ninth Workshop on Algorithms in Bioinformatics (WABI)* 2008. [Cited by 4]
8. Quon G, The YW, Chan ET, Hughes TR, Brudno M, Morris QD. A mixture model for the evolution of gene expression in non-homogeneous datasets. *Proceedings of The Neural Information Processing Systems Conference (NIPS)* 2008. [Cited by 1]
9. *__Lagar-Cavilla A__, __Whitney J__, Scannel A, __Rumble SM__, Patchin P, de Lara E, Brudno M, Satyanarayanan, M. SnowFlock: Rapid Virtual Machine Cloning for Cloud Computing. *Proceedings of the Euro. Conference in Computer Systems (Eurosys)* 2009 [Cited by 37]
10. *__Patchin P__, Lagar-Cavilla HA, de Lara E, Brudno M. Adding the Easy Button to the Cloud with Snowflock and MPI. *3rd Workshop on System-level Virtualization for High Performance Computing (HPCVirt)* 2009 [Cited by 4]
11. *__Lee S,__ Xing EP, Brudno M. MoGUL: Detecting Common Insertions and Deletions in a Population. *Proceedings of the 14th Annual Research in Computational Biology Conference (RECOMB)*, 2010 [Cited by 2]
12. *__Donmez N,__ Brudno M. Hapsembler: An assembler for highly polymorphic genomes. *Proceedings of the 15th Research in Computational Biology Conference (RECOMB)*, 2011
13. __Whitney JA__, Koh J, Costanzo M, Brown GB, Boone C, Brudno M. Clustering with Overlap for Genetic Interaction Networks via Local Search Optimization. *Proceedings of the Twelth Workshop on Algorithms in Bioinformatics (WABI)* 2011.

Book Chapters

1. Brudno M and Dubchak I. Comparison of Long Genomic Sequences: Algorithms and Applications. In S. Aluru, ed. Handbook of Computational Biology, CRC Press, 2006.
2. Brudno M, LAGAN Alignment Toolkit, book chapter in Comparative Genomics, Methods in Molecular Biology Nicholas Bergman, ed. Published by Humana Press, 2007

Unrefereed Publications

1. Brudno M. Building Genomes. Idea&s: The Arts and Science Review, University of Toronto. Fall 2007, p. 21
2. Brudno M, Moret B, Linder R, Warnow T; Beyond Gap Models: Alignment and Phylogeny under genome-scale events: Session Introduction. *Pacific Symposium on Biocomputing (PSB)* 13:1-2, 2008
3. Brudno M, Medvedev P, Stoye J, De La Vega, F. A Report on the 2009 SIG on Short Read Sequencing and Algorithms (Short-SIG). *Bioinformatics,* 25: 2863 – 2864 2009
4. Alkan C, Brudno M, Eichler EE, Kahn M, Sahinalp C. Personal Genomics Session Introduction, *Pacific Symposium on Biocomputing (PSB)*, 15:302-304, 2010

Invited Presentations (altogether >50 in 11 countries)

Keynote Addresses
* Discovering and Visualizing Structural Variation in the Human Genome.
  Journées Ouvertes en Biologie, Informatique et Mathématiques (JOBIM 2011). Paris, France, July 2011.
* Discovering INDEL and CNV Variation in the Human Genome
  2nd Belgium, Netherlands and Luxemburg Next Generation Sequencing User Meeting, Utrecht, Netherlands, July 2009
* Discovering Copy Number Genomic Variation from High-Throughput Sequencing
  1st International Conference on Computational Systems Biology and Bioinformatics (CSBio 2010), Bangkok, Thailand, November 2010

Invited Talks at Conferences and Workshops (12 total)
* CHAOS Local Alignment Algorithm
  Workshop on Comparative Genomics, Bielefeld, Germany, March 2001
* Glocal Alignment: Finding Rearrangements During Alignment
  Recomb Satellite Workshop on Sequencing and Assembly, Stanford, CA, May 2003.
* Next Generation Sequencing Technologies
  Toronto Universities Biotechnology Society Symposium, Toronto, Canada April 2008
* Next Generation Sequencing Technologies
  Canada-Taiwan Biotechnology Symposium, Toronto, Canada, November 2008
* Discovering Genome Variation with Matepair Data
  Rendezvous Sequenage meeting, Genome Quebec, Montreal December 2008
* Discovering INDEL and CNV Variation in the Human Genome
  MonBUG Symposium, Montreal, Canada, September 2009
* Whole Genome Alignment without a Reference Sequence
  CRNG Quantomics Workshop, Barcelona, Spain, September 2009
* Discovering INDEL and CNV Variation in the Human Genome
  NGS2009 Conference, Barcelona, Spain, October 2009

- Discovering INDEL and CNV Variation in the Human Genome
  Toronto NGS Symposium, Toronto, Canada, February 2010
- Tools for Analysis of NGS Data
  European Bioinformatics Institute NGS Conference, Hinxton, UK, December 2010
- Storage, Analysis, and Visualization: Solutions for NGS Data Analysis
  Molecular Medicine Triconference, San Francisco, CA, February 2011
- Discovering and Visualizing Structural Variation in the Human Genome
  Workshop on Statistical Challenges and Biomedical Applications of Deep Sequencing Data.
  Ascona, Switzerland, June 2011

Invited Talks At Institutional/Departmental Lecture Series (20 total)
- Algorithms for Alignment of Whole Genomes
  Biomedical Informatics Departmental Colloquium, Stanford, USA May 2003
- Algorithms for Alignment of Whole Genomes
  Bioinformatics Department Colloquium, Universitat Gottingen, Germany, September 2003
- Algorithms for Alignment of Whole Genomes
  Moscow Seminar on Computational Biology, Moscow, Russia, November 2003
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of British Columbia; January 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, Purdue University, USA; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of Illinois, USA; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Sciences Department Colloquium, University of Pennsylvania, USA; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of Waterloo, Canada; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, Duke University, USA; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of Toronto, Canada; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, Cornell University, USA; February 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Biostatistics & Medical Informatics Dept Colloquium, Univ. of Wisconsin, USA; March 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of Colorado, USA; April 2005
- Alignment of Whole Genomes: Algorithms & Tools
  Computer Science Department Colloquium, University of Texas, USA; April 2005
- Predicting Ancestral Genome Order
  Moscow Seminar on Computational Biology, Moscow, Russia November 2005
- Predicting Ancestral Genome Order
  MIT-CSAIL Bioinformatics Seminar, Cambridge, USA November 2005
- Discovering Genome Variation with Matepair Data
  University of Maryland Computational Biology Seminar Series, February 2008,
- Discovering INDEL and Copy Number Variation from Paired-end Sequencing
  UCLA Bioinformatics Colloquium, November 2009

- Discovering INDEL and Copy Number Variation from Paired-end Sequencing
  SystemsX Lecture Series, ETH Zurich, Switzerland, June 2010
- Detecting (and Visualizing) Structural Variants in the Human Genome
  INRIA – Lille Nord, Lille, France, December 2010

Other Invited Presentations (13 total)
- Algorithms for Alignment of Whole Genomes
  University of British Columbia, Vancouver, Canada, July 2003
- Algorithms for co-Assembling a Genome
  University of Toronto; May 2005
- Alignment of Whole Genomes: Algorithms & Tools
  University of Massachusetts; September 2005
- Chinese Postmen and Virtual Clusters
  Google Inc. Mountain View, CA USA; May 2007
- Assembling Genomes with Next Generation Sequencing Data
  Genelogic Inc., Gaithersburg, MD; February 2008
- Discovering Genome Variation with Matepair Data
  DOE Joint Genome Institutes; February 2008,
- Discovering Genome Variation with Matepair Data
  Stanford University; February 2008
- Variation Discovery and Alignment with Color-space Short Read Data
  Applied Biosystems, Foster City, CA; February 2008
- Alignment of Helicos 2-pass Reads with Weighted Sequence Graphs
  Helicos (Cambridge, MA), June 2008
- Assembling Genomes with Next Generation Sequencing Data
  Ben Gurion University, Be'er Sheva, Israel; September 2008
- Discovering Genome Variation with Matepair Data
  University of Waterloo; November 2008,
- Discovering INDEL and Copy Number Variation from Paired-end Sequencing
  J. Craig Venter Institute, Rockville, MD; June 2009
- Discovering INDEL and Copy Number Variation from Paired-end Sequencing
  Weizmann Institute, Rehovot, Israel; November 2009

Lectures at Summer Schools & Special Courses (8 total)
- Mining the Genome PhD Course, University of Utrecht, Netherlands; October 2003
- PGA Educational Workshop, Lawrence Berkeley Laboratory, California; November 2004
- Mining the Genome PhD Course, University of Utrecht, Netherlands; November 2005
- Course on Genomics, Bioinformatics.ca Workshop, Toronto Canada; February 2006
- Italy Summer School on Bioinformatics, Cluster in Biomedicine, Trieste, July 2007
- Course on Sequencing, Bioinformatics.ca Workshop, Toronto Canada; July 2008
- Course on Sequencing, Bioinformatics.ca Workshop, Toronto Canada; July 2009
- Course on Next-gen Sequencing, Bioinformatics.ca Workshop, Toronto Canada; June 2011

Student supervision

Career Student Numbers		
	In Progress	Completed
Masters	1	5
PhD	4	1
Postdoctoral Fellows	1	0

Current Graduate Students & Postdoctoral Fellows
Orion Buske (MSc 2010-present)
Marc Fiume (BSc 2008-2009, MSc 2009-2010, PhD 2011-present)
Matei David (PDF 2011-present)
Nilgun Donmez (MSc, 2006-2008, PhD 2008-present)
Joseph Whitney (PhD 2007-present)
Vladimir Yanovsky (PhD 2007-present)

Current Undergraduate Research Supervision
Andrew Brook (BSc in CS, 05/2010-present)
Michael Dzamba (BSc in CS & Bioinformatics, 05/2009-present)
Yoni Halpern (BSc in Engineering Sciences, 09/2010-present)

Group Alumni
Elango Cheran (MSc, 2006-2008), now Programmer at SickKids Hospital (Toronto)
Stephen Rumble (BSc 2006-2008), now PhD student at Stanford University
Seunghak Lee (MSc, 2007-2009), now PhD student at Carnegie Mellon University
Adrian Dalca (BSc 2006-2008, MSc 2008-2010) now PhD student at MIT
Paul Medvedev (PhD 2006-2010), now Postdoctoral Fellow with Pavel Pevzner, UCSD

Other Research Supervision
Michael Andruschenko (Undergraduate Research, 05/2007-08/2007)
Botond Ballo (Undergraduate Research, 05/2009-08/2009)
Louie Dinh (Undergraduate Research 05/2010-01/2011)
Daniel Lister (Research Assistant, 09/2009-05/2010)
Aziz M. Mazlini (MSc degree project, 02/2011-07/2011)
Taya Santare (Undergraduate Research, 05/2008-05/2009)
Eric J. Smith (Research Assistant, 10/2010-present)
Tim Smith (Research Assistant, 11/2008-09/2009)
Vanessa Williams (Research Assistant, 01/2010-10/2010)

Teaching

Undergraduate:
CS61B: Data Structures and Advanced Programming (Summer 2000, UC Berkeley)
BCB 410: Applied Bioinformatics (Fall 2007, Fall 2010)
CSC 373: Algorithms (Spring 2009, Spring 2010)

Graduate:
CSC 2431: Topics in Computational Biology (Spring 2008, Spring 2010)
CSC 2417: Algorithms in Genomics (Spring 2006, Fall 2006, Spring 2009, Fall 2010)

Professional Activities

Journal Editorial Positions

- Associate Editor, **Transactions on Computational Biology & Bioinformatics** (2011-present)
- Member of The Editorial Board, **Genome Research** (2010-present)
- Founding Associate Editor, **Algorithms for Molecular Biology** (2006-2010)

Conference Organizer

Founder and Co-organizer of HiTSeq: High Throughput Sequencing Satellite Meeting of ISMB

- 2008 (Toronto, 1 day, 120 attendees)
- 2009 (Stockholm, 1 day, 200 attendees)
- 2010 (Boston, 2 days, 220 attendees)
- 2011 (Vienna, 2 days, 200 attendees)

Steering Committee Member of RECOMB Sequencing Conference (Recomb-seq)

- 2011 (Vancouver, 2 days, 160 attendees)

Session Organizer (responsible for paper/abstract selection)

- Pacific Symposium on Biocomputing (PSB) 2008, Session on Alignment and Evolution
- CSHL/Wellcome Trust Genome Informatics 2009, Session on Next Gen Sequencing
- Pacific Symposium on Biocomputing (PSB) 2010, Session on Personal Genomics
- Intelligent Systems for Molecular Biology (ISMB) 2010, Sequence Analysis Track Chair

Program Committees

- 4th RECOMB Satellite Workshop on Comparative Genomics (Recomb-CG 2006)
- 16th Conference on Intelligent Systems In Molecular Biology (ISMB 2008)
- 8th Workshop on Data Mining in Bioinformatics (BIOKDD 2008)
- 13th Conference on Research in Computational Molecular Biology (RECOMB 2009)
- 15th Computing and Combinatorics Conference (COCOON 2009)
- 17th Conference on Intelligent Systems In Molecular Biology (ISMB 2009),
- 14th Conference on Research in Computational Molecular Biology (RECOMB 2010)
- 18th Conference on Intelligent Systems In Molecular Biology (ISMB) 2010 (Track Chair)
- 10th Workshop on Algorithms in Bioinformatics (WABI 2010)
- 8th RECOMB Satellite Workshop on Comparative Genomics (Recomb-CG 2010)
- 15th Conference on Research in Computational Molecular Biology (RECOMB 2011)
- 11th Workshop on Algorithms in Bioinformatics (WABI 2011)

Reviewing

Peer Reviewer for Science, Nature, Nature Biotechnology, Nature Methods, Nature Communications, Genome Research, Public Library of Science (PLoS) Genetics, PLoS Compuational Biology, Genetics, Molecular Biology and Evolution, Molecular and Systems Biology, Genome Biology, Bioinformatics, Journal of Computational Biology, PLoS ONE, BioMedCentral (BMC) Bioinformatics, BMC Genomics, Journal of Bioinformatics and Computational Biology, ACM/IEEE Transactions on Computational Biology and Bioinformatics, Symposium on Discrete Algorithms (SODA), Foundations of Computer Science Conference (FOCS), IEEE Transactions on Computers.

Grant reviewer: National Institutes of Health (NIH, USA), National Sciences and Engineering Research Council (NSERC, Canada), Health Canada, Netherlands Genomics Institute, Canada Research Chairs Program, French National Research Agency, Foundation for Polish Science.