

Michael Brudno

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University of Toronto

Toronto, ON M5S 3G4 Canada

Assistant Professor and Canada Research Chair in Computational Biology, University of Toronto (start date: January 2006)

- Department of Computer Science
- Banting and Best Department of Medical Research
- Donnelly Centre for Cellular and Biomolecular Research

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

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

Awards & Honors

- Ontario Early Researcher Award (2009-2014)
- Eurosyst 2009 Best Paper Award
- Canada Research Chair in Computational Biology (2006-2011)
- ISMB 2004 Best Paper Award

Refereed Publications (Papers where I am a PI or Corresponding author are noted with a *, students working with me are in **bold**)

1. Dralyuk I, Brudno M, Gelfand M, Zorn M, Dubchak I. ASDB: database of alternatively spliced genes. *Nucleic Acids Res.* **28**:296-7. 2000
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
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
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
5. Brudno M, Morgenstern, B. Fast and sensitive alignment of large genomic sequences. *Proceedings of the IEEE Computer Society Bioinformatics Conference (CSB 2002)*.
6. 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.
7. 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.
8. Brudno M, **Malde S**, Poliakov A, **Do CB**, Couronne O, Dubchak I, Batzoglou S. Global alignment: finding rearrangements during alignment. *Special Issue on the Proceedings of the ISMB 2003, Bioinformatics* **19**: 54i-62i, 2003.
9. Taher L, Rinner O, Garg S, Sczyrba A, Brudno M, Batzoglou S, Morgenstern B. AgenDA: homology-based gene prediction. *Bioinformatics* **19**:1575-1577, 2003.
10. Brudno M, Chapman M, Göttgens B, Batzoglou S, Morgenstern B. Fast and sensitive multiple alignment of large genomic sequences. *BMC Bioinformatics* **4**:66, 2003.
11. Shan 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.
12. Rat Genome Sequencing Project Consortium (RGSPC). Genome sequence of the Brown Norway Rat yields insights into mammalian evolution. *Nature* **428**:493–521, 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.
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.
15. Brudno M, Steinkamp R, Morgenstern B. The CHAOS/DIALIGN WWW server for multiple sequence alignment. *Nucleic Acids Research* **32**:W41 – W44, 2004.
16. 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.

17. **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.
18. The ENCODE Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science*, **306**: 636–640, 2004.
19. Do CB, Mahabhashyam M, Brudno M, Batzoglou S. ProbCons: Probabilistic consistency-based multiple alignment of amino acid sequences. *Genome Res.* **15**: 330–340, 2005
20. 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 Computational Biology* 4:981-998, 2006
21. Small KS, Brudno M, Hill MM, Sidow A. Extreme genomic variation in a natural population. *Proc Natl Acad Sci U S A.* 104(13):5698-703. 2007.
22. Small KS, Brudno M, Hill MM, Sidow A. A haplome alignment and reference sequence of the highly polymorphic *Ciona savignyi* genome. *Genome Biol.* 8(3):R41 2007
23. 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
24. Bazykin GA, Kondrashov FA, Brudno M, Poliakov A, Dubchak I, Kondrashov AS. Extensive parallelism in protein evolution. *Biol Direct.* 2:20 2007
- 25* **Medvedev P**, Georgiou K, Myers EW, Brudno M. Computability and equivalence of models for genome assembly. *Proceedings of the Workshop on Algorithms in Bioinformatics (WABI)*, 2007
- 26* **Dalca AV**, Brudno M. FRESCO: Flexible Alignment with Rectangle Scoring Schemes. *Proceedings of the Pacific Symposium on Biocomputing (PSB)* 2008
- 27* **Medvedev P**, Brudno M. Ab initio Whole Genome Shotgun Assembly with Mated Short Reads *Proceedings of the 12th Annual Research in Computational Biology Conference (RECOMB)*, 2008
- 28* **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
- 29* **Yanovsky V, Rumble S**, Brudno M. Read Mapping Algorithms for Single Molecule Sequencing Data. *Proceedings of the Workshop on Algorithms in Bioinformatics (WABI)* 2008.
30. 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.
- 31* **Donmez N**, Bazykin G, Brudno M, Kondrashov A. Polymorphism due to multiple amino acid substitutions at a codon site within *Ciona savignyi*. *Genetics*, 181: 685–690 2009
- 32* Lagar-Cavilla A, **Whitney JA**, Scannel A, **Rumble SM**, Patchin P, de Lara E, Brudno M, Satyanarayanan, M. SnowFlock: Rapid Virtual Machine Cloning for Cloud Computing. *Proceedings of the European Conference in Computer Systems (Eurosys)* 2009 (**Best Paper Award**).
- 33* Dubchak I, Poliakov A, Kislyuk A, Brudno M. Multiple Whole Genome alignment without a Reference Sequence. *Genome Res.* 19:682-689 2009.

- 34*. 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
35. 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
- 36*. **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
- 37*. **Medvedev P**, Brudno M. Maximum Likelihood Genome Assembly. *Journal of Computational Biology*, in press. (Extended journal version of #27).
- 38*. Lee S, Hormozdiari F, Alkan C, Brudno M. MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions *Nature Methods*, in press 2009

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

Conference Presentation Abstracts Delivered as Talks

1. Brudno M, Kim M, Batzoglou S. Multiple alignment of genomic sequences. *Genome Informatics* September 4–8 Wellcome Trust Genome Campus, Hinxton, United Kingdom, 2002.
2. Brudno M, Do CB, Kim M, Batzoglou S. Multiple genomic sequence alignment. In *BCATS 2002 Symposium Proceedings*, p.23, 2002.
3. Brudno M, Do CB, Cooper GM, Kim M, Davydov E, Green ED, Sidow A, Batzoglou S. Multiple genomic sequence alignment. *Advances in Genome Biology and Technology (AGBT)* Marco Island, Florida, February 2003.
4. Brudno M, Poliakov A, Couronne O, Do CB, Batzoglou S, Dubchak I. Multiple alignment of whole genomes: a pipeline approach. *Genome Informatics* May 7-11 Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 2003.
5. Brudno M, Malde S, Poliakov A, Do CB, Couronne O, Dubchak I, Batzoglou S. Glocal alignment: finding rearrangements during alignment. *Genome Informatics* May 7-11 Cold Spring Harbor Lab, Cold Spring Harbor, New York, 2003.
6. Brudno M, Novichkov PS, Mironov AA. Variable length Seeds for Sequence Alignment. *Genome Informatics* September 22–24 Wellcome Trust Genome Campus, Hinxton, United Kingdom, 2004.
7. Do CB, Brudno M, Batzoglou S. ProbCons: Probabilistic consistency-based multiple alignment of amino acid sequences. ISMB 2004 (Best paper award)
8. Brudno M, Davidson S, Myers G. Using String Graphs for Genome Assembly. *Genome Informatics* Oct 28-31 Cold Spring Harbor Lab, Cold Spring Harbor, New York, 2005.
9. Poliakov A., Soloviev M., Kislyuk A., Dubchak I., Brudno M, All animals are equal – Non-referenced whole genome multiple alignments. *Genome Informatics* September 13–17. Wellcome Trust Genome Campus, Hinxton, United Kingdom, 2006
10. Chan ET, Quon GT, The YW, Brudno M, Hughes TR, Morris QD. Inferring the ancestral vertebrate transcriptome: investigating the evolution of vertebrate gene expression and regulation. Intelligent Systems in Molecular Biology PLoS Track 2007

11. Rumble SR, Yanovsky V, Brudno M, SHRiMP: The SHort Read Mapping Package. *Genome Informatics* September 10–13. Wellcome Trust Genome Campus, Hinxton, United Kingdom, 2008

Unrefereed Publications

1. 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)
2. Brudno M. Building Genomes. *Idea&s: The Arts and Science Review*, University of Toronto. Fall 2007, p. 21

Invited Talks (last 5 years)

- **Assembling Genomes with Next Generation Sequencing Data**
September 2008, Ben Gurion University (Be'er Sheva, Israel)
July 2008, Canadian Bioinformatics Workshop, Toronto CA
- **Next Generation Sequencing Technologies**
November 2008, Canada-Taiwan Biotechnology Symposium
April 2008, Toronto Universities Biotechnology Society
February 2008, Genelogic Inc.
- **Discovering Genome Variation with Matepair Data**
December 2008, Rendezvous Sequenage meeting, Genome Quebec.
November 2008, University of Waterloo
February 2008, DOE Joint Genome Institutes
February 2008, Stanford University
February 2008, Applied Biosystems (Foster City, CA)
February 2008, University of Maryland
June 2008, Helicos (Cambridge, MA)
- **Bioinformatics & Computer Science (8 lecture series)**
July 2007, Trieste, Italy
- **Chinese Postmen and Virtual Clusters**
May 2007, Google
- **Predicting Ancestral Genome Order**
November 2005, Moscow Seminar on Computational Biology
November 2005, MIT-CSAIL Bioinformatics Seminar
- **Algorithms for co-Assembling a Genome**
May 2005, University of Toronto
- **Alignment of Whole Genomes: Algorithms & Tools**
September 2005, University of Massachusetts
- **How's What's and Why's of Alignment**
February 2006, Bioinformatics.ca Workshop, Toronto Canada
June 2005, Lawrence Berkeley Laboratory, California; PGA Educational Workshop
November 2005, University of Utrecht, Netherlands; Mining the Genome PhD Course

Student supervision

Graduate

Adrian Dalca (BSc 2006-2008, MSc 2008-present)
Marc Fiume (BSc 2008-2009, MSc 2009-present)
Seunghak Lee (MSc, 2007-2009, PhD 2009-present)
Paul Medvedev (PhD 2006-present, co-supervised with Allan Borodin)
Nilgun Donmez (MSc, 2006-2008, PhD 2008-present)
Joseph Whitney (PhD 2007-present)
Vladimir Yanovsky (PhD 2007-present)

Undergraduate

Botond Ballo (BSc in Math and Computer Science, 05/2009-present)
Michael Dzamba (BSc in Bioinformatics, 05/2009-present)
Taya Santare (BSc in Math and Computer Science, 05/2008-present)

Alumni

Elango Cheran (MSc, 2006-2008), now Programmer at Sick Children's Hospital (Toronto)
Stephen Rumble (BSc 2007-2008), now PhD Student at Stanford University

Teaching

Undergraduate:

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

Graduate:

CSC 2431: Topics in Computational Biology – Next Generation Sequencing (Spring 2008)
CSC 2417: Algorithms in Genomics (Spring 2006, Fall 2006, Spring 2009)

Professional Activities

Associate Editor of the Algorithms for Molecular Biology journal

Guest associate editor for the PLoS Computational Biology journal

Meeting organizer

- Pacific Symposium for Biocomputing (PSB) 2008 Session on Alignment and Evolution
- Intelligent Systems for Molecular Biology SIG on Next Gen Sequencing (2008, 2009)

Program Committees: Recomb Comparative Genomics 2006, ISMB 2008, 2009, BIODDD 2008, RECOMB 2009, COCOON 2009.

Referee for Genome Research, RECOMB, ISMB, IEEE CSB, Bioinformatics Journal, BMC Bioinformatics, BMC Genomics, Molecular and Systems Biology, Journal of Bioinformatics and Computational Biology, PLoS Genetics, PLoS Computational Biology, Genetics, Molecular Biology and Evolution, SODA, FOCS, Transactions on Computers.

Grant reviewer for NSERC, Health Canada, Netherlands Genomics Institute, French National Research Agency.