

Paul Medvedev

CONTACT INFORMATION	University of California, San Diego Department of Computer Science 9500 Gilman Dr., Mail Code 0404 La Jolla, CA 92093-0404, USA	Web: http://www.cs.toronto.edu/~pashadag/ Email: pmedvedev@cs.ucsd.edu Tel: +1 818 212 1591
RESEARCH INTERESTS	Genome analysis, high-throughput sequencing data analysis, cancer genomics, theoretical computer science, algorithm design and analysis.	
EDUCATION & TRAINING	University of California, San Diego, Aug. 2010 – present <ul style="list-style-type: none">• Post Doctoral Scholar at the Dept. of Computer Science and Engineering• Supervisor: Pavel Pevzner University of Toronto, 2005-2010 <ul style="list-style-type: none">• Ph.D. in Computer Science• Thesis title : Genome Graphs• Supervisors: Michael Brudno and Allan Borodin University of Southern Denmark at Odense (SDU), 2002 – 2004 <ul style="list-style-type: none">• M.Sc. in Computer Science• Thesis title : The Relative Worst Order Ratio Applied to Seat Reservation• Supervisor: Joan Boyar University of California, Los Angeles (UCLA), 1998 – 2002 <ul style="list-style-type: none">• B.S. <i>magna cum laude</i> in Computer Science• Minor Field: Astrophysics• GPA: 3.8	
PROFESSIONAL EXPERIENCE	UCLA, Institute for Pure and Applied Mathematics, Visitor, Sep – Dec 2011 <ul style="list-style-type: none">• Mathematics and Computational Approaches in High-Throughput Genomics Program Universität Bielefeld, Genome Informatics Group, Research Visitor, Oct 2007 – July 2008 <ul style="list-style-type: none">• Host: Jens Stoye• Investigated problems in genome rearrangements Altera Corporation, Advanced Software Engineer, 1/2005 – 8/2005 <ul style="list-style-type: none">• Participated in all aspects of developing compiler software for field-programmable gate arrays (FPGAs), including requirements gathering, detailed design, development, testing and documentation.	
AWARDS AND HONORS	Named one of 2011's "Tomorrow's PIs" by Genome Technology Magazine Platform Computing Graduate Fellowship in Computer Science, 2010 DAAD Research Grant, Oct 2007 – July 2008 <ul style="list-style-type: none">• Salary and support for research project to study genome rearrangements Regents Scholarship, University of California, 1998-2002 <ul style="list-style-type: none">• Full scholarship and stipend Other <ul style="list-style-type: none">• Travel Funding Awards: ISMB 2011, RECOMB 2011, RECOMB 2008• Dean's Honor List, UCLA: Winter 1999, Fall 1998	

**PEER-REVIEWED
JOURNAL
PUBLICATIONS**

Joint first authors are indicated with (*). Author lists denoted using “with“ are alphabetical.

Computational Biology

1. Paul Medvedev*, Son Pham*, Mark Chaisson, Glenn Tesler and Pavel Pevzner, Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers, *Journal of Computational Biology*, in press.
2. Paul Medvedev, Eric Scott, Boyko Kakaradov, and Pavel Pevzner, Error correction of high-throughput sequencing datasets with non-uniform coverage, *Bioinformatics* 27 (13): i137-i141, 2011 (special ISMB proceedings issue).
3. Paul Medvedev, Marc Fiume, Misko Dzamba, Tim Smith, Michael Brudno, Detecting copy number variation with mated short reads, *Genome Research*, 20:1613–1622, 2010 (featured on the cover).
4. Rearrangement models and single-cut operations, with Anne Bergeron and Jens Stoye, *Journal of Computational Biology*, 17(9):1213-1225, 2010.
5. Paul Medvedev, Monica Stanciu, Michael Brudno, Computational methods for discovering structural variation with next generation sequencing, *Nature Methods*, 6(11):S13-S20, 2009.
6. Paul Medvedev and Michael Brudno, Maximum likelihood genome assembly, *Journal of Computational Biology*, 16(8):1101-1116, 2009.

Other Computer Science

7. Shortest paths between shortest paths, with Marcin Kamiński and Martin Milanič, *Theoretical Computer Science*, 412(39):5205–5210, 2011.
8. The plane-width of graphs, with Marcin Kamiński and Martin Milanič, *Journal of Graph Theory*, 68(3):229–245, 2011.
9. The relative worst order ratio applied to seat reservation, with Joan Boyar, *ACM Transactions on Algorithms*, 4(4):1-22, 2008.

**PEER-REVIEWED
CONFERENCE
PUBLICATIONS**

Papers which I presented at the conference are indicated with (†).

Computational Biology

- † Paul Medvedev, Eric Scott, Boyko Kakaradov, and Pavel Pevzner, Error correction of high-throughput sequencing datasets with non-uniform coverage, *19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2011)*, simultaneously published in *Bioinformatics* (see above).
1. Paul Medvedev*, Son Pham*, Mark Chaisson, Glenn Tesler and Pavel Pevzner, Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers, *Proceedings of the 16th International Conference on Research in Computational Molecular Biology (RECOMB 2011)*, LNCS 6577:238-251.
 2. † Rearrangement models and single-cut operations, with Jens Stoye, *Proceedings of the Seventh Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG 2009)*, LNCS 5817:84-97.
 3. † Paul Medvedev and Michael Brudno, Ab initio whole genome shotgun assembly with mated short reads, *Proceedings of the 13th International Conference on Research in Computational Molecular Biology (RECOMB 2008)*, LNCS 4955:50-64.
 4. † Paul Medvedev, Konstaninos Georgiou, Gene Myers, and Michael Brudno, Computability of models for sequence assembly, *Proceedings of the 7th International Workshop of Algorithms in Bioinformatics (WABI 2007)*, LNCS 4645:289-301.

Other Computer Science

5. † Shortest paths between shortest paths and independent sets, with Marcin Kamiński and Martin Milanič, *Proceedings of the 21st International Workshop on Combinatorial Algorithms (IWOCA 2010)*, LNCS 6460:56-67.
6. On the plane-width of graphs, with Marcin Kamiński and Martin Milanič, *European Conference on Combinatorics, Graph Theory and Applications (EuroComb 2009)*, ENDM 34 (2009) 633-637.
7. † The relative worst order ratio applied to seat reservation, with Joan Boyar, *Proceedings of the Ninth Scandinavian Workshop on Algorithm Theory (SWAT 2004)*, LNCS 3111:90-101.
8. Haiyun Luo, Paul Medvedev, Jerry Cheng and Songwu Lu, A self-coordinating approach to distributed fair queueing in ad hoc wireless networks, *Proceedings of the 20th Annual Joint Conference of the IEEE Computer and Communications Societies (INFOCOM 2001)*.

OTHER PUBLICATIONS

1. A report on the 2009 SIG on short read sequencing and algorithms (Short-SIG), with Michael Brudno, Jens Stoye, and Francisco M. de la Vega, *Bioinformatics* 25(21): 2863-2864, 2009.

PROFESSIONAL SERVICE

Program Committee Co-Chair

- RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq 2012)

Program Committee Member

- RECOMB-seq 2011

Peer-Reviewer

- Genome Research, Bioinformatics, RECOMB, ISMB, WABI, IEEE/ACM Transactions on Computational Biology and Bioinformatics, BMC Bioinformatics, Algorithms for Molecular Biology, ESA, SODA, Discrete Applied Mathematics, Theoretical Computer Science

INVITED TALKS

Algorithms for High-Throughput Genomics

- UCLA, Computer Science Seminar, Oct 2011

Genome Rearrangements

- Bioinformatics for Cancer Genomics, Canadian Bioinformatics Workshops, Sep 2011, Toronto

Paired de Bruijn Graphs for Genome Assembly

- Bioinformatics Minisymposium at Canadian Discrete and Algorithmic Mathematics Conference, June 2011, Victoria

Predicting Copy-Counts in Genome Graphs Using Maximum Likelihood: Applications to Assembly and Copy Number Variation Detection

- Wellcome Trust Sanger Institute (UK), July 2010
- Illumina, Inc. (UK), July 2010

Maximum Likelihood Genome Assembly and Variation Discovery

- UC San Diego, Bioinformatics Seminar, July 2010

Computability of Models for Sequence Assembly

- University of Southern Denmark, Computer Science Colloquia, Jan 2008
- University of Waterloo Mini-Symposium on Bioinformatics, 2007

Ab Initio Whole Genome Shotgun Assembly With Mated Short Reads

- Computational Biology Session at Institute for Operations Research and the Management Sciences Annual Meeting (INFORMS 2008), Washington DC

**PRESENTED
ABSTRACTS /
LOCAL TALKS**

(for presentations at conferences with published proceedings, see publication sections)

Copy Number Variation Discovery Using Mated Shorts Reads

- Int. Conf. on Research in Computational Mol. Bio. (RECOMB 2009), Arizona
- Int. Conf. on Intelligent Systems for Mol. Bio. (ISMB 2009), Stockholm
- Cold Spring Harbor Laboratory/Wellcome Trust Conference on Genome Informatics (2009), Cold Spring Harbor

The Plane-Width of Graphs

- Canadian Disc. and Alg. Math. Conf. (CanaDAM 2009), Montreal
- University of Toronto, Theoretical Computer Science Seminar, 2009

On Single Cut and Join

- Universität Bielefeld, Genome Informatics Seminar, Aug 2008

Models for Sequence Assembly and Short Read Sequencing

- NRW Graduate School in Bioinformatics and Genome Research Retreat, 2007, Beverungen-Blankenau, Germany

Sorting Signed Permutations

- University of Toronto, Theory Student Seminar, 2006

The Relative Worst Order Ratio Applied to Seat Reservation

- Workshop on On-Line Algorithms (OLA 2004), Denmark

TEACHING

Algorithm Design and Analysis, University of Toronto, CSC373

- Co-instructor, Spring 2009
- TA, Spring 2007
- TA, Spring 2006

Introduction to the Theory of Computation, University of Toronto, CSC236

- TA, Spring 2010
- TA, Fall 2009

Information Theory, University of Toronto, CSC310

- TA, Fall 2008

Communication Skills for Computer Scientists, University of Toronto, CSC290

- TA, Fall 2006

Software Engineering I, University of Toronto, CSC444

- TA, Fall 2005

Programming Languages, University of Southern Denmark, DM22

- TA, Spring 2004
- TA, Spring 2003

Algorithms and Complexity, University of Southern Denmark, DM19

- TA, Fall 2003
- TA, Fall 2002

LANGUAGES

Fluent in Russian and English, conversational French, some Danish and Spanish