

# Iman Hajirasouliha, Ph.D.

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**Contact Information** S-260 James H. Clark Center, 318 Campus Drive  
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<http://www.imanh.org>

**Current Affiliation** **Department of Computer Science, Stanford University, California, USA**  
*Post Doctoral Research Scholar* **Since July 2014**

**Areas of Expertise** Algorithms for biomolecular sequence analysis  
Computational cancer genomics, including tumor heterogeneity and evolution  
Machine Learning, Combinatorics, Approximation algorithms

**Education** **Simon Fraser University**, Burnaby, BC, Canada  
*Ph.D. in Computing Science* **Jan 2008 – Aug 2012**

- Thesis: Algorithms for structural variation discovery and protein-protein interaction prediction
  - ◊ My dissertation was noted "exceptional" by the external examiner.
- Senior Supervisor: S. Cenk Sahinalp

**Simon Fraser University**, Burnaby, BC, Canada

*M.Sc. in Computing Science* **Sep 2005 – Dec 2007**

- Thesis: Convergence to Nash Equilibria in Distributed, Selfish Reallocation Processes
- Senior Supervisor: Petra Berenbrink

**Sharif University of Technology**, Tehran, Iran

*B.Sc. in Computer Engineering* **Sep 2001 – Jul 2005**

- Thesis: Selfish Routing
- Advisor: Mohammad Ghodsi

**Honours and Awards**

- ◊ Simons-Berkeley Research Fellowship (program: Algorithmic Challenges in Genomics) 2016
- ◊ NSERC Postdoctoral Fellowships (\$90,000) 2014–2016
- ◊ NSERC-CGS Michael Smith Foreign Study Supplements (\$6,000) 2012
- ◊ NSERC Alexander Graham Bell Canada Graduate Scholarship (\$70,000) 2010–2012
- ◊ Simon Fraser University Graduate Fellowship (\$6,250) 2012
- ◊ **Best Paper Award**, ISMB-HiTSeq 2011
- ◊ Ebco/Eppich Graduate Scholarship in Intelligent Systems (\$700) 2011
- ◊ Brian J. Blaha Memorial Annual Graduate Scholarship in Computing Science (\$1,000) 2009
- ◊ SFU Computing Science Graduate Scholarships (\$6,000) 2008
- ◊ SFU Computing Science Graduate Scholarships (\$6,000) 2007
- ◊ Simon Fraser University, Entrance Scholarships (\$2,000) 2005
- ◊ 2nd Ranked, National Graduate Entrance Examination in Computer Science, Iran 2005
- ◊ Silver Medal, The 10th National Olympiad in Informatics, Iran 2000
- ◊ Numerous travel awards to attend the following conferences: STACS'07, ISMB'08, RECOMB'09, ISMB'10, ISMB'11, ISMP'12, HitSeq'15
- ◊ Erdős Number 2!

**Research Experience** **Department of Computer Science, Stanford University, CA, USA**  
*Post Doctoral Research Scholar* **Jul 2014 – present**

- Member of **Serafim Batzoglou's** group. Research on algorithms for genomics, structural variation discovery in cancer genomes, combinatorial optimization, computational cancer genomics.

**Department of Computer Science and Center for Computational Molecular Biology, Brown University**, Providence, RI, USA

*Post Doctoral Research Associate* **Jan 2013 – Jun 2014**

- Member of **Ben Raphael's** group. Research on big data analytics on computational biology, combinatorial optimization, copy number variation, cancer genomics, including heterogeneity.

**School of Computing Science, Simon Fraser University**, Burnaby, BC, Canada

*Ph.D. student, Research Assistant and NSERC-CGS scholar*

**Jan 2008 – Aug 2012**

- Member of the lab for computational biology at SFU (**Cenk Sahinalp's** group). Research on bioinformatics algorithms, combinatorial optimization, next generation sequencing (NGS), protein-protein Interaction (PPI) networks. Contributed to the 1000 Genomes Project.

**Genome Sciences Department, University of Washington**, Seattle, WA, USA

*Visiting Scholar*

**Feb 2009 – Jul 2009**

- Research on structural variation discovery in human genomes under supervision of **Evan Eichler**. Became a member of the 1000 Genomes Project. Developed methods for analyzing large next-generation sequencing (NGS) data sets.

**Centrum Wiskunde and Informatica (CWI)**, Amsterdam, The Netherlands

*NSERC CGS-MSFSS Visiting Scholar*

**Summer 2012**

- Research on discovering and genotyping midsize and long indels in next-gen sequencing data. Worked with Alexander Schönhuth in the life sciences group.

**Canada's Michael Smith Genome Sciences Centre**, Vancouver, BC, Canada

*Student Collaborator*

**Sep 2009 – Aug 2012**

- Research on algorithms for next generation sequencing technologies. Worked with Inanc Birol.

**PIMS-IGTC in Mathematical Biology**, Vancouver, BC, Canada

*Enrolled and completed the training program as a Ph.D. student*

**May 2010 – Aug 2012**

- Fulfilled the requirements of the Pacific Institute for the Mathematical Sciences (PIMS) Graduate Training program. PIMS-IGTC focuses on the training of graduate students in mathematical biology. The IGTC graduate training elements include annual research summits, summer courses, new term-time courses, seminars, graduate student exchanges, and international visitors.

**Bilkent and Sabanci Universities**, Turkey and **University of Durham**, England, UK

*Visiting Student*

**Sep 2007 – May 2008**

- Spent two semesters abroad working closely with my advisors during their sabbatical leave. Research on network motif discovery, randomized and approximation algorithms.

**Simon Fraser University**, Burnaby, BC, Canada

*M.Sc. student, Research Assistant*

**May 2006 – Aug 2007**

- Research on algorithmic game theory and randomized algorithms with Petra Berenbrink.

**Peer-Reviewed  
Journal  
Publications**

1. V. Popic, R. Salari, **I. Hajirasouliha**, D. Kashef-Haghighi, RB West, and S. Batzoglu

*Fast and scalable inference of multi-sample cancer lineages.*

**Genome Biology** (2015) May 6;16(1):91.

2. Ritz A., Bashir A., Sindi S., Hsu D., **Hajirasouliha I.**, Raphael BJ.

*Characterization of Complex Structural Variants with Single Molecule and Hybrid Sequencing Approaches.* **Bioinformatics** (2014) 30 (24): 3458-3466

3. **Hajirasouliha I.**, Mahmoodi A. and Raphael BJ.

*A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data* **Bioinformatics** (2014) 30 (12), i78-i86

4. Wu H., **Hajirasouliha I.**, Raphael BJ.

*Detecting independent and recurrent copy number aberrations using interval graphs* **Bioinformatics** (2014) 30 (12), i195-i203.

5. Marschal T., **Hajirasouliha I.**, Schönhuth A.

*MATE-CLEVER: Mendelian-Inheritance-Aware Discovery and Genotyping of Midsize and Long Indels* **Bioinformatics** (2013), December 15;29 (24): 3143-3150.

6. 1000 Genomes Project Consortium.  
An integrated map of genetic variation from 1,092 human genomes.  
**Nature** (2012) Nov 1;491(7422):56-65.
7. Lapuk AV, Wu C, Wyatt AW, McPherson A, McConeghy BJ, Brahmabhatt S, Mo F, Zoubeidi A, Anderson S, Bell RH, Haegert A, Shukin R, Wang Y, Fazli L, Hurtado-Coll A, Jones EC, Hach F, Hormozdiari F, **Hajirasouliha I.**, Boutros PC, Bristow RG, Zhao Y, Marra MA, Fanjul A, Maher CA, Chinnaiyan AM, Rubin MA, Beltran H, Sahinalp SC, Gleave ME, Volik SV, Collins CC  
From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer.  
**The Journal of Pathology** (2012) Jul;227(3):286-97.
8. **Iman Hajirasouliha**, Alexander Schönhuth, David Juan, Alfonso Valencia, S. Cenk Sahinalp  
Mirroring co-evolving trees in the light of their topologies  
**Bioinformatics** (2012) May 1;28(9):1202-8.
9. Chunxiao Wu, Alexander W Wyatt, Anna V Lapuk, Andrew McPherson, Brian J McConeghy, Robert H Bell, Shawn Anderson, Anne Haegert, Sonal Brahmabhatt, Robert Shukin, Fan Mo, Estelle Li, Ladan Fazli, Antonio Hurtado-Coll, Edward C Jones, Yaron S Butterfield, Faraz Hach, Fereydoun Hormozdiari, **Iman Hajirasouliha**, Paul C Boutros, Robert G Bristow, Steven J M Jones, Martin Hirst, Marco A Marra, Christopher A Maher, Arul M Chinnaiyan, S Cenk Sahinalp, Martin E Gleave, Stanislav V Volik, Colin C Collins Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer  
**The Journal of Pathology** (2012) May;227(1):53-61
10. Petra Berenbrink, Tom Friedetzky, **Iman Hajirasouliha** and Zengjian Hu †  
Convergence to Equilibria in Distributed, Selfish Reallocation Processes with Weighted Tasks  
**Algorithmica**, 62(3-4): 767-786 (2012)  
† Authors are listed alphabetically.
11. Fereydoun Hormozdiari\*, **Iman Hajirasouliha\***, Andrew McPherson, Evan E. Eichler, S. Cenk Sahinalp Simultaneous structural variation discovery in multiple paired-end sequenced genomes.  
**Genome Research**, (2011) Dec;21(12):2203-12 [\* Joint First Authorship.]  
◊ Featured on the cover of the journal!  
◊ Highlighted in: **Nature Biotechnology**, 29, 1101 (2011).
12. Andrew McPherson, Chunxiao Wu, **Iman Hajirasouliha**, Fereydoun Hormozdiari, Faraz Hach, Anna Lapuk, Stanislav Volik, Sohrab Shah, Colin Collins, S. Cenk Sahinalp.  
Comrad: a novel algorithmic framework for the integrated analysis of RNA-Seq and WGSS data.  
**Bioinformatics** 2011 Jun 1;27(11):1481-8. Epub 2011 Apr 9.
13. Mills, R. E., K. Walter, D. A. Stewart, R. Handsaker, K. Chen, C. Alkan, A. Abyzov, S. C. Yoon, K. Ye, R. K. Cheetham, A. Chinwalla, D. F. Conrad, Y. Fu, F. Grubert., **I. Hajirasouliha**, F. Hormozdiari, L. M. Iakoucheva, Z. Iqbal, J. M. Kidd, M. K. Konkel, J. Korn, E. Khurana, D. Kura, H. J. K. Lam, J. Leng, R. Li, Y. Li, C.-Y. Lin, R. Luo, X. J. Mu, J. Nemesh, H. E. Peckham, T. Rausch, A. Scally, X. Shi, M. P. Stromberg, A. M. Stutz, A. E. Urban, J. A. Walker, J. Wu, Y. Zhang, Z. Zhang, M. A. Batzer, L. Ding, G. T. Marth, G. McVean, J. Sebat, M. Snyder, J. Wang, K. Ye, K. Ye, E. E. Eichler, M. B. Gerstein, M. E. Hurles, C. Lee, S. A. McCarroll and J. O. Korbel on behalf of the 1000 Genomes Project.  
Mapping copy number variation at fine-scale by population-scale genome sequencing  
**Nature** 2011, 470: 59-65.
14. Fereydoun Hormozdiari, Can Alkan, Mario Ventura, **Iman Hajirasouliha**, Maika Malig, Faraz Hach, Deniz Yorukoglu, Phuong Dao, Marzieh Bakhshi, S. Cenk Sahinalp, Evan E. Eichler  
Alu repeat discovery and characterization within human genomes.  
**Genome Research** June 2011 21: 840-849.
15. The 1000 Genomes Project Consortium  
A map of human genome variation from population-scale sequencing.  
**Nature** 2010, 467: 1061-1073.  
◊ Featured on the cover of the journal!  
◊ See the 1000 Genomes Project page for media coverage

16. Fereydoun Hormozdiari, **Iman Hajirasouliha**, Phuong Dao, Faraz Hach, Deniz Yorukoglu, Can Alkan, Evan E. Eichler, S. Cenk Sahinalp  
Next Generation VariationHunter: Combinatorial Algorithms for Transposon Insertion Discovery  
**Bioinformatics** 2010 Jun 15;26(12):i350-i357.
17. **Iman Hajirasouliha**, Fereydoun Hormozdiari, Can Alkan, Jeffrey M. Kidd, Inanc Birol, Evan E. Eichler, S. Cenk Sahinalp  
Detection of locus and content of novel sequence insertions using paired-end next-generation sequencing  
**Bioinformatics** 2010 May 15;26(10):1277-83.
18. Rahele Salari, Cagri Aksay, Emre Karakoc, Peter Unrau, **Iman Hajirasouliha**, and S. Cenk Sahinalp  
smRNA: A novel ab initio ncRNA gene finder  
**PLoS ONE**, (5): e5433, doi:10.1371/journal.pone.0005433, May 2009
19. **Iman Hajirasouliha**, Fereydoun Hormozdiari, S. Cenk Sahinalp, and Inanc Birol  
Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies  
**Bioinformatics** 2008 Jul 1;24 (13):i32-40.
20. Noga Alon, Phuong Dao, **Iman Hajirasouliha**, Fereydoun Hormozdiari and S. Cenk Sahinalp †  
Biomolecular Network Motif Counting and Discovery by Color Coding  
**Bioinformatics** 2008 Jul 1;24 (13):i241-9.  
† Authors are listed alphabetically.

**Peer-Reviewed Conference Publications** *Papers which I presented at the conference are indicated with ‡.*

1. ‡ **Iman Hajirasouliha** and Benjamin Raphael  
*Reconstructing mutational history in multiply sampled tumors using perfect phylogeny mixtures*  
**WABI 2014**, Workshop on Algorithms in Bioinformatics, Wroclaw, Poland, September 8-10, 2014.
2. ‡ **Iman Hajirasouliha**, Ahmad Mahmoodi and Benjamin Raphael  
*A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data*  
**ISMB 2014**, Annual International Conference on Intelligent Systems for Molecular Biology, Boston, USA, July 11-15 2014.  
◊ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
3. Hsin-Ta Wu, **Iman Hajirasouliha**, Benjamin Raphael  
*Detecting independent and recurrent copy number aberrations using interval graphs*  
**ISMB 2014**, Annual International Conference on Intelligent Systems for Molecular Biology, Boston, USA, July 11-15 2014.  
◊ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
4. Ritz A., Bashir A., Sindi S., Hsu D., **Hajirasouliha I.**, Raphael B.J.  
*Characterization of Complex Structural Variants with Single Molecule and Hybrid Sequencing Approaches*. **ISMB-HitSeq 2014** Conference on High Throughput Sequencing Analysis and Algorithms (Special Interest Group of ISMB 2014) Boston, MA, July 9-10 2014.  
◊ Extended work was published in *Bioinformatics* (see Journal Publications).
5. Tobias Marschal, **Iman Hajirasouliha**, Alexander Schönhuth *MATE-CLEVER: Mendelian-Inheritance-Aware Discovery and Genotyping of Midsize and Long Indels*  
**ISMB-HiTSeq 2013**: Conference on High Throughput Sequencing Analysis and Algorithms (Special Interest Group of ISMB 2013) July 15-16, 2013 Berlin, Germany  
◊ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
6. ‡ Fereydoun Hormozdiari, **Iman Hajirasouliha**, Andrew McPherson, Evan E. Eichler, S. Cenk Sahinalp. *Simultaneous structural variation discovery in multiple paired-end sequenced genomes*.  
**RECOMB 2011**, Annual International Conference on Research in Computational Molecular Biology, Vancouver, Canada, March 28-31 2011  
◊ Extended work was published in *Genome Research* (see Journal Publications).

7. Andrew McPherson, Chunxiao Wu, **Iman Hajirasouliha**, Fereydoun Hormozdiari, Faraz Hach, Anna Lapuk, Stanislav Volik, Sohrab Shah, Colin Collins, S. Cenk Sahinalp.  
*Comrad: a novel algorithmic framework for the integrated analysis of RNA-Seq and WGSS data.*  
**ISMB-HiTSeq 2011**, Conference on High Throughput Sequencing Analysis and Algorithms (Special Interest Group of ISMB 2011) Vienna, Austria, July 15-16 2011.  
**Winner of the Best Paper Award**  
 ◇ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
  
8. Fereydoun Hormozdiari, **Iman Hajirasouliha**, Phuong Dao, Faraz Hach, Deniz Yorukoglu, Can Alkan, Evan E. Eichler, S. Cenk Sahinalp  
*Next Generation VariationHunter: Combinatorial Algorithms for Transposon Insertion Discovery*  
**ISMB 2010**, Annual International Conference on Intelligent Systems for Molecular Biology, Boston, USA, July 11-13 2010  
 ◇ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
  
9. ‡ **Iman Hajirasouliha**, Fereydoun Hormozdiari, Can Alkan, Jeffrey M. Kidd, Inanc Birol, Evan E. Eichler, S. Cenk Sahinalp  
*Detection of locus and content of novel sequence insertions using paired-end next-generation sequencing*  
**ISMB-HiTSeq 2010**, Conference on High Throughput Sequencing Analysis and Algorithms (Special Interest Group of ISMB 2010) Boston, USA, July 9-10 2010  
 ◇ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
  
10. Phuong Dao, Alexander Schönthuth, Fereydoun Hormozdiari, **Iman Hajirasouliha**, Cenk Sahinalp, Martin Ester Quantifying systemic evolutionary changes by color coding confidence-sored PPI networks **WABI 2009**, Workshop on Algorithms in Bioinformatics, Philadelphia, USA, September 12-13 2009, pages 37-48.
  
11. **Iman Hajirasouliha**, Fereydoun Hormozdiari, S. Cenk Sahinalp, and Inanc Birol *Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies*  
**ISMB 2008**, Annual International Conference on Intelligent Systems for Molecular Biology, Toronto, Canada, July 19-23 2008  
 ◇ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
  
12. ‡ Noga Alon, Phuong Dao, **Iman Hajirasouliha**, Fereydoun Hormozdiari and S. Cenk Sahinalp  
*Biomolecular Network Motif Counting and Discovery by Color Coding*  
**ISMB 2008**, Annual International Conference on Intelligent Systems for Molecular Biology, Toronto, Canada, July 19-23 2008  
 ◇ Simultaneously published in the journal *Bioinformatics* (see Journal Publications).
  
13. Petra Berenbrink, Tom Friedetzky, **Iman Hajirasouliha** and Zengjian Hu  
*Convergence to Equilibria in Distributed, Selfish Reallocation Processes with Weighted Tasks*  
**ESA 2007**, The European Symposium on Algorithms, Eilat, Israel, October 8-10, 2007, pages 41-52  
 ◇ Extended work was published in *Algorithmica* (see Journal Publications).
  
14. ‡ **Iman Hajirasouliha**, Hossein Jowhari, Ravi Kumar, and Ravi Sundaram On Completing Latin Squares **STACS 2007**, Annual Symposium on Theoretical Aspects of Computer Science, Aachen, Germany, February 22-24 2007, pages 524-535

**Book Chapter** Phuong Dao, Fereydoun Hormozdiari, **Iman Hajirasouliha**, Martin Ester, S. Cenk Sahinalp  
*Proteome Network Emulating Models*  
 In *Functional Coherence of Molecular Networks*, Pages 69-95, edited by Mehmet Koyuturk, Shankar Subramaniam and Ananth Grama; Springer, 1st Edition (September 30, 2011)

<b>Teaching Experience</b>	<b>Tutorial Instructor</b> , ACM-BCB 2015, Atlanta, GA, USA	
	<ul style="list-style-type: none"> <li>Computational methods for analyzing intra-tumor heterogeneity</li> </ul>	September 2015
	<b>Guest Lecturer</b> , Stanford University , CA, USA	
	<ul style="list-style-type: none"> <li>CS262-Computational Genomics (Prof. Serafim Batzoglou)</li> </ul>	Winter 2015
	<b>Guest Lecturer</b> , RI-INBRE Bioinformatics Core, University of Rhode Island, RI, USA	
	<ul style="list-style-type: none"> <li>Bioinformatics (Dr. Hany Alashwal)</li> </ul>	Spring 2014
	<b>Guest Lecturer</b> , Department of Computing Science, SFU, BC, Canada	
	<ul style="list-style-type: none"> <li>Bioinformatics Algorithms (Prof. Cenk Sahinalp)</li> </ul>	Fall 2012
	<b>Teaching Assistantship</b> , Simon Fraser University, BC, Canada	
	<ul style="list-style-type: none"> <li>Bioinformatics Algorithms</li> <li>Data Communications and Networking</li> <li>Data Communications and Networking</li> <li>Introduction to Internet and Multimedia</li> <li>Introduction to Internet and Multimedia</li> <li>Introduction to Computer Science</li> </ul>	Fall 2009 Fall 2009 Summer 2007 Fall 2006 Spring 2006 Fall 2005
<b>Conference Presentations</b>	<b>Teaching Assistantship</b> , Sharif University of Technology, Tehran, Iran	
	<ul style="list-style-type: none"> <li>Data Structures and Algorithms</li> <li>Design and Analysis of Algorithms</li> <li>Data Structures and Algorithms</li> <li>Discrete Structures</li> <li>Discrete Structures</li> </ul>	Fall 2004 Spring 2004 Fall 2003 Spring 2003 Fall 2002
	<b>Instructor and Head of summer camp</b> , Iranian National Olympiad in Informatics (INOI), 2003	
	<ul style="list-style-type: none"> <li>Thought a summer long course on Combinatorial Problem Solving</li> <li>Coordinated trainers and teaching material, made teaching schedule, planned and held exams to select the national olympiad team.</li> </ul>	
	<i>I try to attend and/or present at one or two major international conferences in computational biology each year. I also occasionally visit selected institutes and give research talks.</i>	
	<b>Leveraging tumor lineage trees to predict and genotype somatic structural variations using paired-end sequencing</b>	
	<ul style="list-style-type: none"> <li>ISMB-HiTSeq (High Throughput Sequencing Analysis and Algorithms), Dublin, Ireland, Jul 2015</li> </ul>	
	<b>Reconstructing mutational history in multiply sampled tumors using perfect phylogeny mixtures</b>	
	<ul style="list-style-type: none"> <li>The 14th Workshop on Algorithms in Bioinformatics (WABI), Wroclaw, Poland, Sep 2014</li> </ul>	
	<b>A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data</b>	
	<ul style="list-style-type: none"> <li>The 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston, MA, Jul 2014</li> </ul>	
	<b>Next-generation sequence characterization of complex genome structural variation</b>	
	<ul style="list-style-type: none"> <li>The 21st International Symposium on Mathematical Programming (ISMP), Berlin, Germany, Aug 2012</li> </ul>	
	<b>Simultaneous structural variation discovery among multiple sequenced genomes</b>	
	<ul style="list-style-type: none"> <li>The 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB), Vancouver, Canada, Mar 2011</li> </ul>	
	<b>Detection of locus and content of novel sequence insertions</b>	
	<ul style="list-style-type: none"> <li>ISMB-HiTSeq (High Throughput Sequencing Analysis and Algorithms), Boston, USA, Jul 2010</li> </ul>	

### **Biomolecular Network Motif Counting and Discovery by Color Coding**

- The 16th Annual International Conference Intelligent Systems for Molecular Biology ISMB, Toronto, Canada, July 2008

### **On Completing Latin Squares**

- The 24th Annual Symposium on Theoretical Aspects of Computer Science (STACS), Aachen, Germany, Feb 2007

### **Invited talks**

#### **Leveraging tumor lineage trees to predict and genotype somatic structural variations using paired-end sequencing**

- Biomod Club, Center for Cancer Systems Biology, Stanford University, CA Aug 2015
- Bioinformatics & Genomic Medicine, HoChiMinh City, Vietnam Jul 2015

#### **Algorithmic developments in structural variation detection and cancer progression**

- Salk Institute for Biological Studies, San Diego, CA Aug 2014

#### **Combinatorial algorithms for genome variation and cancer evolution**

- School of EE & CS, Washington State University, Pullman, WA Apr 2014
- Department of Computer Science, Stanford University, CA Apr 2014
- Department of Computer Science, Iowa State University, Ames, IA Apr 2014
- Department of Computer Science, Colorado State University, Fort Collins, CO Feb 2014

#### **A combinatorial approach for constructing ancestral history of tumors**

- Exact algorithms for bioinformatics research, Shonan Village Center, Japan Mar 2014

#### **Next-generation sequence characterization of complex genome structural variation**

- Centrum Wiskunde & Informatica (CWI), Amsterdam, The Netherlands Sep 2012

#### **Algorithmic Methods for Structural Variation Discovery**

- Department of Computer Science, Brown University, Providence, RI Apr 2012
- Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD Apr 2012
- Department of Computer Science, University of Toronto, Toronto, ON Apr 2012
- Genome Informatics, Bielefeld University, Bielefeld, Germany Apr 2012
- Department of Genetics, Stanford University, Stanford, CA Jan 2012

#### **Simultaneous structural variation discovery among multiple paired-end sequenced genomes**

- NCBI, NLM, NIH Computational Biology Branch, Bethesda, MD Mar 2011

#### **Bioinformatics Analysis of Pseudomonas Genomes and Transcriptomes**

- BCID (Bioinformatics for Combating Infectious Diseases), Simon Fraser University, BC Jun 2010

#### **Detection of locus and content of novel sequence insertions**

- MoCSSy (Modelling of Complex Social Systems), Simon Fraser University, BC Mar 2010
- Sharif University of Technology, Tehran, Iran Jan 2010

#### **Biomolecular Network Motif Counting and Discovery by Color Coding**

- University of Durham, Durham, England May 2008
- Sabanci University, Istanbul, Turkey Apr 2008

#### **Convergence to Nash Equilibria**

- Northeastern University, Boston, MA May 2007

<b>Poster Presentations</b>	<i>Only those posters that I was the presenter are listed here.</i>	
	<b>Leveraging tumor lineage trees to predict and genotype somatic structural variations using paired-end sequencing</b>	
	<ul style="list-style-type: none"> <li>ASHG 2015, Baltimore, MD, USA Oct 2015</li> <li>◊ Reviewers' Choice Abstract. Selected among the top 10% of poster abstracts, by topic as determined by the reviewers' scores.</li> </ul>	
	<b>A combinatorial approach for analyzing intra-tumor heterogeneity</b>	
	<ul style="list-style-type: none"> <li>RECOMB 2014, Pittsburgh, PA, USA Apr 2014</li> </ul>	
	<b>A combinatorial approach for constructing ancestral history of tumors</b>	
	<ul style="list-style-type: none"> <li>Genome Informatics, Cold Spring Harbor, NY, USA Oct 2013</li> </ul>	
	<b>Detection of locus and content of novel sequence insertions</b>	
	<ul style="list-style-type: none"> <li>PIMS-IGTC annual summit, Naramata, BC, Canada Oct 2012</li> <li>Annual Frontiers in Biophysics conference, Simon Fraser University, BC, Canada Mar 2010</li> </ul>	
<b>Memberships</b>	Genome in a Bottle Consortium (GIAB)	2015 - present
	The 1000 Genomes Project, Structural Variation Group	2009 - present
	The 1000 Genomes Project, Analysis Group	2009 - present
	ISCB - International Society for Computational Biology	2008 - present
	Scientific Committee of Iranian National Computer Olympiad	2002-2004
	Scientific Committee, ACM-ICPC Regional Contest, Tehran	2004
<b>Mentoring Experience</b>	William Zeng. Undergraduate student. <i>Stanford University</i> Can Kockan. Undergraduate student. <i>Currently Ph.D. student at Simon Fraser University</i> Pinar Kavak. Visiting graduate student, SFU. <i>Currently Ph.D. student at Bilkent University</i> Reza Shahidi-Nejad. M.Sc. student, SFU. <i>Currently Software Developer Engineer II at Amazon</i>	
<b>Reviews</b>	<b>Grants:</b> The Wellcome Trust and Royal Society of the UK. (reviewed a Sir Henry Dale Fellowship which was budgeted over £1,000,000).  <b>Journals:</b> Bioinformatics, BMC Bioinformatics, Algorithmica, Information Processing Letters (IPL), Nature Medicine [sub-reviewer], Genome Research [sub-reviewer].  <b>Conferences:</b> Intelligent Systems for Molecular Biology (ISMB), International Conference on Research in Computational Molecular Biology (RECOMB), RECOMB satellite workshop on sequencing (RECOMB-seq), Combinatorial Pattern Matching (CPM), IEEE International Conference on Bioinformatics and Biomedicine (BIBM), String Processing and Information Retrieval (SPIRE), Asia Pacific Bioinformatics Conference (APBC), Pacific Symposium on Biocomputing (PSB), ACM-SIAM Symposium on Discrete Algorithms (SODA), Approx-Random, European Symposium on Algorithms (ESA), IEEE International Parallel and Distributed Processing Symposium (IPDPS), GIW/InCoB, The ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)	
<b>Program Committee</b>	<b>ISMB/ECCB 2015</b> , Dublin, Ireland, Jul 10-14, 2015. Program Committee <b>Genome Medicine 2015</b> , Ho Chi Minh City, Vietnam, Jul 20-23, 2015. Program Committee <b>GIW/InCoB 2015</b> , Tokyo, Japan, Sep 9-11, 2015. Program Committee	
<b>Technical Skills</b>	C/C++, Python, Linux, Shell script, L <sup>A</sup> T <sub>E</sub> X	
<b>Citizenship &amp; Immigration</b>	Canada: citizen. USA: permanent resident.	



## **Press**

**July 8, 2014:** Brown CS And CCMB To Enjoy Record Participation At ISMB 2014. **CS Brown**

**March 14, 2014** Iman Hajirasouliha Receives NSERC Fellowship. **CS Brown News**

**November 8, 2012:** Scientists find more genome variants **SFU News** article on our contribution to map the largest and most varied number of human genomes to date.

**October 31, 2012:** Bigger human genome pool uncovers more rare variants. **SFU Public Affairs and Media Relations** story on my contribution to our 1000 Genomes Nature paper.

**December 14, 2011:** Human genome research leaps ahead at SFU **SFU Public Affairs and Media Relations** story on our Genome Research paper.

**November 8, 2010:** SFU researchers help map human variation **The Peak** story on our contribution to the 1000 Genomes Project (See page 7 of the newspaper).

**October 28, 2010:** SFU behind genetic leap **SFU Public Affairs and Media Relations** story on our contribution to the 1000 Genomes Project.

## **References**

Available upon request