

Iman Hajirasouliha, Ph.D.

Last modified: October 2, 2018

Contact Information

1305 York Avenue (Room: 13.08, Box: 140)
New York, NY 10021
imh2003@med.cornell.edu
www.imanh.org

Work Experience

Weill Cornell Medical College of Cornell University, New York, NY, USA

Assistant Professor (tenure-track) of Computational Genomics **Sep 2016 – present**
Department of Physiology and Biophysics
Institute for Computational Biomedicine
Englander Institute for Precision Medicine
Meyer Cancer Center

University of California at Berkeley, Berkeley, CA, USA

Simons Institute Research Fellow (mentor: Ron Shamir) **Jan 2016 – May 2016**

Department of Computer Science, Stanford University, Stanford, CA, USA

Post Doctoral Research Scholar (advisor: Serafim Batzoglou) **Jul 2014 – Jul 2016**

Department of Computer Science, Brown University, Providence, RI, USA

Post Doctoral Research Associate (advisor: Ben Raphael) **Jan 2013 – Jun 2014**

Education

Simon Fraser University, Burnaby, BC, Canada

Ph.D. in Computing Science (Senior Supervisor: S. Cenk Sahinalp) **Jan 2008 – Sep 2012**
• Thesis: Algorithms for structural variation discovery and protein-protein interaction prediction ◊ My dissertation was noted "exceptional" by the external examiner.

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

Sharif University of Technology, Tehran, Iran

B.Sc. in Computer Engineering **Sep 2001 – Jul 2005**
• Thesis: Selfish Routing

Trainings and other Research Experience

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. H Toosi, A Moeini and **I Hajirasouliha**

BAMSE: Bayesian model selection for tumor phylogeny inference among multiple tumor samples **BMC special issue in BMC Genomics or BMC Bioinformatics**. (2018) In Press.

2. C Ricketts, V Popic, H Toosi, **I Hajirasouliha**

Using LICHeE and BAMSE for Reconstructing Cancer Phylogenetic Trees
Current protocols in bioinformatics (2018) e49

3. P Khosravi, E Kazemi, M Imielinski, O Elemento, **I Hajirasouliha**

Deep convolutional neural networks enable discrimination of heterogeneous digital pathology images
EBioMedicine (2017) 27, 317-328

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

Fast and scalable inference of multi-sample cancer lineages.
Genome Biology (2015) May 6;16(1):91.

5. 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

6. **Hajirasouliha I.**, Mahmoody A. and Raphael BJ.

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

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

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

8. 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.

9. 1000 Genomes Project Consortium.

An integrated map of genetic variation from 1,092 human genomes.
Nature (2012) Nov 1;491(7422):56-65.

10. Lapuk AV, Wu C, Wyatt AW, McPherson A, McConeghy BJ, Brahmhatt 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.

11. **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.

12. Chunxiao Wu, Alexander W Wyatt, Anna V Lapuk, Andrew McPherson, Brian J McConeghy, Robert H Bell, Shawn Anderson, Anne Haegert, Sonal Brahmhatt, 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

13. 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.

14. 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).

15. 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.

16. 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. Nemes, 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. Korb on behalf of the 1000 Genomes Project.

Mapping copy number variation at fine-scale by population-scale genome sequencing

Nature 2011, 470: 59-65.

17. 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.

18. 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

19. 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.
20. **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.
21. Rahele Salari, Cagri Aksay, Emre Karakoc, Peter Unrau, **Iman Hajirasouliha**, and S. Cenk Sahinalp
smyRNA: A novel ab initio ncRNA gene finder
PLoS ONE, (5): e5433, doi:10.1371/journal.pone.0005433, May 2009
22. **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.
23. 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. S Ciccolella, MS Gomez, M Patterson, G Della Vedova, **I Hajirasouliha**, P Bonizzoni
gpps: An ILP-based approach for inferring cancer progression with mutation losses from single cell data
ICCABS 2018, 8th IEEE International Conference on Computational Advances in Bio and Medical Sciences, Las Vegas, NV, October 18-20, 2018.
(Also, invited for BMC journal special issue.)
2. C Ricketts, D Seidman, V Popic, F Hormozdiari, S Batzoglou and **I Hajirasouliha**
Meltos: Multi-Sample Tumor Phylogeny Reconstruction for Structural Variants
RECOMB-CCB 2018, RECOMB-Computational Cancer Biology, Paris, April 19-20 , 2018.
(Also, invited and under minor revision at the journal **Bioinformatics**.)
3. S Ciccolella, MS Gomez, M Patterson, G Della Vedova, **I Hajirasouliha**, P Bonizzoni
Inferring Cancer Progression from Single Cell Sequencing while allowing loss of mutations
RECOMB-CCB 2018, RECOMB-Computational Cancer Biology, Paris, April 19-20 , 2018.
4. ‡ Hosein Toosi, Ali Moeini and **Iman Hajirasouliha**
BAMSE: Bayesian model selection for tumor phylogeny inference among multiple tumor samples **ICCABS 2017**, 7th IEEE International Conference on Computational Advances in Bio and Medical Sciences, Orlando, FL, October 19-21, 2017.
5. ‡ **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.
6. ‡ **Iman Hajirasouliha**, Ahmad Mahmoody 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**).

7. 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).
8. 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).
9. 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).
10. † 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).
11. 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).
12. 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).
13. † **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).
14. Phuong Dao, Alexander Schönhuth, 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.
15. **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).
16. † 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).

17. 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*).

18. ‡ **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 Subramanian and Ananth Grama; Springer, 1st Edition (September 30, 2011)

Manuscripts I am dedicated to make scientific publications available as soon as possible. Below is a list of preprints posted on bioRxiv that are currently under review at different journals.

1. P Khosravi, E Kazemi, Q Zhan, M Toschi, JE Malmsten, C Hickman, M Meseguer, Z Rosenwaks, O Elemento, N Zaninovic, **I Hajirasouliha**
Robust Automated Assessment of Human Blastocyst Quality using Deep Learning
Preprint Available: bioRxiv, 394882

2) NH Motlagh, M Jannesary, HR Aboulkheyr, P Khosravi, O Elemento, M. Totonchi, **I. Hajirasouliha**
Breast Cancer Histopathological Image Classification: A Deep Learning Approach
Preprint Available: bioRxiv, 242818

3) Ciccolella, MS Gomez, M Patterson, G Della Vedova, **I Hajirasouliha**, P Bonizzoni
Inferring Cancer Progression from Single Cell Sequencing while allowing the loss of mutations
Preprint Available: bioRxiv, 268243

4) Karaoglanoglu, C Ricketts, ME Rasekh, E Ebrein, **I Hajirasouliha***, C Alkan*
Characterization of segmental duplications and large inversions using Linked-Reads
Preprint Available: bioRxiv, 394528 (* Joint Last Author)

5) S Ciccolella, MS Gomez, M Patterson, G Della Vedova, **I Hajirasouliha**, P Bonizzoni
gpps: An ILP-based approach for inferring cancer progression with mutation losses from single-cell data
Preprint Available: bioRxiv, 365635

6) DC Danko, D Meleshko, D Bezdán, C Mason, **I Hajirasouliha**
Minerva: an alignment and reference free approach to deconvolve linked-reads for metagenomics
Preprint Available: bioRxiv, 217869 (provisionally accepted in *Genome Research*)

7) S Malikic, S Ciccolella, FR Mehrabadi, C Ricketts, MK Rahman, E. Haghshenas, D. Seidman, F Hach, **I Hajirasouliha***, SC Sahinalp*
PhISCS-A Combinatorial Approach for Sub-perfect Tumor Phylogeny Reconstruction via Integrative use of Single Cell and Bulk Sequencing Data
Preprint Available: bioRxiv, 376996 (* Joint Last Author)

Other submitted manuscripts 1) D Meleshko, H Mohimani, V Tracanna, **I Hajirasouliha**, MH Medema, A Korobeynikov, PA Pevzner
BiosyntheticSPAdes: Reconstructing Biosynthetic Gene Clusters From Assembly Graphs

Patents Integrated framework for evaluating human embryos using AI (US Patent Application Filed)

Honours and Awards	◇ Simons-Berkeley Research Fellowship	2016
	◇ NSERC Postdoctoral Fellowships	2014–2016
	◇ NSERC-CGS Michael Smith Foreign Study Supplements	2012
	◇ NSERC Alexander Graham Bell Canada Graduate Scholarship	2010–2012
	◇ Simon Fraser University Graduate Fellowship	2012
	◇ Best Paper Award , ISMB-HiTSeq	2011
	◇ Ebco/Eppich Graduate Scholarship in Intelligent Systems	2011
	◇ Brian J. Blaha Memorial Annual Graduate Scholarship in Computing Science (\$1,000)	2009
	◇ SFU Computing Science Graduate Scholarships	2008
	◇ SFU Computing Science Graduate Scholarships	2007
	◇ Simon Fraser University, Entrance Scholarships	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!	

Teaching Experience	Course Director and Instructor , Weill Cornell Medicine, NY, USA	
	• Data Structure and Algorithms for Computational Biology	Fall 2018
	Co-Instructor , Weill Cornell Medicine, NY, USA	
	• Seminar and journal club, Tri-I Computational Biology & Medicine	Fall 2017-18, Spring 2018-19.
	Tutorial Instructor , ACM-BCB 2015, Atlanta, GA, USA	
	• Computational methods for analyzing intra-tumor heterogeneity	September 2015
	Guest Lecturer , Stanford University, CA, USA	
	• CS262-Computational Genomics (Prof. Serafim Batzoglou)	Winter 2016
	• CS262-Computational Genomics (Prof. Serafim Batzoglou)	Winter 2015
	Guest Lecturer , RI-INBRE Bioinformatics Core, University of Rhode Island, RI, USA	
	• Bioinformatics (Dr. Hany Alashwal)	Spring 2014
	Guest Lecturer , Department of Computing Science, SFU, BC, Canada	
	• Bioinformatics Algorithms (Prof. Cenk Sahinalp)	Fall 2012
	Teaching Assistantship , Simon Fraser University, BC, Canada	
	• Bioinformatics Algorithms	Fall 2009
	• Data Communications and Networking	Fall 2009
	• Data Communications and Networking	Summer 2007
	• Introduction to Internet and Multimedia	Fall 2006
• Introduction to Internet and Multimedia	Spring 2006	
• Introduction to Computer Science	Fall 2005	
Teaching Assistantship , Sharif University of Technology, Tehran, Iran		
• Data Structures and Algorithms	Fall 2004	
• Design and Analysis of Algorithms	Spring 2004	
• Data Structures and Algorithms	Fall 2003	
• Discrete Structures	Spring 2003	
• Discrete Structures	Fall 2002	
Instructor and Head of summer camp , Iranian National Olympiad in Informatics (INOI), 2003		
• Thought a summer long course on Combinatorial Problem Solving		
• Coordinated trainers and teaching material, made teaching schedule, planned and held exams to select the national olympiad team.		

I attend and/or present at a few major international conferences in computational biology each year. I also occasionally visit selected institutes and give research talks.

**Accepted
Conference
Presentations**

Listed only those papers that I was the presenting author

Deep convolutional neural networks enable discrimination of heterogeneous digital pathology images

- Highlight Talk at RECOMB-CCB, Paris, France, April 2018

Bayesian model selection for tumor phylogeny inference among multiple samples

- ICCABS, Orlando, FL, USA, October 2017

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

- ISMB-HiTSeq (High Throughput Sequencing Analysis and Algorithms), Dublin, Ireland, Jul 2015

Reconstructing mutational history in multiply sampled tumors using perfect phylogeny mixtures

- The 14th Workshop on Algorithms in Bioinformatics (WABI), Wroclaw, Poland, Sep 2014

A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data

- The 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston, MA, Jul 2014

Simultaneous structural variation discovery among multiple sequenced genomes

- The 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB), Vancouver, Canada, Mar 2011

Detection of locus and content of novel sequence insertions

- ISMB-HiTSeq (High Throughput Sequencing Analysis and Algorithms), Boston, USA, Jul 2010

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

Accepted Poster Presentations *Only those posters that I was the presenter are listed here.*

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

- ASHG 2015, Baltimore, MD, USA Oct 2015
◊ Reviewers' Choice Abstract. Selected among the top 10% of poster abstracts, by topic as determined by the reviewers' scores.

A combinatorial approach for analyzing intra-tumor heterogeneity

- RECOMB 2014, Pittsburgh, PA, USA Apr 2014

A combinatorial approach for constructing ancestral history of tumors

- Genome Informatics, Cold Spring Harbor, NY, USA Oct 2013

Detection of locus and content of novel sequence insertions

- PIMS-IGTC annual summit, Naramata, BC, Canada Oct 2012
- Annual Frontiers in Biophysics conference, Simon Fraser University, BC, Canada Mar 2010

Invited talks at conferences/ workshops	Tumor phylogeny reconstruction using bulk and single cell sequencing data	
	• Cancer, Development and Complexity Workshop, Como Lake, Italy	May 2018
	Genomic characterization and applications of read-cloud sequencing technologies	
	• Algorithmic Challenges in Genomics Reunion, University of California, Berkeley, CA	Jun 2017
	Combinatorial approaches for analyzing intra-tumor heterogeneity from NGS data	
	• Models for Oncogenesis, Clonality and Tumor Progression, OSU, Columbus, OH	Sep 2016
	Leveraging tumor lineage trees to predict and genotype somatic structural variations using paired-end sequencing	
	• Bioinformatics & Genomic Medicine, HoChiMinh City, Vietnam	Jul 2015
	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	
	• The 21st International Symposium on Mathematical Programming (ISMP), Berlin, Germany	Aug 2012
Invited talks at Institutes	TBD	
	• Department of Computational Biology, Carnegie Mellon University, Pittsburgh, PA	Jan 2019
	Computational methods for characterizing large-scale structural variations human genome variations and tumor phylogenies	
	• Department of Computer Science, University of Milano-Bicocca, Italy	May 2018
	Computational methods for characterizing large-scale human genome variations with applications to cancer	
	• Institute for Genomics and Multiscale Biology, Mount Sinai, NY	Nov 2016
	• Institute for Precision Medicine, WCM, Cornell University, NY	Sep 2016
	• Department of Computer Engineering, Sharif University, Tehran, Iran	Aug 2016
	• Institute for Research in Fundamental Sciences, Tehran, Iran	Aug 2016
	• Department of Computer Science, University of Central Florida, FL	Mar 2016
	• Institute for Computational Biomedicine, WCM, Cornell University, NY	Mar 2016
	• The Jackson Laboratory, Bar Harbor, ME	Mar 2016
	• Institute for Precision Medicine, UNLV, Las Vegas, NV	Mar 2016
• MIR/BMI Seminar, University of Wisconsin Madison, WI	Mar 2016	
• Toyota Institute at the University of Chicago (TTIC), Chicago, IL	Feb 2016	
• Department of Computer Science, University of Florida, FL	Feb 2016	
• Simons Institute, University of California, Berkeley, CA	Feb 2016	
• Department of Computer Science, Stanford University, CA	Feb 2016	
	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
	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
	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

Memberships

The Cancer Genome Atlas Lung Adenocarcinoma (TCGA-LUAD) group	2017 - present
TCGA Heterogeneity and Tumor Evolution group	2017 - present
10x Genomics Metagenomic Consortium	2017 - present
Genome in a Bottle Consortium (GIAB)	2015 - present
The 1000 Genomes Project, Structural Variation Group	2009 - 2012
The 1000 Genomes Project, Analysis Group	2009 - 2012
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

Mentoring Experience

Zakieh Tayyebi, Rotating PhD student (Tri-I CBM)	Since Summer 2018
Vianne Gao, Rotating PhD student (Tri-I CBM)	Since Summer 2018
Xiang (Steve) Niu, PhD student (Tri-I CBM)	since April 2018
Dmitrii Meleshko, PhD student (Tri-I CBM)	since August 2017
Pegah Khosravi, Postdoc Fellow	Since April 2017
David Danko, Rotating PhD student (Tri-I CBM)	Since April 2017
Camir Rickets, PhD student (Tri-I CBM)	Since November 2016
Hongyi Xin, visiting Ph.D. student from Carnegie Mellon University	Since October 2017
Simone Ciccolella, visiting M.Sc student from University of Milan	August-October 2017
Daniel Seidman, Rotating PhD student (Tri-I CBM)	May-July 2017
Nicole Lustgarten, Rotating PhD student (PBSP)	March-May 2017
Aditya Deshpande, Rotating PhD student (Tri-I CBM)	March-May 2017

Thesis Committee

Syed Ali Ahmed, <i>City University of New York (CUNY)</i>	PhD thesis examiner (2017)
Hongyi Xin, <i>Carnegie Mellon University (CMU)</i>	PhD advisory committee (2017)
Jamal Elkhader, <i>Weill Cornell Medical College</i>	PhD ACE committee (2017)
Xiaotong Yao, <i>Weill Cornell Medical College</i>	PhD ACE committee (2017)
Kevin Matthew Hadi, <i>Weill Cornell Medical College</i>	PhD ACE committee (2017)

Program Committee **ACM-BCB 2018**, Washington, D.C., Aug 29-Sep 1, 2018.
ISMB 2018, Chicago, Illinois, USA, July 6-10, 2018.
WABI 2018, Helsinki, Finland, August 20-24, 2018.
RECOMB-SEQ 2018, Paris, France, Apr 19-20, 2018.
ICCABS 2017, Orlando, FL, USA Oct 18-21, 2017.
ACM-BCB 2017, Boston, MA, August 20-23, 2017.
WABI 2017, Boston, MA, August 20-23, 2017.
ISMB/ECCB 2017, Prague, Czech Republic, July 21-25, 2017.
RECOMB-SEQ 2017, Hong Kong, China, May 7-8, 2017.
GIW 2016, Shanghai, China Oct 4-6, 2016.
ISMB 2016, Orlando, Florida, July 8-12, 2016.
RECOMB-CCB 2016, UCLA Campus, California, April 16-17, 2016.
AlCoB 2016, Trujillo, Spain, June 21-23, 2016.
GIW/InCoB 2015, Tokyo, Japan, Sep 9-11, 2015.
ISMB/ECCB 2015, Dublin, Ireland, Jul 10-14, 2015.
Genome Medicine 2015, Ho Chi Minh City, Vietnam, Jul 20-23, 2015.

Reviews **Grants:** The Wellcome Trust and Royal Society of the UK. (reviewed a Sir Henry Dale Fellowship which was budgeted over £1,000,000). NSF Panel Review, Information and Intelligent Systems (2017)

Journals: Genome Research, Genome Biology, Bioinformatics, BMC Bioinformatics, Algorithmica, Information Processing Letters (IPL), IEEE/ACM Transactions on Computational Biology and Bioinformatics, Nature Medicine [sub-reviewer], Genome Research [sub-reviewer].

Conferences: 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)

Technical Skills C/C++, Python, Linux, Shell script, L^AT_EX

Press **August 24, 2018:** EIPM and ICB Team Translates AI Benefits to In-Vitro Fertilization. **EIPM Weill Cornell Medicine**

February 9, 2018: Artificial Intelligence Aids in Cancer Diagnosis. **Weill Cornell Medicine**

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.

Active Grants • National Science Foundation (NSF) Award Number:1840275
 • NVIDIA GPU Grant

08/15/18-07/31/20
10/17/17

References Available upon request