BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Iman Hajirasouliha, PhD	**Postdoctoral Research Scholar of Computer Science, Stanford University**
eRA COMMONS USER NAME (credential, e.g., agency login) IHAJIRASOULIHA	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Sharif University of Technology, Iran	B.Sc.	07/05	Computer Engineering
Simon Fraser University, Canada	M.Sc.	12/07	Computing Sciences
Simon Fraser University, Canada	PhD	09/12	Computing Sciences
Brown University, Providence, RI, USA	Postdoc	06/14	Computer Science

A. PERSONAL STATEMENT

I am passionate about applications of computational and mathematical methods to molecular biology. My training is in computer science and I have been focused on computational genomics (including cancer genomics) and biomolecular sequence analysis in recent years. My postdoctoral plans include understanding cancer genomes and evolution, and work on related computational biology problems. I have also experience in analyzing large-scale genomic data sets, and developed several methods for detecting structural variations in sequenced genomes. I was a participant in the 1000 Genomes Project, an ambitious international effort to map human structural variations with fine resolution. Since the launch of the project, I presented my results and contributed as a co-author to three papers in the journal Nature. My research is highly collaborative and I worked with genome scientists and cancer biologists on many recent projects. You can see the highlight of those collaborations in the Publications Section.

B. POSITIONS AND HONORS

Positions and Employment

2013-2014 Postdoctoral Research Associate, Dept of Computer Science and Center for Computational Molecular Biology, Brown University
2014 - Postdoctoral Research Scholar, Dept of Computer Science, Stanford University

Teaching, Other Experience, and Professional Memberships (recent)

2009 - Member of the 1000 Genomes Project, Structural Variation and Analysis Groups
2008 - Member of the International Society for Computational Biology

Honors

2016 Simons-Berkeley Research Fellowships
2014-2016 NSERC Postdoctoral Fellowship
2012 NSERC-CGS Michael Smith Foreign Study Supplements
2010-2012 NSERC Alexander Graham Bell Canada Graduate Scholarship

C. SELECTED PEER-REVIEWED PUBLICATIONS

1. Popic V, Salari R, Hajirasouliha I, Kashef-Haghighi D, West RB, Batzoglou S. (2014) Fast and scalable inference of multi-sample cancer lineages. **Genome Biol.** 2015 May 6;16(1):91.

2. Hajirasouliha I, Mahmoody A, Raphael BJ (2014) A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data. **Bioinformatics**. 30(12):i78-86.

3. Wu HT, Hajirasouliha I, Raphael BJ (2014) Detecting independent and recurrent copy number aberrations using interval graphs. **Bioinformatics.** 30(12):i195-203..

4. Marschall T, Hajirasouliha I, Schönhuth A (2013) MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. **Bioinformatics**. 29(24):3143-50.

5. 1000 Genomes Project Consortium (2012) An integrated map of genetic variation from 1,092 human genomes. **Nature.** 491(7422) 56-65.

6. Lapuk AV et al. (2012) From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. **J Pathol.** 227(3):286-97.

7. Hajirasouliha I, Schönhuth A, de Juan D, Valencia A, Sahinalp SC (2012) Mirroring co-evolving trees in the light of their topologies. **Bioinformatics.** 28(9):1202-8.

8. Wu C et al. (2012) Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer. **J Pathol.** 227(1):53-61.

9. Hormozdiari F, Hajirasouliha I, McPherson A, Eichler EE, Sahinalp SC (2011) Simultaneous structural variation discovery among multiple paired-end sequenced genomes. **Genome Res.** 21(12):2203-12.

10. McPherson A, Wu C, Hajirasouliha I, Hormozdiari F, Hach F, Lapuk A, Volik S, Shah S, Collins C, Sahinalp SC (2011) Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. **Bioinformatics.** 27(11):1481-8.

11. Mills RE et al. (2011) Mapping copy number variation by population-scale genome sequencing. **Nature**. 470(7332):59-65.

12. Hormozdiari F, Alkan C, Ventura M, Hajirasouliha I, Malig M, Hach F, Yorukoglu D, Dao P, Bakhshi M, Sahinalp SC, Eichler EE (2011) Alu repeat discovery and characterization within human genomes. **Genome Res.** 21(6):840-9.

13. 1000 Genomes Project Consortium (2010) A map of human genome variation from population-scale sequencing. **Nature**. 467(7319):1061-73.

14. Hormozdiari F, Hajirasouliha I, Dao P, Hach F, Yorukoglu D, Alkan C, Eichler EE, Sahinalp SC (2010) Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. **Bioinformatics.** 26(12):i350-7.

15. Hajirasouliha I, Hormozdiari F, Alkan C, Kidd JM, Birol I, Eichler EE, Sahinalp SC (2010) Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. **Bioinformatics.** 26(10):1277-83.

16. Hajirasouliha I, Hormozdiari F, Sahinalp SC, Birol I (2008) Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. **Bioinformatics.** 24(13):i32-40.

17. Alon N, Dao P, Hajirasouliha I, Hormozdiari F, Sahinalp SC (2008) Biomolecular network motif counting and discovery by color coding. **Bioinformatics.** 24(13):i241-9.