سخنرانی علمی

Computational methods for characterizing large-scale human genome variations with applications to cancer

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We may be at the cusp of major leaps in personal genome and cancer genome interpretation over the next several years, with profound impact in human health. Large-scale projects based on Next Generation Sequencing technologies have been sequencing thousands of individual genomes and the technologies enabled the sequencing of many cancer genomes and multiple tumor samples from cancer patients. In this talk, I will present some of my major contributions during my Ph.D. and postdoctoral training for characterizing human genomes. In particular, I will present algorithms for detecting various types of large-scale structural variations in sequenced genomes, including NovelSeq, a state-of-the-art method for detecting novel sequence insertions, Next-generation Variation Hunter, a computational method for identifying Mobile Element Insertions (MEI), and CommonLAW, a combinatorial framework for detecting Structural Variations in multiple genomes.

I will also discuss applications of those methods for analyzing cancer genomes and will present computational problems related to the evolution of somatic mutations and intra-tumor heterogeneity. I will present novel algorithms for reconstructing tumor lineage trees and detecting somatic structural variations and will discuss several future directions. These studies are considered first

necessary steps for understanding tumor genomics landscape and the challenges in biomarker development.

Bio:

Starting September 2016, Iman Hajirasouliha will be Assistant Professor of Computational Genomics in the Institute for Computational Biomedicine at Weill Cornell Medicine of Cornell University and a member of the Institute for Precision Medicine. He recently completed a Postdoctoral Scholarship at the Computer Science Department, Stanford University, and a Simons Research Fellowship at the University of California, Berkeley. His research focuses on computational genomics, large-scale sequence analysis, and characterizing somatic variations and intra-tumor heterogeneity in cancer.

Iman received his B.Sc. in Computer Engineering from Sharif University and his M.Sc. in Computing Science from Simon Fraser University (SFU). He obtained his Ph.D. with Exceptional Recognition from SFU and also held a postdoctoral appointment at Brown University. During his Ph.D., Iman was also a student collaborator at Canada's Michael Smith Genome Sciences Centre and a visiting scholar at the Department of Genome Sciences, University of Washington.

Iman received an NSERC Alexander Graham Bell Canada Graduate Scholarship (CGS-D), the best paper award at ISMB-HitSeq 2011, an NSERC Postdoctoral Fellowship and a Simons-Berkeley Research Fellowship. He is on the program committee of several bioinformatics conferences, including ISMB and RECOMB-CCB.

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