Spring 2016 Seminar Series

ALGORITHMS FOR CHARACTERIZING INTRA-TUMOR HETEROGENEITY IN CANCER GENOMES

MONDAY, APRIL 18, 2016 ● 10:00 AM – HEC 438

Next-generation sequencing (NGS) technologies have enabled the sequencing of many cancer genomes. Recent studies of tumor samples have shown that most tumors exhibit extensive intra-tumor heterogeneity, with multiple subpopulations of tumor cells containing different somatic mutations. In this talk, I will discuss several recent computational methods for the purpose of characterizing intra-tumor heterogeneity. In particular, I will present novel algorithms for inferring clonal evolution and reconstructing tumor phylogenies from single or multiple NGS samples.

DR. IMAN HAJIRASOULIHA
Stanford University

Iman Hajirasouliha is a postdoctoral scholar at the Computer Science Department, Stanford University, and a Simons Research Fellow 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). Prior to moving to the bay area, he obtained his Ph.D. with Exceptional Recognition from SFU and 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.

Hosted by: Dr. Gary Leavens