VanBUG
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presents Guest Speaker:

Ben Raphael

Associate Professor of Computer Science, Brown University

Computational Analysis of Mutational Heterogeneity in Cancer Genomes

Recent sequencing projects have demonstrated that somatic mutations in cancer genomes are highly heterogeneous. This mutational heterogeneity is apparent on two levels. First, individual cells within a tumor typically have different complements of somatic mutations. Second, different individuals with the same type of cancer often exhibit different combinations of causal, or driver, mutations. We describe algorithms to address both of these sources of heterogeneity. In the first case, we present an algorithm to infer clonal and subclonal copy number aberrations in the presence of admixture by normal (non-cancerous) cells. In the second case, we describe two algorithms to identify driver pathways, groups of genes containing driver mutations, in a large cohort of cancer samples. The first algorithm, HotNet, uses prior information about interactions between genes and identifies subnetworks of a genome-scale interaction network that are recurrently mutated. The second algorithm, Dendrix, optimizes a measure derived from the statistical properties of mutations on driver pathways. We apply these algorithms to genome/exome sequencing and array copy number data from several cancer types in The Cancer Genome Atlas (TCGA). We identify both known pathways and novel combinations of mutations, the latter suggesting previously uncharacterized interactions, or crosstalk between pathways.

Introductory speaker (10 mins):

Andrew Roth
Shah Lab, BC Cancer Research Centre

Studying the Evolutionary Dynamics of Cancer Using Next Generation Sequencing

Thursday, November 8th, 2012, 6:00 pm

Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue

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