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Friday, December 9, 2016
12:00-1:00 p.m.
Biotech Auditorium

Bayesian inference of intra-tumor heterogeneity based on next-generation sequencing data

Abstract: I will cover a suite of tools that we developed for the inference of intra-tumor heterogeneity using next-generation sequencing data. The goal is to infer the subpopulations of tumor cells and normal cells in a set of tumor samples. Each subclone is defined as a set of unique mutation events, such as sequence or structure mutations. We develop feature allocation models, namely extensions of the Indian buffet process, to capture the mutational structure of the subclones. Heavy biology is used to facilitate prior modeling which helps improves inference. Also, a couple of computational techniques, including a training/testing set split in the Markov chain Monte Carlo simulations and parallel tempering facilitates the mixing of Markov chains in the posterior inference. Examples will be given to demonstrate the utility of the Bayesian inference for understanding the tumor subclonal structure.