

The Department of Computational and Systems Biology  
presents...

Special Seminar



10:30 am Thursday, November 19, 2015  
Room 3073, Biomedical Science Tower 3

## Deciphering Cancer Biology using Boolean Methods

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Cancer is a complex disease characterized by a large number of point mutations, large structural changes and epigenetic dysregulation. Cancer genome sequencing projects such as The Cancer Genome Atlas (TCGA) have profiled tens of different tumor types with hundreds of samples per tumor type. These projects have demonstrated convincingly that cancer genomes exhibit considerable heterogeneity among different individuals. New analytical techniques are needed to extract common biological principles from massive amounts of data to provide useful mechanistic insights about cancer and thereby guide effective therapy.

I will present Boolean implications, a new data mining method that can be used to mine large, heterogeneous cancer data sets and demonstrate its application to derive new actionable hypotheses with the potential for biological discovery and targeted therapy. First, I will describe the use of Boolean implications to understand the role of a common mutation in leukemia in driving aberrant DNA hypermethylation, which subsequently led to the identification of a targeted therapy for patients with the mutation. In the second half of my talk, I will describe MiSL, a new method for mining synthetic lethal partners of recurrent cancer mutations by analyzing pan-cancer primary tumor data. Initial results are promising, and indicate that MiSL can be widely applicable and can greatly accelerate target discovery for cancer-specific mutations.

Host: Jim Faeder ([faeder@pitt.edu](mailto:faeder@pitt.edu))