

# On April 25, 2013, PED Seminar Series Presents

## Passenger mutation rates in cancer: why they are important and how they can be investigated?

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Important progress has been made in our understanding of cancer thanks to the ever growing amount of data originated by sequencing technologies. The integration of mathematical modeling and statistical analysis with sequencing and clinical data represents a new powerful approach for better understanding the evolutionary dynamics of cancer, and for implementing quantitative approaches to cancer classification and treatment.

In this talk, we will present some of the stochastic models we have formulated in order to shed light on various processes of accumulation of somatic mutations in cancer. For example, a mathematical model - where, for the first time, all relevant phases of a tissue's history are considered - makes unexpected predictions, validated by the analysis of sequencing data, on the number of somatic mutations that occur prior to the onset of neoplasia, in tumors of self-renewing tissues. It also provides a novel way to estimate the in-vivo tissue-specific somatic mutation rates from the sequencing data of tumors.