Stochastic modeling of the accumulation of passenger and driver mutations in cancer

Cristian Tomasetti[1]

Abstract

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 I will present some of the stochastic models I 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.

---

[1]Department of Biostatistics, Harvard School of Public Health, and Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, MA, USA