Cancer is the result of a stochastic evolutionary process characterized by the accumulation of mutations that are responsible for tumor growth, immune escape, and drug resistance, as well as mutations with no effect on the phenotype. Stochastic modeling can be used to describe the dynamics of tumor cell populations and to obtain insights into the hidden evolutionary processes leading to cancer. I will present recent approaches that use branching process models of cancer evolution to quantify intra-tumor heterogeneity and the development of drug resistance, and their implications for interpretation of cancer sequencing data and the design of optimal treatment strategies. (Received February 01, 2018)