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Marek Kimmel* (kimmel@rice.edu), **Khanh N Dinh** and **Roman Jaksik**, , Poland, **Amaury Lambert**, , France, and **Simon Tavaré**. *Statistical inference for the evolutionary history of cancer genomes*.

Recent years have produced a large amount of work on inference about cancer evolution from mutations identified in cancer samples. Much of the modeling work has been based on classical models of population genetics, generalized to accommodate time-varying cell population size. Reverse-time genealogical views of such models, commonly known as coalescents, have been used to infer aspects of the past of growing populations. Another approach is to use branching processes, the simplest scenario being the linear birth-death process (lbdp), a binary fission Markov age-dependent branching process. A genealogical view of such models is also available. The two approaches lead to similar but not identical results. In this paper, we examine how the statistics based on birth-death processes differ from those based on the coalescent model. We also present a model of tumor evolution with selective sweeps, based on coalescence, and demonstrate how it may help in understanding the past history of tumor as well the influence of data pre-processing. We illustrate the theory with applications to several examples of The Cancer Genome Atlas tumors. (Received March 01, 2020)