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Julia Chifman* (chifman@american.edu) and **Laura Kubatko**. *Modeling the Evolutionary History of a Tumor Given Single-Cell Sequencing Data*. Preliminary report.

Advances in genomic technologies and specifically in single-cell sequencing have made cancer evolution a central topic among researchers, resulting in a great need for accurate computational models and methods that are able to produce realistic pictures of the diversity of cancer. The idea of tumor progression as an evolutionary process driven by somatic mutations and clonal expansions was established in the late 1970's, and thus insights into the complexity of cancer can be gained using classical evolutionary principles. We present a model that computes true site pattern genotype probabilities on the tumor tree by using a finite-sites continuous-time Markov model together with a model for single-cell sequencing errors and explore the mathematical properties of this model, such as rank conditions of flattenings of the 4-dimensional probability distribution. We evaluate the performance of the proposed method for the genotype model using simulation and empirical data. (Received January 23, 2018)