Genetic Composition of Supercritical Branching Populations under Rare Mutation Rates

Vianney Brouard*[1]

[1]UMPA – Université de Lyon, ENS de Lyon – France

Résumé

We aim at understanding the evolution of the genetic composition of cancer cell populations. To this aim, we consider a branching individual based model representing a cell population where cells divide, die and mutate along the edges of a finite directed graph (V,E). The process starts with only one cell of trait 0. Following typical parameter values in cancer cell populations we study the model under large population and rare mutations limit, in the sense that the mutation probabilities are parameterized by negative powers of n and the typical sizes of the population of our interest are positive powers of n. Under {non-increasing growth rate condition} (namely the growth rate of any sub-population is smaller than the growth rate of trait 0), we describe the time evolution of the first-order asymptotics of the size of each sub-population on the $log(n)$ time scale, as well as in the random time scale at which the initial population, resp. the total population, reaches the size n^{t}. In particular, such results allow to characterize whose mutational paths along the edges of the graph are actually contributing to the size order of the sub-populations. Up to our knowledge, it is the first time that a model considering the large population rare mutations limit captures the first-order asymptotics of the size of the sub-populations. Without any condition on the growth rate, we describe the time evolution of the orders of magnitude of each sub-population. Adapting techniques from Durrett and Mayberry 2011, we show that these converges to positive deterministic non-decreasing piecewise linear continuous functions, whose slopes are given by an algorithm.

Mots-Clés: cancer evolution, multitype branching processes, finite graph, long time behavior, rare mutation rates, population genetics

*Intervenant