

Controlled branching processes in Biology: a model for cell proliferation

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Branching processes are relevant models in the development of theoretical approaches to problems in applied fields such as, for instance, growth and extinction of populations, biology, epidemiology, cell proliferation kinetics, genetics and algorithm and data structures. The most basic model, the so-called Bienaymé-Galton-Watson process, consists of individuals that reproduce independently of the others following the same probability distribution, known as offspring distribution. A natural generalization is to incorporate a random control function which determines the number of progenitors in each generation. The resulting process is called controlled branching process.

In this talk, we deal with a problem arising in cell biology. More specifically, we focus our attention on experimental data generated by time-lapse video recording of cultured *in vitro* oligodendrocyte cells. In A.Y. Yakovlev et al. (2008) (Branching Processes as Models of Progenitor Cell Populations and Estimation of the Offspring Distributions, *Journal of the American Statistical Association*, 103(484):1357–1366), a two-type age dependent branching process with emigration is considered to describe the kinetics of cell populations. The two types of cells considered are referred as type T_1 (immediate precursors of oligodendrocytes) and type T_2 (terminally differentiated oligodendrocytes). The reproduction process of these cells is as follows: when stimulating to divide under *in vitro* conditions, the progenitor cells are capable of producing either their direct progeny (two daughter cells of the same type) or a single, terminally differentiated nondividing oligodendrocyte. Moreover, censoring effects as a consequence of the migration of progenitor cells out of the microscopic field of observation are modelled as the process of emigration of the type T_1 cells.

In this work, we propose a two-type controlled branching process to describe the embedded discrete branching structure of the age-dependent branching process aforementioned. We address the estimation of the offspring distribution of the cell population in a Bayesian outlook by making use of disparities. The importance of this problem yields in the fact that the behaviour of these populations is strongly related to the main parameters of the offspring distribution and in practice, these values are unknown and their estimation is necessary. The proposed methodology introduced in M. González et al. (2017) (Robust estimation in controlled branching processes: Bayesian estimators via disparities. *Work in progress*), is illustrated with an application to the real data set given in A.Y. Yakovlev et al. (2008).

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