BINARY BRANCHING PROCESSES WITH APPLICATIONS IN BILOLOGY

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Abstract:

We discuss three recent applications of binary branching processes to the study of biological problems. The first one by Schinazi (2006), evaluate the risk of drug resistance during a induced treatment, the aim is to compute the probability of pathogen eradication before drug resistance appears. The second model by Bozic et al. (2010) calculate the number of passenger mutations in a tumor that has accumulate a certain number of driver mutations. Finally, we consider a model also by Bozic et al. (2013), which describes the dynamics of cancer progression in response to a specific combination therapy. We review the mathematical formulation of these models, the main results and further modifications. This work is part of the Master dissertation of the author under the supervision of Prof. Pablo Rodriguez.