

Inferential Problems for Y-linked Gene Branching Models with Blind Choice

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In the paper of González, Martínez and Mota (Journal of Theoretical Biology 258, 478-488, 2009) a two-dimensional bisexual branching process was introduced to analyze the evolution of the number of carriers of some alleles of genes linked to the Y chromosome from generation to generation in a two-sex monogamic population. They assumed that the gene has no influence on the mating process and then, females choose blindly their mates, and showed that the behavior of the alleles of these Y-linked genes is strongly related to the reproduction law of each genotype. In fact, the average numbers of female and male offspring per mating unit constitute the key to determine the extinction or survival of each allele. In practice these offspring distributions are usually unknown, so in order to apply this model to real situations it is necessary to develop its estimation theory. In this work, we deal with the development of this theory. A non-parametric frequentist framework is considered and it is assumed that the only available data are the total number of females, the total number of males of each genotype and the total number of each type of couple in each generation. The estimation problem is tackled as an incomplete data problem. Maximum likelihood estimators for the main parameters of the model are derived using expectation-maximization method. Predictive distributions for as yet unobserved generations are approximated, and the accuracy of the algorithm is illustrated by way of simulated examples.

Key Words: Sex-linked bisexual branching processes; maximum likelihood estimators; expectation-maximization method.

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