

On Y-linked branching models

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Abstract

A pair of chromosome, called X and Y, determine the sex of many animal species, including most of mammals and human beings among them. In this system females have XX chromosome and males have two distinct chromosome XY. Recent investigations have shown the importance of some Y-linked genes in populations of humans (see e.g., www.nature.com/nature/focus/ychromosome/) or for other species (see the review [1]). Determining the evolution of Y-linked characters in a population plays an important role to solve some relevant questions from a practical viewpoint, such as, the problem of Y-chromosomal Adam, infertility problems in males, or the extinction/spreading of marks such as the surnames or melanistic pigmentation. Recently, two bidimensional bisexual branching models have been introduced to explain the evolution of alleles associated to these genes (see [2] and [3]). In this work we summarize the results obtained for these models, related to their extinction conditions and asymptotic behaviours, and we also present new results about their estimation theories, from frequentist and Bayesian viewpoints.

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