Two-sex branching models in Genetics

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It is well-known that in human and some animal populations the sex of the individuals is determined by a pair of chromosomes X and Y. A female has XX chromosomes, while a male has XY chromosomes. Certain characteristics are due to genes carried on the X chromosome (X-linked). Others due to genes carried on the Y chromosome (Y-linked) and still others to genes carried on both chromosome (XY-linked). From a practical viewpoint, it is of interest to model and analyze the evolution of sex-linked genes from generation to generation.

Focusing our attention in the Y-chromosome, it is worth mentioning that some of the Y-linked genes are expressed in males and play a relevant role in the mating of these males, whereas some others (really, the majority) are not expressed or if they are, they do not play any role in their mating.

Recently, (see Mathematical Biosciences (2006), 202, 227-247 and Journal of Theoretical Biology (2009), 258, 478-488) two different multitype bisexual branching processes have been introduced to analyze the evolution of the number of carriers of both types of Y-linked genes. In the first one it is assumed the preference of females for males with a specific genetic characteristic determined by an allele of the gene. The second model considers that females choose their mates blindly, without caring the genotype they have. Moreover the possibility of mutation has also been considered (see Journal of Theoretical Biology (2012), 307, 104-116).

In this talk we review the main probabilistic and inferential results obtained until now for these models. The probabilistic results are related to the extinction and/or survival of the Y-linked genes and to their growth rates into the population. In general, the behavior of such genes depends on the average number of female and male offspring per mating unit. These parameters of the offspring distributions have been estimated in a Bayesian context, using Monte-Carlo Markov Chain and Approximate Bayesian Computation methodologies.

Finally, by means of simulations, we show different behaviors of Y-linked genes in some special cases as well as the behavior of the obtained estimates for the main parameters of the models.

Keywords: Two-sex branching processes; extinction probability; asymptotic behavior; Markov chain Monte-Carlo; Approximate Bayesian Computation.