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Age statistics in the Moran population model

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Abstract

We analyze the age structure in the Moran model for population genetics. Limit distributions for the age of an individual and the order statistics are computed. The limiting distribution for the life of an individual is shown to be a (shifted) geometric distribution. By an argument that draws on recent conclusions from a model for solitons the limiting order statistics are shown to be convolutions of geometric random variables. Finally, the number of individuals at a certain age is shown to be associated with limiting Bernoulli random variables, via a class of difference-differential functional equations.

Keywords: Moran model; Population mathematics; Random structure; Limit distribution; Gametes

1. Introduction

Instead of assuming that all the individuals of a biological population reproduced then died at the same time (as in Wright's (1951) model for gametes), Moran (1958) assumes that at each instant at which the state of the model may change one randomly chosen gamete dies and is replaced by a new gamete. Moran (1958) kept his process discrete, but Karlin and McGregor (1962) considered extension to processes embedded in real time. Moran (1962) surveys several variations.

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Moran (1958) and the following variants of the model focused on the frequencies of gametes in the population. Our aim here is to study the age structure of a biological population evolving in the same way. Certain aspects of this structure can be connected to some recent developments in a model for solitons. Itoh et al. (2004) study a stochastic model for solitons. The positions of the jumping particles of a wave are investigated, with the chief aim of determining the wavelength and stationary distributions therein. In that paper the particles were assumed indistinguishable. In the present research we endow each particle with an arbitrary label (starting age), and our goal is to study statistics of the particle ages both individually, and globally across the population. Rather minor modification of the soliton model makes it equivalent to the Moran model in population genetics and we can easily apply the soliton results.

In the Moran model we have a population of k living gametes, who evolve in time. Assume these gametes have ages $a_1, \ldots, a_k$. We refer to this configuration as the initial population, or generation 0. The evolution proceeds in discrete steps, and the configuration of ages after n steps is called the nth generation. The rules of the evolution are stochastic: in generation $n-1$, a gamete is chosen at *random* (all gametes being equally likely) for ‘‘rebirth’’. That is, the gamete dies and is replaced by a new gamete (of age 0) in generation n; all the other living gametes survive to the next generation, but they all age by one unit of time. We shall take the time unit to be one year. The process is perpetuated across generations. See Fig. 1 for an illustration; a starred gamete in a generation is the one chosen for rebirth in the next.

A natural model of randomness is to assume that at any stage, the jth gamete, for $j = 1, \ldots, k$, is chosen for rebirth with probability $\frac{1}{k}$. Note that the model allows for a newly born gamete (of age 0) to be chosen randomly for rebirth. It is thus a case of a gamete that never makes it to be 1 year of age.

							Generation Number
6	9*	6	18	15	6	6	0
7	0	7	19	16	7*	7	1
8	1	8	20	17	0*	8	2
9	2	9	21	18*	0	9	3
10*	3	10	22	0	1	10	4
0	4*	11	23	1	2	11	5
			⋮				

Fig. 1. The evolution of a gamete population under the Moran model.