On the Mean Convergence Time of Evolutionary Algorithms without Selection and Mutation

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Abstract. In this paper we study random genetic drift in a finite genetic population. Exact formulae for calculating the mean convergence time of the population are analytically derived and some results of numerical calculations are given. The calculations are compared to the results obtained in population genetics. A new proposition is derived for binary alleles and uniform crossover. Here the mean convergence time $\tau$ is almost proportional to the size of the population and to the logarithm of the number of the loci. The results of Monte Carlo type numerical simulations are in agreement with the results from the calculation.

1 Introduction

Two opposite tendencies operate on natural populations: natural selection, or the propensity to adapt to a given environment; and polymorphism, or the propensity to produce variation to cope with changing environments. With the explosion of data reporting polymorphism on the biochemical level, the long-standing problem of the relative importance of nonrandom and random processes in the genetic structure of populations has revived in the form of a selectionist-neutralist controversy. The most prominent neutralist is Kimura[8].

The controversy has stimulated the study of many stochastic models including the infinite alleles model and the sampling formula. Later Kimura and many others extensively applied diffusion analysis to the study of stochastic genetic models[7]. The problems considered include the analysis of random sampling effects due to small populations, the balance in small populations of recurrent mutation and random genetic drift, the expected time of fixation of a mutant gene.

Random genetic drift is also important for evolutionary algorithms. It is a source of reducing the variation of the population. But if the variation is reduced then the response to selection i.e. the increase of the mean fitness becomes less in the next generation [10]. In this paper we will compute the expected time until convergence for different genetic models. Convergence means that all genotypes in the population become equal. The most complex genetic model deals with recombination by uniform crossover. For this model the genetic drift has not
been investigated before. We derive exact formulae for calculating the mean convergence time and compare them with the results from Monte Carlo type simulations. These results show that uniform crossover recombination increases the convergence time only slightly.

The outline of the paper is as follows. In the next section we analyze the classical simple sampling case as a preparation for treating the case with uniform crossover. In section 3 we present the main result. It is compared with simulations in section 4. Section 5 is for discussion and conclusion.

2 Random drift with simple sampling

2.1 One gene with two alleles

Let the population consist of \( N \) individuals. Assume that each individual has only one gene (one locus) in which there are two different alleles termed "A" and "a". There is no mutation, crossover, and selection. The generations are discrete and the size of the population is fixed, that is, in each new generation we sample \( N \) offspring from the gene pool of \( N \) ancestors with replacements. This model is approximately equivalent with the classical diploid model with \( N/2 \) individuals which is usually treated in the literatures of quantitative genetics.

We can describe the status of the population by the number of individuals which have genotype "A". Let the set of possible states be \( \Theta = \{0, 1, \ldots, N\} \). The development of the state of the population can be described by a simple Markov chain\[2\][6]. We denote the probability of the population to be in state \( i \in \Theta \) at time \( t \) as \( P_i(t) \). Then the transition probability of the Markov chain from the state \( i \) to the state \( j \) is denoted as \( q(j|i) \), \( i, j \in \Theta \).

The product law leads us to the following formula for \( q(j|i) \)

\[
q(j|i) = \binom{N}{j} \left( \frac{i}{N} \right)^j \left( \frac{N - i}{N} \right)^{N-j},
\]

and the relation

\[
P_j(t) = \sum_{i=0}^{N} q(j|i)P_i(t - 1)
\]

holds.

In vector-matrix notation, we denote the transition probability matrix as \( Q = (q_{ji}) \), where \( q_{ji} = q(j-1|i-1) \) and the probability vector as \( P(t) \). The \( i \)-th element of \( P(t) \) is \( P_{i}(t) \). Then we can write the equation (2) as

\[
P(t) = QP(t - 1)
\]

By iteration we obtain

\[
P(t) = Q^tP(0).
\]

Here \( Q^t \) is the power \( t \) of the matrix \( Q \).