Modelling Hierarchical Genetic Strategy as a Family of Markov Chains

Joanna Kołodziej

Institute of Mathematics and Computer Science, Łódź Technical University Branch
in Bielsko-Biała, Bielsko-Biała, Poland,
`jkolodziejpb.bielsko.pl`

Abstract. We present Hierarchical Genetic Strategy (HGS) as a family of Markov chains applying Vose's mathematical model for Simple Genetic Algorithm. Studying its asymptotic properties and performing simply experiments we try to compare efficiency of HGS and sequential genetic algorithms.

1 Introduction

The main idea of Hierarchical Genetic Strategy (HGS) is running in parallel a set of dependent genetic processes (see [1]). The lower order ones represent chaotic search with lowest accuracy. They only detect the promising regions on the optimization landscape in which more accurate processes of higher order are activated. HGS has a tree structure. Every single process builds a branch in this structure and can be described as a sequence of evolving populations. Simple Genetic Algorithm (SGA) is implemented as the basic mechanism of evolution, which governs the progression from one generation to the next. A metaepoch of fixed period $k \in \mathbb{N}$ in evolution is defined as a discrete process, which terminates after at most k generations by selection of the best adapted individual. After every metaepoch new branch called *child* can be created from given one (*parental branch) by sprouting operation.*

We say that the branch has degree $j \in \mathbb{N}$ if it is created by populations containing chromosomes of the length $s_j \in \mathbb{N}$. The unique branch of the lowest degree is called root . If the parental branch has the degree j, then the degree of its child equals $j+1$. The full specification of HGS with formal definitions of all operations was presented in [1]. In this paper we apply the exact Markov model of SGA investigated by Vose and coop. (see [4]) for a construction of simple Markov model of HGS.

2 Simple Mathematical Model of HGS

Let us denote by Ω_s the set of all possible binary coded genotypes of fixed length $s \in \mathbb{N}$. A collection of n elements of Ω_s is called *a population of size n* and can be represented by its *frequency vector* :

$$p = [p_0, ..., p_{r-1}]^T : p_j \geq 0, \ \sum_j p_j = 1 \tag{1}$$

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where p_j is a proportion of element j in the population. The coordinates of this vector are identical with baricentric coordinates of some point in the standard unit of $(r-1)$-dimensional simplex Λ^{r-1}, where $r = 2^s$. We denote by X_n^r a set of all possible populations of the size n.

Let $D \subset \mathrm{I\!R}^N$ be the admissible set to global optimization problem and let $D_r \subset D$ be the finite subset of points in D, which are called *individual phenotypes*. For the future use we define an operator $\Theta : \Lambda^{r-1} \to M(D_r) \subset M(D)$ by:

$$\Theta(p)(A) = \sum_{i \in I} p_i, \quad \forall A \tag{2}$$

where $p \in \Lambda^{r-1}$ is a population vector, $M(D_r)$ and $M(D)$ denote sets of probabilistic measures over D_r and D respectively and $i \in I \subset [0, ..., r-1]$ if and only if its phenotype is in A. $\Theta(p)$ is a probabilistic measure on D induced by the vector p.

Let $G = M \circ F : \Lambda^{r-1} \to \Lambda^{r-1}$ be heuristic function which can be defined as the superposition of recombination (M) and selection (F) operators. According to the Vose's theory (see [4]) in case of finite size of population and positive mutation SGA forms an ergodic Markov chain with states in X_n^r. When the size of population is infinite, then SGA is modelled as the sequence of trajectories of G and converges to the fixed points of this operator, if they exist.

Because SGA is implemented as a basic mechanism of evolution, then every branch in HGS can be modelled as a Markov chain described above. After running several metaepochs we have finite family of Markov chains C_{ij}^t, where j is branch degree, t is local time measured in genetic epochs starting from the branch creation, and $i = (i_1, ..., i_m)$, $i_p = 0$ for $p > j$, is the unambiguous branch identifier, which describes the "history of creation" of every branch (see [1]). In this family we have $b = \sharp\{C_{im}^t\}$ branches of the maximal degree m. That means that there are b copies of Markov chain with states in the set $X_{n_m}^{r_m} \subset \Lambda^{r_m - 1}$, where n_m denotes the size of populations evolving in these branches, s_m is length of genotypes of individuals sampled in these populations, and $r_m = 2^{s_m}$.

There are two main questions concerning this model:

- Will HGS detect an optimum in some point $x \in D$, if SGA can find it there?
- Is HGS more effective than SGA in finding the multiple local optima?

We give the patrial answer to the first question studying asymptotic properties of HGS.

3 Asymptotic Behavior of HGS

Assume that after t_0 genetic epochs there are b branches of maximal degree and no new branch can be sprouted. Let $P = \{p_{1,m}^t; ...; p_{b,m}^t\}$, $t > t_0$, be the set of the frequency vectors, which represent the populations of size m_n evolving in these branches. The partial answer to the question from the previous section is given by the following theorem: