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**MODELING THE GENETIC ALGORITHM BY
A NONHOMOGENEOUS MARKOV CHAIN:
WEAK AND STRONG ERGODICITY**

Эволюционные алгоритмы используются для поиска экстремумов функции. В одном из таких алгоритмов, каноническом генетическом алгоритме, обычно фиксируются два параметра: вероятность мутации и вероятность перекреста. В данной работе мы допускаем возможность изменения этих параметров в процессе работы алгоритма и исследуем сходимость алгоритмов такого типа. Мы также предлагаем новый подход к доказательству слабой эргодичности неоднородных цепей Маркова, не опирающийся на явное использование коэффициента эргодичности Добрушина δ .

Ключевые слова и фразы: неоднородные марковские цепи, слабая и сильная эргодичность, генетические алгоритмы.

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1. Introduction. Canonical Genetic Algorithms (CGA) as introduced in [6] are often used to search for optimal points of functions; that is, they are used to find

$$\arg \max_{x \in B^i} f(x) \text{ or equivalently } \max\{f(b)/b \in B^i\}, \quad (1.1)$$

where B^i is the discretization of the domain of the function f , and f is supposed to be a nonconstant function, limited over its domain. In optimization theory, an algorithm is said to converge to the global optimum if it generates a sequence of solutions or functions values in which the global optimum is a limit value.

Markov chains offers an appropriate model to analyze CGAs, and it has been used in [4] and [5] to prove probabilistic convergence of the best solution within a population to the global optimum under elitist selection (best individual survives with probability one). In [8], CGAs global convergence properties were analyzed and a modified version of the CGA was presented in which they kept the best element of the population in an extra place, but it is not used in the evolutionary process. This element just changes if throughout the evolution of the algorithm a better element appears in the population. In [2] some operations were used in order to obtain an expression for transition probabilities, and some conditions were given for the convergence of the algorithm. In the previously mentioned papers, the mutation and crossover probabilities were kept fixed through the evolution of the algorithm.

In this paper, we extend the ideas presented in [8] to the cases where mutation and crossover parameters are allowed to change through the evolution of the algorithm. In [1] and [2], Cerf modeled the mutation and crossover steps using Markovian operators instead of using crossover and mutation parameters obtaining what he called new genetic algorithm.

This paper is divided into 4 sections. In Section 2, we present the definitions and results we use in the rest of the paper. In Section 3, we introduce the model of CGA in which the crossover and mutation parameters are allowed to vary through time. In Theorem 3.2, we give conditions to guarantee the convergence of the algorithm when only the mutation parameter is allowed to change. In Theorem 3.3, we give conditions to guarantee the convergence of the algorithm when both the crossover and mutation parameters are allowed to change through time.

2. Preliminaries. Let $\{X_n\}$ be a nonhomogeneous Markov chain with finite state space $E = \{1, \dots, N\}$ and with transitions matrices given by $\{P_m\}_{m \geq 0}$, where

$$P_m(i, j) = P(X_{m+1} = j | X_m = i) = P^{(m, m+1)}(i, j), \quad i, j \in E.$$

By the properties of nonhomogeneous Markov chains, the k step transition is given by the product of the transitions matrices $P_m P_{m+1} \cdots P_{m+k-1}$, for all $m \geq 0$. Thus,

$$P^{(m, m+k)}(i, j) = \sum_{i_1 \in E, \dots, i_{k-1} \in E} P_m(i, i_1) P_{m+1}(i_1, i_2) \cdots P_{m+k-1}(i_{k-1}, j)$$

and we can write the Chapman–Kolmogorov equation as

$$P^{(m, m+k)} = P^{(m, m+r)} P^{(m+r, m+k)}, \quad 1 \leq r < k.$$

Definition 2.1. A nonhomogeneous Markov chain $\{P_n\}_{n \in \mathbf{N}}$ is said to be weakly ergodic if it satisfies

$$\lim_{k \rightarrow \infty} \|\mu_0 P^{(m, k)} - \mu_1 P^{(m, k)}\| = 0, \quad \forall m \geq 0, \quad (2.1)$$

where μ_0 and μ_1 are probability distributions, $\|P\| = \sup_i \sum_{j \in E} |P_{ij}|$ and $\|\mu\| = \sum_{j \in E} |\mu_j|$. When the state space is finite (2.1) is equivalent to

$$\lim_{k \rightarrow \infty} \|P_{ij}^{(m, m+n)} - P_{kj}^{(m, m+n)}\| = 0, \quad \forall i, j, k \in E, \quad \forall m \geq 0.$$

In [7], it is proved that (2) is equivalent to

$$\lim_{k \rightarrow \infty} \alpha(P^{(m,k)}) = 1 \quad \text{or} \quad \lim_{k \rightarrow \infty} \delta(P^{(m,k)}) = 0, \quad \forall m \geq 0.$$

Here, for a stochastic matrix $Q = (q_{ij})_{i,j \in E}$, Dobrushin's ergodic coefficient is defined by

$$\alpha(Q) = 1 - \sup_{i,k \in E} \sum_{j \in E} [q_{ij} - q_{kj}]^+ \quad \text{with} \quad [q_{ij} - q_{kj}]^+ = \max\{0, q_{ij} - q_{kj}\}$$

and $\delta(Q) = 1 - \alpha(Q)$ is called the delta coefficient. We see easily that $\delta(P) \leq 1$, for any stochastic matrix P .

Definition 2.2. A constant transition matrix is a transition matrix which has all its lines equal to a vector.

Definition 2.3. A nonhomogeneous Markov chain $\{P_n\}_{n \in \mathbf{N}}$ is said to be *strongly ergodic* if there exists a constant transition matrix P_∞ such that

$$\lim_{k \rightarrow \infty} \|P^{(m,k)} - P_\infty\| = 0, \quad \forall m \geq 0.$$

The following preliminaries results will be used to prove the strong ergodicity of the nonhomogeneous Markov chain in Section 3.

Theorem 2.1 (see [3]). *If P_∞ is a weakly ergodic transition matrix and a discrete nonhomogeneous Markov chain $\{P_n\}_{n \in \mathbf{N}}$ satisfies*

$$\lim_{n \rightarrow \infty} \|P_n - P_\infty\| = 0,$$

then $\{P_n\}_{n \in \mathbf{N}}$ is strongly ergodic.

The previous theorem will be used extensively in this paper and it is an extension of the Theorem V.4.5. presented in [7].

Lemma 2.1 (see [7]). *Let P, Q , and R be transition matrices, then*

$$\|P.Q\| \leq \|P\|.\|Q\|, \quad \delta(P.Q) \leq \delta(P)\delta(Q), \quad (2.2)$$

$$|\delta(P) - \delta(Q)| \leq \|P - Q\|. \quad (2.3)$$

Theorem 2.2. *Let $\{P_n\}_{n \in \mathbf{N}}$ be a discrete weakly ergodic nonhomogeneous Markov chain and assume there exists a probability distribution $\pi_n = (\pi_n(j))_{j \in E}$ such that $\pi_n = \pi_n P_n$ and*

$$\sum_{k \geq 1} \sum_{j \in S} |\pi_k(j) - \pi_{k+1}(j)| < \infty,$$

then $\{P_n\}_{n \in \mathbf{N}}$ is strongly ergodic.

Theorem 2.2, which is presented in [7], as well as Theorem 2.1 have their hypotheses easily checked in practical problems, which make them very useful.

3. Nonhomogeneous genetic algorithm: results. In [8], it is explained that a genetic algorithm consists of an n -tuple of binary strings b_i of length l , where the bits of each string are considered to be the *genes* of an *individual chromosome* and where the n -tuple of individual chromosomes is said to be a *population*. So, the algorithm evolves in following way: first, a random population is generated and it is called initial population. Afterwards, three operations are performed on the initial population, namely: mutation, crossover, and selection. Each of these operations is modeled by a stochastic matrix which describes such operation. Each individual b_i represents a feasible solution of the problem (1) and its objective function value $f(b_i)$ is said to be its *fitness* which is to be maximized. The algorithm can be sketched as follows: an initial population is randomly generated

repeat
 perform selection
 perform crossover
 perform mutation
until some stopping criterion applies

There are a lot of ways to perform each operation above. The transition matrix for the selection step, when using so-called *proportional selection*, is built in the following way: Suppose the initial population is given by $x = (x_1, x_2, \dots, x_n)$, so the probability that after the selection step we get the population $y = (y_1, y_2, \dots, y_n)$ is

$$S(x, y) = \begin{cases} \frac{\prod_{k=1}^n f(y_k)}{(\sum_{k=1}^n f(y_k))^n} & \text{if } \{y_1, y_2, \dots, y_n\} \subset \{x_1, x_2, \dots, x_n\}, \\ 0, & \text{otherwise.} \end{cases}$$

The parameter p_c , which is called crossover probability, is used to select population's elements which will participate in the crossover process. Although many crossover operators have been proposed, there is not a closed expression to the inputs of the transition matrix for crossover, except in very particular situations. Fortunately, even not having the knowledge of the inputs of the transition matrix for crossover, we will be able to proceed the convergence analysis of the Markov chain, which is generated in this process.

The parameter p_m , which is called mutation probability, is used to select which genes will change in each individual chromosome of the population. In contrary to transition matrix for crossover, there is a closed expression to each input of the transition matrix for mutation. For example, suppose the population before the mutation step is given by $x = (x_1, x_2, \dots, x_n)$, so the probability that after the mutation step we get the population $y = (y_1, y_2, \dots, y_n)$ is

$$M(x, y) = p_m^{H(x, y)} (1 - p_m)^{n - H(x, y)},$$

where $H(x, y)$ is the Hamming distance between x and y , x and y are considered as a string obtained by the concatenation of the strings $x_1, x_2, \dots, x_n$ and $y_1, y_2, \dots, y_n$, respectively.

The CGA is modeled by a Markov chain whose transition matrix P , which represents the algorithm, is the product of three stochastic matrices (S), (C), and (M), which describe the intermediate transitions caused by selection, crossover, and mutation, respectively. Thus, the transition matrix is given by $P = SCM$, where C , M , and S are kept fixed throughout the evolution of the algorithm.

In this section, we allow the mutation probabilities to change throughout time, p_m^n will represent the mutation probability on the n th step of the algorithm, and we represent this allowance by representing the mutation matrix as

$$M = M_n = (m_n(i, j))_{i, j \in E}, \quad n \in \mathbf{N},$$

and we consider the transition matrix P_n as the following product:

$$P_n = SCM_n, \quad (3.1)$$

where S and C are the selection and crossover matrices, respectively, as in [8]. This product order is seemed to us more natural than the order used in [8]. Thus, we have a nonhomogeneous Markov chain $\{P_n\}_{n \in \mathbf{N}}$.

Lemma 3.1. *Let $\{P_n\}_{n \in \mathbf{N}}$ be the nonhomogeneous Markov chain given in (5). If the mutation probabilities p_m^n are such that $p_m^n \in (0, 1)$ for any $n \in \mathbf{N}$, then there exists a sequence $\{\alpha_n\}$, with $\alpha_n > 0$, for any n such that*

$$\inf_{i \in E} P_n(i, j) \geq \alpha_n \quad \forall j \in E.$$

P r o o f. S and C are stochastic matrices and M_n is a positive stochastic matrix for all $n \in \mathbf{N}$ because $p_m^n \in (0, 1)$ for any $i, j \in E$ for all $n \in \mathbf{N}$, so $P = SCM_n$ is a

positive matrix for all $n \in \mathbf{N}$. By the hypothesis, E is finite; hence, for each $n \in \mathbf{N}$, we can guarantee the existence of $\alpha_n > 0$ such that

$$\inf_{i \in E} P_n(i, j) \geq \alpha_n, \quad \forall j \in E.$$

Lemma 3.1 is proved.

Theorem 3.1. *Suppose that for $m = 0, 1, \dots$ there exist an integer ν_m , a constant $\delta_m > 0$, and a subset $E_m \subset E$, with $\#E_m = N_m \geq 1$ (where $\#E$ is the cardinality of E) such that*

$$\inf_{i \in E, j \in E_m} P_{ij}^{(m, m+\nu_m)} \geq \delta_m. \quad (3.2)$$

Then we have the following upper bound:

$$|P_{ij}^{(m, m+n)} - P_{kj}^{(m, m+n)}| \leq \prod_{u=0}^{k(m, n)} (1 - \delta_{r_u}), \quad (3.3)$$

where $r_0 = m, r_u = r_{u-1} + \nu_{r_{u-1}}$, and $k(m, n) = \max\{u: r_u < m + n\}$.

Moreover, if $\sum_{u=1}^{\infty} \delta_{r_u} = \infty$ then $\{P_n\}$ is weakly ergodic.

P r o o f. First of all, note that if (3.3) and $\lim_{n \rightarrow \infty} \prod_{u=0}^{k(m, n)} (1 - \delta_{r_u}) = 0$ are true, then we have not only the weak ergodicity but also

$$\lim_{n \rightarrow \infty} \sup_{u, v} |P_{uj}^{(k, k+n)} - P_{vj}^{(k, k+n)}| = 0.$$

Because $\nu_m \geq 1$, we have $r_0 < r_1 < \dots$. By the hypotheses, $\sum_{u \geq 0} \delta_{r_u} = \infty$, then it follows that $\prod_{u=0}^n (1 - \delta_{r_u}) \xrightarrow{n} 0$. So we have only to prove that $k(m, n) \xrightarrow{n} \infty$. Observe that given m_0 , there always exists $u_0 > m_0$ such that $r_{u_0} < m + n$ for n sufficient large, so $k(m, n) \xrightarrow{n} \infty$. In order to prove (3.3), we define

$$\begin{aligned} L_j^{(m, m+n)} &= \sup_{i \in E} P_{ij}^{(m, m+n)}, \quad l_j^{(m, m+n)} = \inf_{i \in E} P_{ij}^{(m, m+n)}, \\ E^+ &= E^+(i, k, u, v) = \{l: l \in E, P_{il}^{(u, v)} \geq P_{kl}^{(u, v)}\}, \\ E^- &= E^-(i, k, u, v) = \{l: l \in E, P_{il}^{(u, v)} < P_{kl}^{(u, v)}\}. \end{aligned}$$

Using the Chapman–Kolmogorov equation we can write

$$\begin{aligned} L_j^{(m, m+n)} - l_j^{(m, m+n)} &= \sup_{i, k} (P_{ij}^{(m, m+n)} - P_{kj}^{(m, m+n)}) \\ &= \sup_{i, k} \sum_{l \in E} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) P_{lj}^{(m+\nu_m, m+n)}. \end{aligned}$$

Note that

$$\begin{aligned} \sum_{l \in E^+} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) P_{lj}^{(m+\nu_m, m+n)} \\ \leq \sum_{l \in E^+} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) L_j^{(m+\nu_m, m+n)} \end{aligned}$$

and

$$\begin{aligned} \sum_{l \in E^-} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) P_{lj}^{(m+\nu_m, m+n)} \\ \leq \sum_{l \in E^-} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) l_j^{(m+\nu_m, m+n)}. \end{aligned}$$

Using that $\sum_{l \in E} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) = 0$ and $E = E^+ \cup E^-$, we have

$$\sum_{l \in E^+} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}) = - \sum_{l \in E^-} (P_{il}^{(m, m+\nu_m)} - P_{kl}^{(m, m+\nu_m)}).$$

Thus,

$$L_j^{(m,m+n)} - l_j^{(m,m+n)} \leq \sup_{i,k} \sum_{l \in E^+} \left(P_{il}^{(m,m+\nu_m)} - P_{kl}^{(m,m+\nu_m)} \right) \left(L_j^{(m+\nu_m,m+n)} - l_j^{(m+\nu_m,m+n)} \right).$$

We will show later that

$$\sum_{l \in E^+} \left(P_{il}^{(m,m+\nu_m)} - P_{kl}^{(m,m+\nu_m)} \right) \leq 1 - \delta_m. \quad (3.4)$$

After (3.4) proved, we can conclude that

$$L_j^{(m,m+n)} - l_j^{(m,m+n)} \leq \sup_{i,k} (1 - \delta_m) \left(L_j^{(m+\nu_m,m+n)} - l_j^{(m+\nu_m,m+n)} \right).$$

Using $r_0 = m$ and $r_1 = r_0 + \nu_{r_0}$ we can rewrite the previous equation as

$$L_j^{(r_0,m+n)} - l_j^{(r_0,m+n)} \leq \sup_{i,k} (1 - \delta_{r_0}) \left(L_j^{(r_1,m+n)} - l_j^{(r_1,m+n)} \right).$$

Repeating this procedure until $k(m, n) = \max\{u: r_u < m + n\}$, we have

$$\begin{aligned} L_j^{(r_0,m+n)} - l_j^{(r_0,m+n)} &\leq \prod_{u=0}^{k(m,n)} \left(1 - \delta_{r_u} \right) \left(L_j^{(r_{k(m,n)},m+n)} - l_j^{(r_{k(m,n)},m+n)} \right) \\ &\leq \prod_{u=0}^{k(m,n)} (1 - \delta_{r_u}). \end{aligned} \quad (3.5)$$

In the last inequality we used the fact that $0 \leq L_j(\cdot, \cdot) - l_j(\cdot, \cdot) \leq 1$. From (3.5) we have (3.3). Now we are going to prove (3.4). For $r_0 = m$ and $r_1 = m + \nu_m$ we have

$$\sum_{l \in E^+} P_{il}^{(r_0,r_1)} = 1 - \sum_{l \in E^-} P_{il}^{(r_0,r_1)}$$

and

$$\sum_{l \in E^+} \left(P_{il}^{(r_0,r_1)} - P_{kl}^{(r_0,r_1)} \right) = 1 - \sum_{l \in E^-} P_{il}^{(r_0,r_1)} - \sum_{l \in E^+} P_{kl}^{(r_0,r_1)}.$$

Using (3.2) and the fact that $\#E_m = \#(E^+ \cap E_m) + \#(E^- \cap E_m)$, we have

$$\begin{aligned} \sum_{l \in E^+} \left(P_{il}^{(r_0,r_1)} - P_{kl}^{(r_0,r_1)} \right) &\leq 1 - \sum_{l \in E^- \cap E_m} P_{il}^{(r_0,r_1)} - \sum_{l \in E^+ \cap E_m} P_{kl}^{(r_0,r_1)} \\ &\leq 1 - \delta_m \#(E^- \cap E_m) - \delta_m \#(E^+ \cap E_m) \\ &\leq 1 - \delta_m \#E_m \leq 1 - \delta_m. \end{aligned}$$

Theorem 3.1 is proved.

Note that Theorem 3.1 is an alternative approach to prove the weak ergodicity without using Dobrushin's ergodic coefficient and it is easier to use.

Corollary 3.1. *Let $\{P_n\}_{n \in \mathbf{N}}$ be the nonhomogeneous Markov chain given in (5) and the mutation probabilities p_m^n be such that $p_m^n \in (0, 1)$ for any $n \in \mathbf{N}$. If the sequence $\{\alpha_n\}_{n \in \mathbf{N}}$ obtained in Lemma 3.1 satisfies*

$$\sum_n \alpha_n = \infty,$$

then $\{P_n\}_{n \in \mathbf{N}}$ is weakly ergodic.

P r o o f. Using Theorem 3.1 with $\nu_m = 1, \delta_m = \alpha_m$, and $E_m = E$ we obtain $k(m, n) = n$ and with the additional information that $\sum_n \alpha_n = \infty$ we obtain that $\{P_n\}_{n \in \mathbf{N}}$ is weakly ergodic.

Corollary 3.1 is proved.

Corollary 3.2. *Let $\{P_n\}_{n \in \mathbf{N}}$ be the nonhomogeneous Markov chain given in (5). If the mutation probabilities p_m^n are such that $p_m^n > \gamma > 0$ for all $n \in \mathbf{N}$, then $\{P_n\}_{n \in \mathbf{N}}$ is weakly ergodic.*

Since M_n is positive for all $n \in \mathbf{N}$ this implies that $P_n = SCM_n$ is positive, and we can conclude, from the homogeneous Markov chain theory, that for each n there exists a probability distribution π_n that satisfies $\pi_n = \pi_n P_n$. Thus, using Theorem 2.2 and under the same hypothesis of Corollary 3.1, if the probability distributions π_n guaranteed above satisfies

$$\sum_{k \geq 1} \sum_{j \in E} |\pi_k(j) - \pi_{k+1}(j)| < \infty,$$

then $\{P_n\}_{n \in \mathbf{N}}$ is strongly ergodic.

E x a m p l e 3.1. The CGA introduced by [6] fits in all cases discussed above when we consider $P_n = P$ since the transition matrix does not change through time.

O b s e r v a t i o n 1. If $Q = (q_{ij})_{i,j \in E}$ is a nonconstant positive stochastic matrix, then $\delta(Q) < 1$. In fact, since each element of Q is positive, we can write

$$\sum_{j \in E} |q_{ij} - q_{kj}| = \sum_A (q_{ij} - q_{kj}) + \sum_B (q_{kj} - q_{ij}),$$

where $A = \{j: q_{ij} \geq q_{kj}\}$ and $B = \{j: q_{ij} < q_{kj}\}$. Q is nonconstant, it follows that $A, B \neq \emptyset$. Thus

$$\sum_{j \in E} |q_{ij} - q_{kj}| \leq \sum_A q_{ij} + \sum_B q_{kj} < 2.$$

As the last inequality holds for any i and k , the observation follows.

Theorem 3.2. *If there exist $\gamma < 1$ and $k \in \mathbf{N}$ such that $\delta(M_n) < \gamma$ for $n \geq k$ and M_∞ such that*

$$\|M_n - M_\infty\| \rightarrow 0, \quad (3.6)$$

then $\{P_n\}$ is strongly ergodic and $\{P_n\}_{n \in \mathbf{N}}$ converges in law to a unique stationary distribution of SCM_∞ .

P r o o f. Let $P_\infty = SCM_\infty$. By Lemma 2.1 (2.2) we have

$$\|P_n - P_\infty\| = \|SCM_n - SCM_\infty\| \leq \|M_n - M_\infty\| \rightarrow 0.$$

By (2.3) we have

$$\|\delta(M_n) - \delta(M_\infty)\| \leq \|M_n - M_\infty\| \rightarrow 0.$$

By the hypotheses we have $\delta(M_n) < \gamma$ for n large, so $\delta(M_\infty) < \gamma$. Thus

$$\delta(SCM_\infty) < \delta(SC)\delta(M_\infty) < \gamma < 1,$$

hence SCM_∞ is weakly ergodic. By Theorem 2.1 we obtain that $\{P_n\}$ is strongly ergodic. The convergence in law of $\{P_n\}$ to a unique stationary distribution of SCM_∞ is guaranteed by Theorem 2 in [3].

Theorem 3.2 is proved.

In the prior theorem we proved the ergodicity of the Markov chain $\{P_n\} = \{SCM_n\}$ keeping the crossover and selection matrices fixed through time. Now we allow the crossover matrix to change through time by allowing changes in crossover probabilities. We will call p_c^n the crossover probability at the n th step of the algorithm and we set conditions in order to guarantee the ergodicity of the Markov chain $\{P_n\} = \{SC_n M_n\}$.

Theorem 3.3. *If there exist $\gamma < 1$ and $N \in \mathbf{N}$ such that $\delta(M_n) < \gamma$ for $n \geq N$ or $\delta(C_n) < \gamma$ for $n \geq N$ and*

$$\|M_n - M_\infty\| \rightarrow 0 \quad \text{and} \quad \|C_n - C_\infty\| \rightarrow 0,$$

then $\{P_n\}$ is strongly ergodic and $\{P_n\}_{n \in \mathbf{N}}$ converges in law to a unique stationary distribution of $SC_\infty M_\infty$.

P r o o f. The proof is similar to that of Theorem 3.2.

O b s e r v a t i o n 2. In [8] Rudolph modeled the CGA by $\tilde{P}_n = CMS$. If we consider $\tilde{P}_n = CMS_n$ and suppose for S_n the same hypothesis we considered for M_n , we can guarantee the convergence of the nonhomogeneous Markov chain $\tilde{P}_n$.

Conclusions. These results give us an infinite number of possibilities to vary the parameters and study the convergence of the algorithm, for this reason we are still developing simulations and exploring those possibilities. We hope in the future be able to present a policy of changing parameters that improve the performance of the traditional genetic algorithm.

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CONTINUOUS DISINTEGRATIONS OF GAUSSIAN PROCESSES¹⁾

Цель настоящей статьи — описать условное распределение случайного процесса по наблюдениям за ним на интервале. Вводится понятие непрерывного дезинтегрирования — регулярная условная вероятностная мера, непрерывно зависящая от параметра в условии. Обусловливание бесконечномерно по своему характеру, что приводит нас к рассмотрению общего случая вероятностных мер в банаховых пространствах. Наш основной результат состоит в том, что для некоторого числа M , зависящего от ковариационной структуры, условие $M < \infty$ является необходимым и достаточным для того, чтобы гауссовская мера допускала непрерывное дезинтегрирование. Условие $M < \infty$ довольно разумно: в случае стационарных процессов $M = 1$.

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