ISNN:2181-1296



SHAROF RASHIDOV NOMIDAGI
SAMARQAND DAVLAT UNIVERSITETI

САМАРКАНДСКИЙ ГОСУДАРСТВЕННЫЙ
УНИВЕРСИТЕТ ИМЕНИ ШАРОФА РАШИДОВА

SAMARKAND STATE UNIVERSITY NAMED
AFTER SHAROF RASHIDOV

ILMIY AXBOROTNOMA

НАУЧНЫЙ ВЕСТНИК
SCIENTIFIC JOURNAL

ANIQ VA TABIIY FANLAR SERIYASI

Matematika, Mexanika, Informatika
Fizika, Kimyo, Biologiya, Geografiya

№ 1/1 (149)
2025

ISSN 2181-1296

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Samarqand viloyat matbuot boshqarmasida ro‘yxatdan o‘tish tartibi 09-25.
Jurnal 1999-yildan chop qilina boshlagan va OAK ro‘yxatiga kiritilgan.

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tashkilot, korxonalar uchun **- 5584**

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UDC: 681.14 https://doi.org/10.59251/2181-1296.2025.v1.149.1.3167

ALGORITHMS FOR USING EVALUATION METHODS IN DATABASE DESIGN

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Received: 07.02.2025
Revised: 26.02.2025
Accepted: 15.03.2025
Published: 29.03.2025

Publisher: Samarkand State University named after Sharof Rashidov.

Abstract. The increase in the volume of information leads to an increase in the technologies and research for their processing. The study proposes a parallel implementation technology for matching records with the same characteristics of the algorithm, and the sequence of solving the problem using genetic algorithms is presented. In the proposed algorithm, the selection and replacement stages are determined by the parallel increase in the fitness function using replacement with sets. A genetic algorithm model is presented for the file design problem and the method of encoding chromosomes is explained. The process of working with existing methods for constructing the fitness function is described. At the end of the study, the reliability of the proposed model and algorithms is proven using experimental results.

Keywords: information, fitness function, genetic algorithms, database, adaptation, mutation, population, selection.

Ma’lumotlar bazasini loyihalashtirishda evolyutsion usullarini qo‘llash algoritmlari

Annotatsiya. Axborotlar hajmini oshish ortida ularni qayta ishlash texnologiyalari va tadqiqotlarini kuchayishiga olib kelmoqda. Tadqiqotda Algoritm bir xil xuxusiyatga ega bo‘lgan yozuvlar o‘rtasida moslashishtirishni parallel amalga oshirish texnologiyalrini taklif etilgan bo‘lib genetik algoritmlar yordamida muammoni qanday yechim topish ketma ketligi keltirib o‘tilgan. Taklif etilayotgan algoritmda tanlash va almashtirish bosqichlari aniqlangan to‘plamlar bilan almashtirishni qo‘llab fitnes funksiya parallel ravishda ko‘payishning tasdiqlar keltirib o‘tilgan. Fayl dizayni muammosi uchun genetik algoritm modeli keltirib o‘tilgan va xromosomalarni kodlash uslubiyati tushuntirilgan. Fitness funksiyani qurishda mavjud usllar yordamida ishlash jarayoni baayon etilgan. Tadqiqot songida taklif etilgan model va lagoritmlar ishonchliligi tajriba natijalari yordamida isbotlangan.

Kalit so‘zlar: axborot, fitness funksiya, genetic algoritmlar, ma’lumotlar bazasi, moslahstirish, mutatsiya, populyatsiya, seleksiya.

Алгоритмы использования эволюционных методов в проектировании баз данных

Аннотация. Увеличение объема информации приводит к росту технологий ее обработки и исследований. В исследовании предлагается технология параллельной реализации для сопоставления записей с одинаковыми характеристиками, а также представлена последовательность шагов решения задачи с использованием генетических алгоритмов. Предложенный алгоритм демонстрирует параллельный рост функции приспособленности с использованием замены с определенными наборами шагов

выбора и замены. Представлена модель генетического алгоритма для задачи проектирования файлов и объяснен метод кодирования хромосом. Описан процесс построения функции приспособленности с использованием существующих методов. Надежность предложенной модели и алгоритмов в конце исследования была доказана с использованием экспериментальных результатов.

Ключевые слова: информация, функция приспособленности, генетические алгоритмы, база данных, адаптация, мутация, популяция, отбор.

Introduction. In the context of a sharp increase in the volume of information, the rapid use of records in a company-wide database consisting of millions of records requires the use of modern methods for their aggregation and processing. One of the pressing issues in data collection is the organization of queries and information processing in database systems in different regions. This process can be achieved by organizing requests for records in the existing database equally across all part servers or by processing the existing records into a single table view (by matching) (Figure 1).

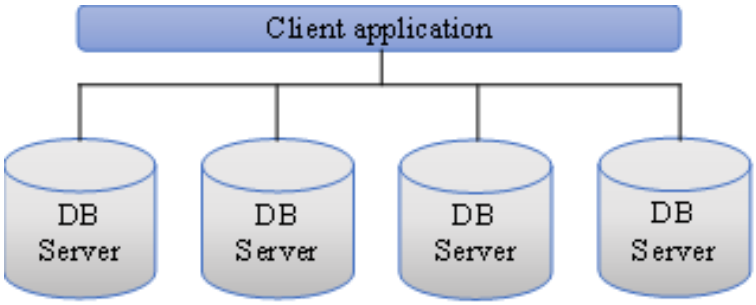

Figure1. Distributed database view.

The use of genetic algorithms (GA) to search for configurations in multiple databases is considered one of the effective methods for solving a given problem [1-2]

Multi-niche crowding genetic algorithm (MNC GA). One of the advantages of MNC GA is that it selects a stable subpopulation of existing solutions. The algorithm uses the concept of group selection to perform adaptation between records with similar characteristics during its operation, thereby ensuring that many members of the population participate in the adaptation. This method identifies several local optima and compares them during the solution search to find the global optimum (Fig 2).

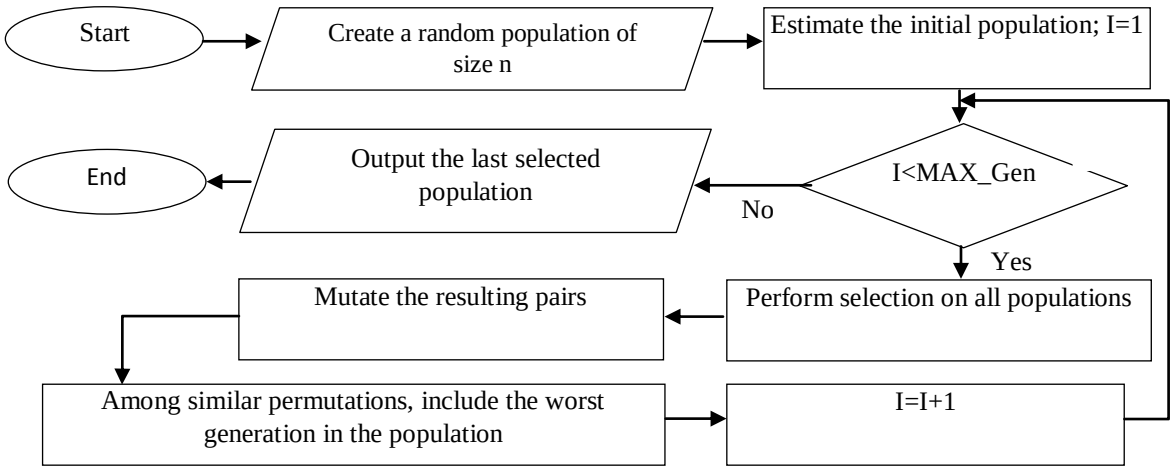

Figure 2. Parallel application algorithm of MNC GA.

The above algorithm states that in the first step, all samples in the population (of size n) are randomly generated and evaluated in parallel. In the second step, the population is generated and

selection, recombination, and mutation substitution operations are applied to a sufficient number of generations. The samples in the resulting population are selected for selection. In the third stage, all n pairs are selected in parallel, resulting in 2n generations. The 2n generations generated are mutated, resulting in the replacement of those that are different from their parents. In the fourth stage, the remaining generations are continued by introducing the worst generation into the population among similar replacements. The above four steps are performed for all the identified generations. One of the main ideas of the algorithm is to use the selection and replacement steps with the identified sets, so that the fitness function can be multiplied in parallel, increasing the number of selections and maintaining the diversity of the search for samples. The algorithm in Figure 2 above gives the following main results:

• maintains constant subpopulations in all cases;
• preserves diversity during the search process;
• an algorithm that converges to local optima emerges.

The algorithm does not impose additional conditions during the search for an optimal solution, which allows exploring other areas of the search space and approaching the best solutions in different spaces [3-4]. The selection process in the algorithm is an integral part of GA, and there are several well-defined methods for this. The study considers the Cowding selection method, which uses parallel external selection to ensure that each sample has a chance of mating in each generation.

1) Each sample from population I_i is selected as a parent for mating.

2) Its mate is selected from a randomly selected group of samples of size C_s (Cowding selection size) from population I_j.

Cowding selection favors mating of samples with similar characteristics and ensures the participation of the entire population [5-6].

Genetic algorithm model for file design problem. The model under study uses multimodality to generate generations by using pairing and replacement among solutions at local optimums, while simultaneously obtaining improved results. The solutions in the population randomly select records from the files. Given K files with b cells, the number of cells in them is N, the cells are numbered from 1 to N in a non-repeating manner. For example, to create two offspring, three steps had to be performed: selecting parents, mating them, and calculating the viability of the offspring. Each parent in the population is allowed to mate at least once in each generation. The average number of files (ANF) to apply single-attribute queries to store (read) N records from K files is minimized. In other words, the goal can be achieved by reading (on average) queries from as few files as possible for records with the same attribute Table 1 [7-8].

TABLE 1. Attributes have values {B, C, F, V} and entries {2, 7, 1, 2} respectively.

File 1	File 2	fex(B)	fex(C)	fex(F)	fex(V)	ANF
C C C C C C	C B B V V F	1	2	1	1	1.25
C C C B V V	C C C C B F	2	2	1	1	1.50
C C C C B V	C C C B V F	2	2	1	2	1.75
C C C B B F	C C C C V V	1	2	1	1	1.25

Chromosome coding. The records under study consist of N allele strings, each corresponding to a record in the file. Each allele can take a value between 0 and K-1, representing the records in the file. To clearly state that the chromosomes are not binary for the records in Table 1, files of size b=4 of size K=3 were chosen, Table 2 [9].

TABLE 2. Encoding of files

Record number	1	2	3	4	5	6	7	8	9	10	11	12
Record attribute	B	B	C	C	C	C	C	C	C	F	V	V
Chromosome 1	0	0	0	0	1	1	1	1	2	2	2	2
Chromosome 2	0	0	1	1	2	2	2	0	0	1	1	2
Record attribute	B	B	C	C	C	C	C	C	C	F	V	V

When calculating the similarity metric, using the data in Table 1, 3 files with 4 attributes are given (Table 3), where each number indicates the file in which the record is located.

TABLE 3. Pair selection using similarity

Writing	**B**	**B**	**C**	**C**	**C**	**C**	**C**	**C**	**C**	**F**	**V**	**V**
Chromosome 1	1	**0**	2	**2**	**0**	**1**	**0**	**1**	1	**0**	2	**2**
Chromosome 2	2	**0**	1	**2**	**0**	**1**	**0**	**1**	2	**0**	1	**2**
Similar tasks		**1**		**2**	**3**	**4**	**5**	**6**		**7**		**8**

Building a fitness function. The Fitness function of the problem captures three important properties of an optimal solution:

• minimum average number of files (ANF);

• matching records with the same attribute

• equal distribution of records with the same attribute in long files among the minimum number of files when storing

The last two properties are considered to be inverse processes and represent the matching and the distribution of records evenly across files. In order to improve the quality of the solution, the value of the matching is considered more important. The average number of files is calculated using the formula (1) [10-11].

$$ANF = \sum_{i=1}^{h} \frac{fex(a_i)}{h} \tag{1}$$

where $fex(a_i)$ is the total number of functions that contain the attributes a_i. Using this formula, we can calculate the upper and lower bounds of the ANF. The lower bound represents the configuration of writing all the record attributes to the minimum number of files. The upper bound represents the configuration of distributing all the record attributes to the maximum number of files. The lower and upper bounds are referred to as *min_anf* and *max_anf*, respectively (2).

$$\min_ anf = \sum_{i=1}^{h} \left\lceil \frac{n_i}{b} \right\rceil / h \le ANF \le \max_ anf = \sum_{i=1}^{h} \min(n_i, K)/h. \tag{2}$$

where n_i is the number of attribute i in the records, h is the number of attributes, b is the size of the files, and K is the number of files.

When calculating the grouping term (GT) value, the ratio of records with the same attribute in each file is determined by how the records of the attribute are located in the files and by grouping records with the same attribute together, as shown in formula (3).

$$GT = \sum_{i=1}^{h} \sum_{j=1}^{K} \left(\frac{attr(a_i, j)}{n_i} \right)^2 \tag{3}$$

where $attr(a_i,j)$ denotes the number of records of attribute a_i in file j.

Balancing term (BT) applies a minimum uniform distribution to files with identical attribute matching, and the result is calculated by adding the difference value between the number of records of the attribute and the balance configuration of the attribute (4) [12-13].

$$BT = \sum_{i=1}^{h}\sum_{j=1}^{K}\left\lfloor \left| \frac{attr(a_i, j) - n_i}{\lceil n_i / b \rceil} \right| \right\rfloor \text{ were } attr(a_i, j) \neq 0 \quad (4)$$

where $\lceil n_i / b \rceil$ denotes the number of files required to store the attribute a_i records, and values of BT closest to zero represent balanced configurations.

When determining the fitness value, it is normalized to return values in the range [0; 1] and a percentage of each of ANF, BT, and GT is added to form the final fitness value (5).

$$fitness = 0.7 * \frac{GT}{h} + 0.25 * \frac{\max_anf - ANF}{\max_anf - \min_anf} + 0.05 * \frac{1.0}{1.0 + BT} \quad (5)$$

The fitness function value can be an arbitrary number in the range [0; 1]. Where 1 represents the configurations in which solutions can achieve the min_anf value[14].

Experimental results. Six tests with different characteristics were selected to evaluate the state of the algorithm, and some of them contain solutions that reach the lower bound of min_anf. Since it is an experimental design, a total of 100 records were used to create different configurations by adding different attributes to the files (Table 4).

TABLE 4. Configuration for all test cases.

Case number	**File number**	**File size**	**Attribute number**	**Number of records by attribute $n_1, n_2, n_3, n_4, \ldots, n_h$**	***min_anf availability***
1	5	20	10	7, 2, 3, 1, 5, 17, 18, 13, 15, 19	Yes
2	10	10	10	7, 2, 3, 1, 5, 17, 18, 13, 15, 19	Yes
3	5	20	10	7, 4, 3, 8, 6, 11, 18, 15, 10, 18	No
4	10	10	10	7, 4, 3, 8, 6, 11,18, 15, 10, 18	No
5	5	20	21	7, 4, 3, 8, 6, 1, 8, 5, 10, 8, 1, 2, 4, 9, 5, 1, 6, 2, 3, 3, 4	Yes
6	5	20	15	7, 4, 9, 7, 7, 4, 9, 5, 9, 7, 9, 5, 6, 7, 5	No

The MNC GA parameters used for the algorithm to run a single run are:

Population size	100
Number of generations	50
Mating probability	0.95
Mutation probability	0.01
Cs for selection	4
Cf for replacement	3
S for replacement	5

During the study, several optimal solutions were found for the test cases and they were stored for generations. In four of the six experiments, at least one optimal solution was found before the 6th generation. For the third and fourth experiment cases, it was found that more generations were needed

and that there were attribute values with unreachable min_anf and the number of records was greater than the file size. In these cases, very small fitness improvements were achieved between the solutions (Table 5).to carefully check their article PDF prior to submission. Perform visual inspections to detect subtle font errors and ensure that all fonts are embedded. With the wide range of tools and software that authors use to create PDFs, and the number of devices and platforms that readers use to view/print them, font embedding by authors is not only “nice-to-have”; it is *essential*

TABLE 5. Best solution and number of generations required for all test cases

Case	Gen	The best solution
1	3	4444444, 11, 333, 0, 22222, 3333333333333333, 11111111111111111, 4444444444444, 22222222222222, 0000000000000000000
2	4	9999999, 77, 111, 6, 88888, 33333333113311111, 22222222277777777, 5555555555999, 44444444488888, 000000000066666666
3	25	2222222, 0000, 222, 44444444, 333333, 4444444444, 000000000100001000, 333333433333333, 2222222222, 11111111111111111
4	15	8888888, 9999, 888, 55555555, 999999, 2222222227, 00000000006666666, 111111111155667, 3333333333, 4444444447777777
5	5	0000000, 3333, 222, 33333333, 222222, 0, 00000000, 11111, 2222222222, 44444444, 2, 44, 4444, 11111111, 3333, 4, 111111, 44, 333, 444, 0000
6	5	0000000, 2222, 222222222, 4444444, 222222, 3333, 333333333, 44444, 000040000, 3333333, 111111111, 111111111, 4444444, 00000

Table 5 shows the solutions for the above-executed experimental tests, the new generation numbers obtained, and the generations represented by each solution. rezord is assigned. The table can be described as follows: in the initial result, the pointers for attribute 1 are to file 4, the pointers for attribute 2 are to file 1, and so on. The optimal configuration in experiment 4 concerns the eighth attribute, which is explained by the fact that the conditions for the value (1111111111155667) are written to 4 different files.

As can be seen from the experiment, in all the remaining rows, we can see that the attribute values are written to only 1 or 2 files. During the study, such cases were achieved in the test results obtained by many operators, but this required more generations. In addition, the MNS GA did not prevent the population from approaching the optimum, which was lost prematurely. In order to achieve the intended goal as a result of the parallel application of the MNS GA, it is recommended to upgrade to four processors with speeds from 2.2 to 2.9 on three different platforms.

Conclusion. In the course of the study, an algorithm for parallel implementation of Multi-Niche Crowding GA was proposed and its block diagram was presented. The use of multimodality inherent in the file design problem led to a more balanced search across the entire space. The use of genetic operators through evolutionary methods enhanced the convergence of the algorithm and at the same time allowed for the existence of multiple solutions. It was experimentally proven that it is

possible to achieve acceleration through parallel operation of the operator using the proposed fitness functions.

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