Application of Adaptive Genetic Algorithm in Mining Industry

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Abstract— **Selection, mutation and crossover are the parameters that stipulate the evolution process. These three methods are used by the genetic algorithms. We've tried to apply genetic algorithms in mining industry, particularly in concentrating the manganese. It's necessary to optimize several parameters for that. In Adaptive genetic algorithms were applied Hamming weight and Hamming distance for selection and crossover. By Hamming Distance we search in chromosomes the similarity combinations and define the crossover point.**

Keywords— *Hamming weight; Hamming distance; fitness function; genetic algorithm*

I. INTRODUCTION

GENETIC algorithms which represent Natural evoluation process, solve the problems and basically optimization problems [1]-[2]. Apart from the classic Genetic Algorithms their modified variants are also widely used like Genetic Micro Algorithms and Adaptive Genetic Algorithms. In classical Genetic Algorithms basically is used the binary representation of chromosomes, roulette wheel selection, mutation and crossover point (basically one–point crossover). To raise the efficiency there are various modifications of genetic algorithms which are based on diverse methods of selection, the operators of crossover, and the ways of coding chromosomes. There are also genetic algorithms that allow finding not only global optimum but local optimum as well [1]-[3].

All other versions of genetic algorithms are used in multicriterial optimizations problems and for short-length chromosome populations genetic micro algorithms are used.

Section 2 reviews selection methods.

Section 3 reviews fitness function, the ranking of chromosomes by Hamming weight and normalized Hamming weight, the operator of mutation and the process of ranking of alleles in chromosomes.

Section 4 reviews mutation operator.

Section 5 reviews crossover operator and is calculated Hamming distance and the point of crossover operator.

Section 6 reviews the application of adaptive genetic algorithms in concentrating the manganese process and its consequences.

Section 7 shows small example of definition1,definition2 and definition3.

II. SELECTION METHOD

The main purpose of initialization or primary population forming is to select randomly from chromosomes combination necessary length and quantity of chromosomes [3]-[4].

Selection of chromosomes foresees selecting of those ones that will take part in forming new posterity for next generations. Based on natural selection, those chromosomes will be selected which ones fitness functions are higher. The higher is fitness function, the more "qualified" is chromosome. It is that fitness function is non-negative. There are meant several various methods of selection [3]-[4]

III. DEFINITION OF FITNESS FUNCTION

Fitness function is the most important conception in genetic algorithms, otherwise it is known as evolution function. It defines given individ's adaptation size in population. It plays special role because it defines concrete individ's adaptation in population, which has decisive purpose in evolution process based on the Principe of surviving the powerful. Form of the fitness function is depending on solving problem, on its nature. We should calculate each chromosome's fitness function and evaluate its selection.

As a rule in optimization problems fitness function is optimized. And it is called purpose function.

In various situations when it is needed to avoid genetic algorithms earlier convergence or when important nonhomogenous takes place in populations, they appeal fitness functions scaling operations like as linear scaling, sigma truncation of fitness function and power-law scaling [3]-[4].

All of them: roulette wheel selection, tournament selection, ranking selection basically use each chromosome ch_i, i=1,2,...N (N – size of population), $v(ch_i)$ – roulette sector size expressed in percents. We can rank chromosomes

$$V(ch_i) = P_s(ch_i)100\%$$

Baku, Azerbaijan

$$P_s(ch_i) = \frac{F(ch_i)}{\sum\limits_{i=1}^{N} F(ch_i)}$$

Where $F(ch_i)$ is chi chromosome fitness function, and $P_s(ch_i)$ – is ch_i chromosome selection probability.

The number of copies in mating pool

$$e(ch_i) = P_s(ch_i) * N, \quad i=1,2\ldots N$$

precisely, the number of copies is equal of $e(ch_i)$-s integer parts.

$$e(ch_i) = \frac{F(ch_i)}{\overline{F}}$$

Where $\overline{F}$ is fitness function average definition in population.

The definition of Hamming weight for binary chromosomes.

Definition 1. $w(ch_i)$ is called (chi) chromosome's Hamming weight and is equal of the number of ones in chromosomes [1].

Definition 2. The chromosomes normalized weight called P_i, binary chromosomes Hamming weight $w(ch_i)$ divided into L – chromosomes length.

We can rank chromosomes in population by P_i.

$$P_i = \frac{W(ch_i)}{L}$$

At the beginning of Algorithm, chromosomes are randomly generated alleles are randomly distributed. We use Hamming weight and by it we put in order the chromosomes

IV. MUTATION

The operator of mutation P_m probability ($0<P_m<1$) changes the meaning of gene in chromosome by its opposite meaning or 0 is changed by 1 and on the contrary. The mean of P_m probability is very small. That's why mutation is chosen comparatively rarely. In adaptive algorithms the process of mutation can be linked to chromosomes fitness function and item of distributing the alleles. Those chromosomes which are in the top rank their Hamming weight are higher and during the mutation 1 will change by 0. In chromosomes which are in the bottom of rank 0 will change by 1 [1] and [3]- [4].

V. CROSSOVER

In classical genetic algorithms crossover operation is used by one-point crossover. Apart from that there are two-point multiply-point uniform and inverse crossovers.

The definition of the crossover point in chromosome is random. Adaptive (modified) genetic algorithms the definition of the crossover point is determined in various methods. We search similar structure in chromosome. Hamming Distance is used to define similarity measure.

Definition 3. The number between two N-length ch_i and ch_j chromosomes is called Hamming distance $D(ch_i, ch_j)$, which is equal of the number of those positions in which chromosomes are different from one another [1].

In [1] Hamming distance measure between the i-th chromosome. In article [5] two different measures for Hamming distance. Long Hamming distance crossover D_i and short Hamming distance crossover

$$D_i{}' - L - D_i$$

Where L is length of chromosome and D_i Hamming distance between two chromosomes.

VI. APPLICATION : CONCENTRATING THE MANGANESE

In technological process of concentrating manganese is measured in input composition of manganese in mine and concentration in output. On the process basically is spent water and air supplied by pressure (the frequency of water pulsation) and etc. All these parameters are correlative with one another. Our goal is to minimize the expenses. By mathematical model which simply describes concentrating process (It is meant that in technological process participate four cameras which have different parameters):

$$Q = \sum_{j=1}^{N} (aB_j + qH_j)^2$$

Where a and q are constants.

B_j and H_j are water and air expenses, Q is totally spent energy. And we manage to minimize Q [6].

For this problem we have used classical genetic algorithm and adaptive genetic algorithm.

Population size 30 chromosome length – L=7.

Roulette wheel selection and one-point crossover 0,8.

Mutation probability is 0,005.

In adaptive genetic algorithms are used ranking by Hamming normalized weight. In mutation operator is used in chromosomes by Hamming weight and by selecting similar combinations in the top rank chromosomes is changed by D.

In the bottom of rank 0 is changed by 1. Crossover operator uses Hamming Distance.

VII. SMALL EXAMPLE OF DEFINITIONS

In order to demonstrate small example based on definition1,definition2 and definition3 , let's take small chromosomes pool. Population size 8 and chromosome length – L=7.We use binary representation of chromosomes.

TABLE I.
CHROMOSOMES BINARY REPRESENTATION WITH HAMMING WEIGHT AND NORMALIZED WEIGHT

Chromosome (ch_i)	Hamming weight $w(ch_i)$	Normalized weight P_i
0001010	2	2/7
0001011	3	3/7
0001100	2	2/7
0001101	3	3/7
0001110	3	3/7
0001111	4	4/7
0010000	1	1/7
0010001	2	2/7

At second step we must select the chromosomes with high hamming weight

TABLE II.
SELECTED CHROMOSOMES WITH HAMMING WEIGHT AND NORMALIZED WEIGHT

0001011	3	3/7
0001101	3	3/7
0001110	3	3/7
0001111	4	4/7

Based on definition 3 compute D_i and D'_i

TABLE III.
LONG HAMMING DISTANCE AND SHORT HAMMING DISTANCE

$D(ch_i, ch_j)$	D_i	D'_i (L-D_i)
$D(ch_1,ch_2)$	2	5
$D(ch_1,ch_3)$	2	5
$D(ch_1,ch_4)$	1	6
$D(ch_2,ch_3)$	2	5
$D(ch_2,ch_4)$	1	6
$D(ch_3,ch_4)$	1	6

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