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A Similarity-based Cellular Selection Mechanisim for Genetic algorithms to Solve Assignment Problems

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Abstract. In this paper, we illustrate a cellular structure mixed with Genetic Algorithms for solving assignment problems which have more than one feasible or optimum solution. Considering similarity among individuals in population, we use two dimensions Cellular Automata in order to place the individuals onto its cells to make the locality and neighborhood on Hamming distance basis. This new structure and using Genetic Algorithm on it, as 2D Cellular Automata Hamming GA, introduces locality for genetic selection and local knowledge for their selection process on cells of 2D Cellular Automata. The cellular selection based on the structure can ensure maintaining population diversity and fast convergence in the genetic search and improve the convergence performance during the genetic search.

Keywords: Genetic Algorithms, Assignment Problems, Cellular Automata, Optimization, NP-hard Multi Solutions Problems

1. Introduction

Genetic Algorithms (GAs) are used to solve difficult optimization problem like many NP-Hard Problems [1] in scientific and engineering areas. Resources distribution [2], management [3] and Assignment: Channel Assignment Problem [4], Graph Colouring Problem [5]; Multi-objective Optimization of Systems: 0/1 Multiple Knapsack Problem [6], Assembly Line Balancing Problem [7]; and etc are considered to solve by GA. But the main disadvantages of genetic algorithms are the disruption of good sub-solutions by crossover and mutation operations and undesired population diversity loss by selection operations, which constantly decreases the variety of its specimens.

Several mechanisms have been integrated with genetic algorithms in various ways to preserve the diversity of species. Reference [8] have presented a binary GA with a modified mutation operator, which is based on the well-known Hill Climbing Algorithm (HCA) and the selection operator preserves the best individual from the GA population during the selection process while maintaining the positive characteristics of the standard tournament selection. Chen and Wang [9] have presented a selection method combining roulette selection with tournament

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selection is presented to reinforce the local search ability. In [10, 11, and 12], some modified selection methods are proposed to increase the gain of resources, reliability and diversity.

In this paper, we introduce the property of multi feasible/optimum solution problems and cellular automata to realize the locality and neighbourhood in the population structure, which is done by using a computational cellular model and mapping individuals based on hamming distances between them. The selection mechanism of individuals (in GA) is controlled by this model to avoid the fast population diversity loss during the genetic search, and then by using the similarity-based cellular selection.

2. Genetic Algorithm and Multi Solution for Assignment Problems

2.1. Variety of solutions

Genetic algorithms (GAs) solve complex optimization problems by manipulating a population of solutions by genetic operators like selection, crossover (recombination) and mutation [15]. For manipulating solutions by means of genetic operators, they have to be encoded in form of so-called individual (or chromosomes) each of which consists of a sequence of genes. For example, a simple graph colouring problem is shown in fig. 1, with 3 colours, there is a string of bits as matrix C that illustrates colours assigned to nodes of graph (in each row of matrix C). In this solution (not exactly correct), colour 1 is assigned to nodes “a” and “d”, colour 2 is assigned to node “c”; colour 3 is assigned to node “b”.

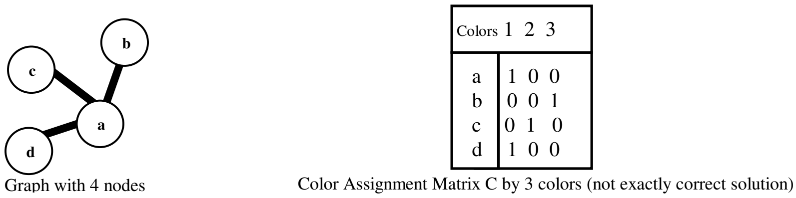
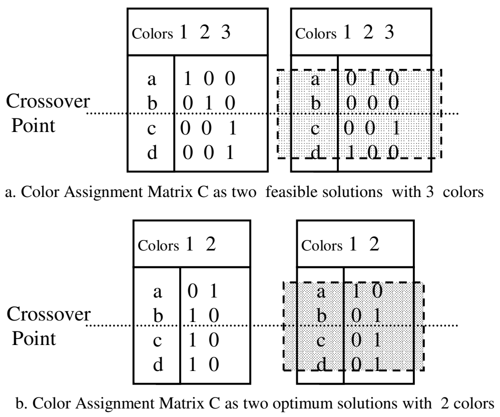


Fig. 1: A Graph colouring Problem with 3 colours.



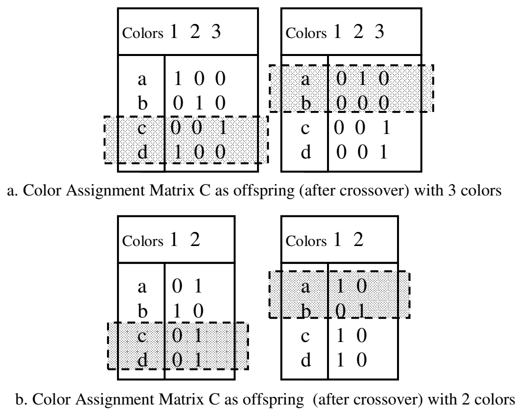


Fig. 2: Two fasible/Optimum Solutions for problem in fig. 1   Fig. 3: Two feasible/Optimum Offspring after do crossover

Fig. 3 shows offspring after crossover operation. As it is clear, the penalty for two new solutions is 1 (fig. 3.a) and for others (fig. 3.b) is 2. This retrogression has resulted from bad selection of couple to create offspring.

2.2. Hamming Distance between Binary Solutions

Some researcher tried to modify the mechanism of selection in order to improve the GA [2, 3, 4 and 5]. In [14] Hamming distance is used for grading the difference between binary strings that have an equal number of bits. Modified new selections have new mechanisms depend to Hamming distance between first and second parents.

2.3. Comparing HGA and Classic GA

To comparing, HGA is applied on the well-known NP-hard Problem in cellular mobile networks, Channel Assignment Problem (CAP) [4] that has Multi feasible/optimum solution with three constraints. All three constraints are considered for the channel assignments: the co-channel constraint, the adjacent channel constraint and the co-site channel constraint. The goal of CAP is the assignment of the channel frequencies which satisfied these constraints with the lower bound number of channels (as feasible/optimum solution).

In next section, we apply 2-Dimensional Cellular Automat to reduce the real time of running HGA and it keeps the improvement as well.

3. 2D Cellular Automata Hamming GA (2DCAHGA)

3.1. Mapping a population of GA onto a 2DCA

Before developing a 2DCAHGA, the individuals of each population are mapped onto all the cells of the cellular automaton, based on the Hamming distances.

Let us consider a population consisting of m individuals, with binary string v. We randomly choose v_i (i=1 … Size of Population), to be the element C (fig. 5), then the neighbourhood of C is constructed as follows. The individuals in population are sorted in ascending order of their corresponding Hamming distances to v_j. Choose the first eight elements v_k as the neighbourhood of C, with other elements scattered outside its neighbourhood, and then the whole population have been mapped onto a cellular automaton. The closest neighbours of C element are marked by # in fig. 5. They usually have smaller Hamming distance to C. This idea has introduced locality in GAs and global knowledge for their selection process. The selection based on this cellular automaton can ensure maintaining population diversity and fast convergence in the genetic search.

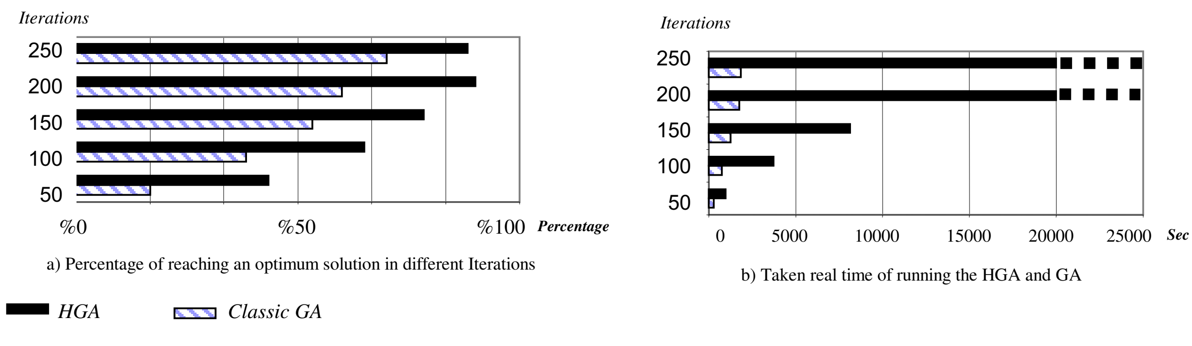


Fig. 4: Comparing HGS with GA for CA Problem (Percentage of success to reach an optimum solution / Real time).

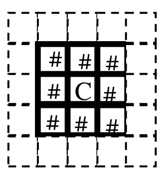


Fig. 5: A part of 2DCA – C cell and its neighbors with mark #

3.2. Steps of 2DCAHGA

Each cell in CA, independently do selection and select one neighbor on the selection rules as own local transition function. This operation can be done in concurrency way too as extra advantage (in some parallel computers which can do). Each cell according to own position on CA would have some candidates to select as mate. The 2DCA based Hamming genetic algorithm can, in essence, be given as follows:

Phase 1 (Making initial population)

- Step 1: generate initial population.

Phase 2 (Mapping on 2CA)

- Step 2: independently select an individual j from the current population. Map the selected individual j onto a cellular automaton, as described in the above subsection (previous sub section).
- Step 3: randomly chose one filled cell of CA such that has at leas an empty neighbor, and then select individuals and map just onto empty its neighbors as described before (previous sub section).
- Sept 4: if all cells of CA are not full, go to step 3.

Phase 3 (Cellular genetic actions)

- Step 5: independently, but they can concurrency, each cell select one of its neighbors as a mate to product a new offspring on their fitness and selection rules (as cellular selection).
- Step 6: in each cell, do crossover on individual in cell and its selected neighbor, and then do Mutation then, the one of the results would be kept instead of previous individual in the cell.

Phase 4 (Checking to finish)

- Step 7: if the best solution is not reached go to step 2.

There are 3 most important phases to do for 2DCAHGA and at the end of cellular genetic phase there is new population on cells. To continue the algorithm in order to reach a better solution, the phases would be continued (phase 4).

4. Simulation Results

The new GA, 2DCAHGA is applied for the same CAP has mentioned in section II. Whatever, 2DCAHGA is able to apply on many multi solution problems such 0/1 multi knapsack, graph coloring, assembly line balancing for manufacturing, placement, and etc. as well as CAP and the results are the same.

There is a noticeable improvement in the real (actual) time taken by running 2DCAGHA as compared to HGA and Classic GA in fig. 6.b. but there is not exactly specific behavior in low iterations (50 to near 150 iterations) to demonstrate that new mechanism of the selection would be better than the mechanism (of HGA) in percentage of reaching an optimum solution (see fig. 6.a). As it is obvious, new mechanism works well (about 90%) in high iterations of running (250 iterations) and the real time (about 1000 sec) too. Totally, the results show that the cellular model is capable of searching feasible/optimum solutions in reasonable time and iterations.

5. Conclusion

By using cellular structure, two dimensional cellular automata based hamming genetic algorithm (2DCAHGA) has been developed to maintain population diversity during the genetic search, which is essential for genetic algorithms to solve the difficult Multi feasible/optimum solution problems such as 0/1 multiple Knapsack, channel assignment in cellular mobile network, graph colouring, and many NP-hard problems which have more than one feasible or optimum solution. The cellular automaton is introduced to realize the locality and neighbourhood in the population structure. The similarity-based cellular selection of individuals is controlled based on the structure of cellular model. Applications of 2CAHGA in optimization problems have shown that 2CAHGA is capable of searching for the global optimum solution of difficult nonlinear optimization problems

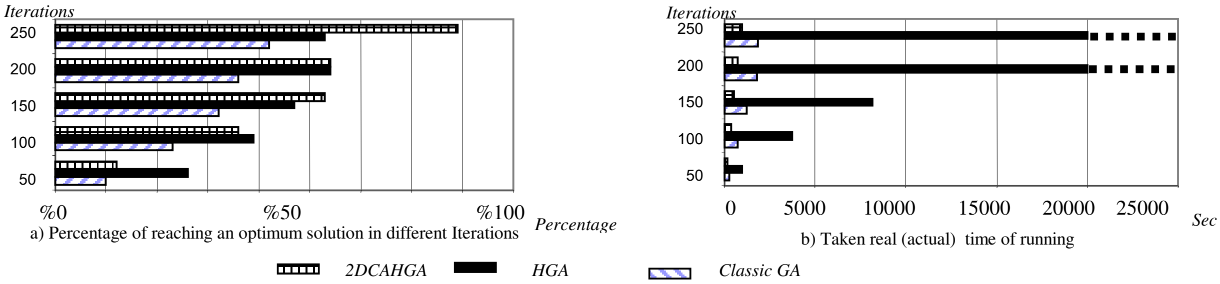


Fig. 6: Property of 2DCAHGA, HGS and Classic GA for CA Problem

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