

**CLASSICAL AND URGENCIES ASSIGNMENT METHODS IN  
*P*-MEDIAN PROBLEMS WITH FUZZY GENETIC ALGORITHM**

**M. Jalali Varnamkhasti<sup>1</sup> and Nasruddin Hassan<sup>2§</sup>**

<sup>1</sup> Department of Mathematics, Dolatabad Branch, Islamic Azad University  
Isfahan, Iran. Email: jalali.m.v@gmail.com

<sup>2</sup> School of Mathematical Sciences, Faculty of Science and Technology  
Universiti Kebangsaan Malaysia, 43600 UKM Bangi,  
Selangor D.E, Malaysia. Email: nas@ukm.edu.my

§ Corresponding author

**ABSTRACT**

The objective in the  $p$ -median problem is to minimize the total demand-weighted distance between facilities and demand points. Two different assignment techniques are considered. These techniques are the classical assignment technique and the assignment through urgencies technique. A fuzzy genetic algorithm, crossover operator and crossover rate are used to compare the behavior and efficiency of these methods. The performances of these techniques are assessed by using the benchmark problems currently available in open literature. It is found that the assignment through urgencies is much superior to the classical assignment method.

**KEYWORDS**

Fuzzy genetic algorithm;  $p$ -median problem; sexual selection; urgencies assignment.

**1. INTRODUCTION**

The four principal problems in the area of the theory of discrete location theory are: the quadratic assignment problem (QAP), the Uncapacitated Facility Location Problem (UFLP), the  $p$ -center problem and the  $p$ -median problem [Mirchandani and Francis (1990)]. Facility location problems have a number of applications, such as communications, industrial transportation and distribution networks. The prototype model of the  $p$ -median problem was considered by Hakimi (1965) who paid attention to network location problems and was proven  $NP$ -hard by Kariv and Hakimi (1979). Several methods based on Genetic Algorithm (GA) have been used in genetic algorithms by Varnamkhasti and Hassan (2012, 2013) and to solve  $p$ -median problems. Hosage and Goodchild (1986) were the first to apply genetic algorithms to the  $p$ -median problem.

Moreno et al. (1994) implemented a genetic algorithm whereby a collection of indices of the demand points represented the solutions. Maniezzo et al. (1998) presented a bionomic algorithm in how the parent set was obtained. Combining genetic algorithms and vertex substitution was considered by Estivill-Castro and Torres-Velázquez (1999) to avoid premature convergence. Cluster seed points was applied by Chiou and Lan (2001) while a dynamic population was used by Lorena and Furtado (2001), followed by

Bozkaya et al. (2002) who considered a GA with each chromosome has a  $p$ -median vertex as an index.

Alp et al. (2003) introduced a simple GA that evolves new solutions using the union of two solutions. Correa et al. (2004) developed heuristic hypermutation and Kratica et al. (2007) proposed new encoding schemes with associated objective functions. Domínguez and Muñoz (2008) considered genetic algorithm and some heuristic methods for solving this problem.

In order to find a solution for the capacitated  $p$ -median problem, we propose a Fuzzy GA (FGA) based on sexual selection, the selection of the crossover operator and crossover rate, by comparing two assignment methods in assigning demand points to those chosen  $p$  medians. The classical assignment method introduced by Kuhn (1955) assigns each randomly selected demand point to its nearest median. On the other hand, the assignment through urgencies used by Viera and Tansini (2004) is a technique to define a superiority relationship between demand points. This superiority relationship determines which demand points are assigned first to medians.

The paper is organized as follows. The  $p$ -median problem is defined in Section 2, while Section 3 discusses the proposed FGA. The computational results are tabled in Section 4, while conclusion remarks are in Section 5.

## 2. $P$ -MEDIAN PROBLEM

The objective is to minimize the total demand-weighted distance between the demand points and the facilities. The following formulation of the  $p$ -median problem is introduced by ReVelle and Swain (1970).

$$\min \sum_{i=1}^n \sum_{j=1}^n w_i d_{ij} x_{ij} \quad (1)$$

$$s.t. \quad \sum_{j=1}^n x_{ij} = 1 \quad \forall i, \quad (2)$$

$$x_{ij} \leq y_j \quad \forall i, j, \quad (3)$$

$$\sum_{j=1}^n y_j = p, \quad (4)$$

$$x_{ij} = 0 \text{ or } 1, \forall i, j \text{ and } y_j = 0 \text{ or } 1 \quad \forall j, \quad (5)$$

where

$n$  = total number of demand points,

$x_{ij} = \begin{cases} 1 & \text{if demand point } i \text{ is assigned to facility point } j, \\ 0 & \text{otherwise} \end{cases}$

$y_j = \begin{cases} 1 & \text{if a facility is located at point } j, \\ 0 & \text{otherwise} \end{cases}$

$w_i$  = demand at point  $i$ ,

$d_{ij}$  = distance between points  $i$  and  $j$

$p$  = number of facilities

The objective function (1) minimizes the total distances between the demand points and the median set. Constraint (2) ensures all demand points are assigned to only one median. Constraint (3) prevents a demand point from being assigned to non-selected facilities. Constraint (4) sets the total number of median points to be  $p$ . Constraint (5) stipulates binary values for the decision variables.

### 3. PROPOSED FUZZY GENETIC ALGORITHM

In this study we develop a sexual selection and Fuzzy Logic Controller (FLC) to achieve a better solution for solving P-Median Problems (PMPs).

#### 3.1 Encoding

The encoding in GA is important because a weak choice may result in a weak algorithm independent of its other characteristics. In a  $p$ -median problem, with  $N$  facilities, indexed as 1, 2... and  $N$ , we use simple encoding corresponding to the indices of facilities. For instance, a capacitated 6-median facility location problem (2, 5, 6, 23, 19, 7) is a chromosome where the demand points 2, 5, 6, 23, 19 and 7 are chosen as location of facilities. Note that each gene in each chromosome appears at most once.

#### 3.2 Population Diversity

We define a measure for diversity of chromosomes and populations based on phenotype characteristics and genotype. The methods proposed by Zhu and Liu (2004) are considered with a little modification as in Varnamkhasti et al. (2011).

$$T_{1,t} = \frac{n_{f_i}}{N} \quad (6)$$

$$T_{2,t} = \frac{f_{\max,t} - f_{avr,t}}{f_{\max,t}} \quad (7)$$

where,

$N$  = number of population.

$n_{f_i}$  = the number of different values of fitness in generation  $t$ .

$f_{\max,t}$  = the maximum value of fitness in generation  $t$ .

$f_{avr,t}$  = the average value of fitness in generation  $t$ .

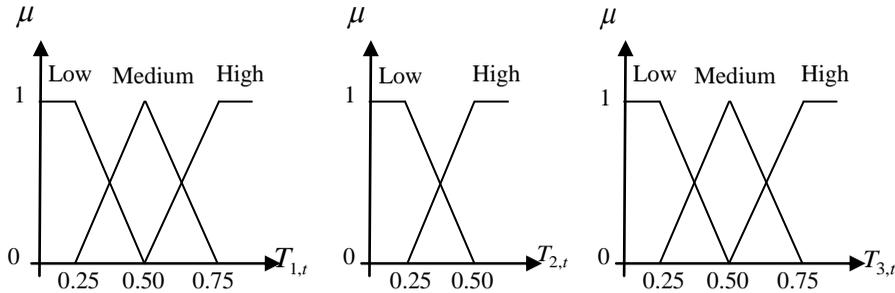
Genotype measure is given as

$$T_{3,t} = \frac{H\left(C_{f_{\max,t}} - C_{f_{\min,t}}\right)}{L} \quad (8)$$

where,  $H\left(C_{f_{\max,t}} - C_{f_{\min,t}}\right)$  is the Hamming Distance (HD) between the worst chromosome and the best one whereby  $L$  is the chromosome's length.

The HD is calculated for the chromosome with maximum and minimum fitness values. Thus, our method requires less time than Jassadapakorn and Chongstitvatana (2003).  $T_{1,t}$ ,  $T_{2,t}$ , and  $T_{3,t}$  belong to the interval  $[0, 1]$ . If these numbers are near zero, the population diversity is low and the algorithm may converge quickly. However, if it is close to 1, the population diversity will be higher.

Three membership functions are defined for  $T_{1,t}$ ,  $T_{2,t}$  and  $T_{3,t}$ . The linguistic labels for  $T_{1,t}$  and  $T_{3,t}$  are low, medium and high. Labels for  $T_{2,t}$  are without medium. Label meanings are illustrated by Figures 1 [Varnamkhasti et al. (2012)].



**Figure 1: Linguistic labels for  $T_{1,t}$ ,  $T_{2,t}$  and  $T_{3,t}$**

### 3.3 Fitness Function

The fitness function must be able to reflect the objective and direct the search towards optimal solution. The fitness of a chromosome assumes the value of the corresponding objective function, and it can be calculated using the problem data.

#### 3.3.1 Fitness Function for Classical Assignment

In classical assignment method for  $p$ -median problem each demand point that was randomly selected should be assigned to the nearest median. Each median has a certain capacity, thus some demand points will be assigned to the next nearest median to it. The assignment is finished when each of the demand points has been assigned to a median. When the assignment procedure has been completed, the fitness of the chromosome is calculated using the formula (1).

#### 3.3.2 Fitness Function for Urgencies Assignment

To determine the urgency of demand points we calculate distance of demand point  $i$  from second nearest median and first nearest median respectively, that is

$$\Delta D(i) = Sm(i) - Fm(i).$$

All demand points are placed in an assignment priority list in decreasing order by their respective  $\Delta D(i)$  ( $i=1,2,\dots,N$ ) values. When two or more demand points have the same  $\Delta D(i)$  value, they are placed in the assignment priority list (in subsequence position) by the order in which they were considered for computation of their  $\Delta D(i)$  values. The assignment process begins by assigning the first demand point in the list with highest

$\Delta D(i)$  value. When a median runs out of capacities, the list is immediately recomputed. The system restarts the assignment procedure for those demand points that have not yet been assigned, and for the medians that still have capacities.

The assignment is completed when each of the demand points has been assigned to a median. When the assignment procedure has been completed, the fitness of the chromosome can then be computed.

### 3.4 Sexual Selection

When integer encoding is used, a wide variety of genes appear within the chromosomes. The relation between the fitness value and Hamming distance (HD) is proposed for sexual selection. In this case, a female chromosome (female\_chro) is chosen from a certain selection size of the female group. Consequently, the male chromosome (male\_chro) will then be selected in preferential order using one of the following:

1. the maximum value of HD between the male\_chro and female\_chro,
2. the largest fitness value of the female\_chro,
3. random selection.

### 3.5 Fuzzy Crossover Operator Selection

In general GA performance is depends on genetic operators, and particularly on the crossover operator type. For selecting a crossover method based on integer encoding, some crossover operators are considered from available literature. Abbreviations for these operators are as in Table 1.

**Table 1**

**Common Abbreviations of Crossover Methods Based on Integer Encoding**

Crossover Methods	Abbreviation
Partially Mapped Crossover	PMX
Order Crossover	OX
Cycle Crossover	CX
Position Based Crossover	PBX
Alternating Position Crossover	APX

The chromosomes genetic diversity is medium ( $0.25 \leq T_{3,t} \leq 0.50$ ) when some gene share the same locations. In such case, the PMX and CX methods are not an excellent choice because the offspring and parent are identical or very similar to others whereas the OX, PBX or APX methods are more appropriate for these types of chromosomes.

When the population genetic diversity is low ( $T_{3,t} < 0.25$ ), some chromosomes are similar and thus the PMX, CX and PBX methods are not useful because the offspring and parent are identical or resemble one another. Under such condition the APX and OX methods are more suitable.

Therefore, we can say that OX and APX operators are appropriate in all cases of population diversity. Note that PBX is not useful when chromosomes are identical and

PMX is not useful when genetic diversity of chromosomes is medium or low. CX is useful for high diversity but time consumption is high.

Three levels of crossover operators based on integer encoding shown in Table 2 are introduced. We refer to them as Low, Medium and High. Low CA implies that the effect of this operator on genetic diversity is low, and this is relative to the structure of crossover operator or time consumption. Medium CA means this operator can increase genetic diversity but not much. CA is high if the effect of this operator on genetic diversity is high.

**Table 2**  
**Crossover Operator Categories**

Low	Medium	High
Cycle Partially Mapped	Position Based	Order Alternating Position

The genetic diversity in itself is not sufficient to handle the diversity of the population. Accordingly,  $T_{1,t}$ ,  $T_{2,t}$  and  $T_{3,t}$  are considered in this research and in compliance with their linguistic labels, fuzzy rules for the selection of the crossover methods are defined.

The AND/OR operator combines the inputs to produce output ( $x_i, \mu_i(CA)$ ) and response values ( $y_i, \mu_i(p_c)$ ) for all the expected inputs [Varnamkhasti et al. (2012)].

$$\mu_i(CA) = \max\{\mu_i(T_{1,t}), \mu_i(T_{2,t}), \mu_i(T_{3,t})\}, \quad (9)$$

$$\mu_i(p_c) = \min\{\mu_i(T_{1,t}), \mu_i(T_{2,t}), \mu_i(T_{3,t})\}, \quad (10)$$

for  $i = 1, 2, \dots$ , number of rules.

Using the Centre of Gravity approach for defuzzification [Varnamkhasti et al. (2012)], we have

$$x_{CA} = \frac{\sum_{i=1}^n \mu_i(CA)x_i}{\sum_{i=1}^n \mu_i(CA)} \quad (11)$$

$$y_{p_c} = \frac{\sum_{i=1}^n \mu_i(p_c)y_i}{\sum_{i=1}^n \mu_i(p_c)} \quad (12)$$

### 3.6 Mutation

The mutation operator is essential in genetic algorithm. Although reproduction and crossover supply much of the processing power, sometimes a particular demand point (facility) from the set of demands points (facilities) may not be eliminated very soon. Then the mutation performed in two steps is used in GA for improvement.

1. A random natural number  $k$ , whose value does not exceed the number of genes in the chromosome, is generated for each chromosome selected,
2. The gene number  $k$  is replaced by another randomly-generated gene (a facility index), provided that facility index is absent from the current genotype.

### 3.7 Stopping condition

The stopping condition for fuzzy genetic algorithm is set to be either the maximum number of generation or a maximum CPU time.

## 4. COMPUTATIONAL ANALYSIS

All experiments were tested on test problems on capacitated p-median location problem from the ORLIB library [Beasley (1990)], coded using C++ and run on a Pentium IV. The problem sizes range from 50 to 100,  $p = 5$  to 10, and capacity = 120. The parameters are as follows:

- Size of population = 50,
- The generation number = 1000, and
- The probability of mutation = 0.2.

The results, with the best solution on 1000 generations at the 10<sup>th</sup> iteration are as in Table 3. The proposed technique in assignment urgency has produced a suitable solution with minimal error. It shows that the urgency assignment is superior to the classical assignment.

**Table 3**  
**Comparison of Classical Assignment and Urgencies Assignment**

<i>Test#</i>	<i>n</i>	<i>p</i>	<i>Capacity</i>	<i>Optimal</i>	<i>Classical</i>	<i>Urgencies</i>
					<i>assignment</i>	<i>assignment</i>
					Error	Error
1	50	5	120	713	1.750	0.630
2	50	5	120	740	1.022	0.827
3	50	5	120	751	1.983	0.661
4	50	5	120	651	1.472	0.590
5	50	5	120	664	4.047	1.805
6	50	5	120	778	2.115	0.962
7	50	5	120	787	1.940	0.539
8	50	5	120	820	1.728	0.744
9	50	5	120	715	1.488	0.530
10	50	5	120	829	2.381	0.880
11	100	10	120	1006	2.062	0.981
12	100	10	120	966	1.720	0.607
13	100	10	120	1026	1.033	0.504
14	100	10	120	982	0.968	0.107
15	100	10	120	1091	1.094	0.408
16	100	10	120	954	2.057	0.820
17	100	10	120	1034	2.991	0.995
18	100	10	120	1043	1.039	0.607
19	100	10	120	1031	1.302	0.501
20	100	10	120	1005	2.170	0.839

## 5. CONCLUSION

In this study a fuzzy genetic algorithm based on sexual selection, the selection of the crossover operator and crossover probability, has been proposed to solve  $p$ -median problems. Two assignment techniques are compared. The urgencies assignment was found to be able to provide better solutions than that of the classical assignment.

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