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## **Scientific Research and Essays**

Full Length Research Paper

## Mobile electronic system integration placement optimization within ankara by using genetic algorithms

### Aysun COŞKUN<sup>1\*</sup> and Bekir HORAT<sup>2</sup>

<sup>1</sup>Department of Computer Education, Faculty of Industrial Arts Education, Gazi University, Gölbaşı, Ankara, Turkey. <sup>2</sup>Department of Computer Education, Gazi University, Institute of Informatics, Beşevler, Ankara, Turkey.

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Due to the increase in criminality, surveillance of society is increasing all over the world. When it comes to urban management just is not right to talk about security aspect. Safety management systems used in the study, the city of surveillance technology and placement methods which are used in the field were investigated. MOBESE, carry out a combination of a lot of function such as transportation, health care, city architecture and emergency response units. These systems are proceeding in parallel with technological advances in the development of urban safety management systems to benefit works. However, planning, infrastructure, installation, management and adapting to changing conditions should be conducted in at the deep. MOBESE is costly, complex and difficult to keep up to date, because application areas of MOBESE are very large cities. In this study, the genetic algorithm solution to the problem of Ankara City in the settlement of the MOBESE and as a result sought out the settlement plan has been optimized. Genetic algorithms demonstrate successful results in classical solutions, time-consuming and difficult to solve problems of this type of hosting of many variables and different criteria. This problem has been resolved by the method used in the solution, and the application has been tested for functionality and reliability.

**Key words:** City security management system, mobile electronic system integration (MOBESE), genetic algorithms, optimization, surveillance.

### INTRODUCTION

Following the emergence of modern state understanding, monitoring and surveillance activities of cities have been executed by governments and improvements have been supported. In today's world, in parallel with increasing magnitudes of criminality and terror crimes, surveillance over society is intensified (Karakehya, 2009; Güven, 2012). Today, all world countries design these systems suitably to their own cities and have been using these systems for a long time. In this regard, KGYS was established in Ankara. System is also known as

\*Corresponding author. E-mail: bekir.horat@gazi.edu.tr Abbreviations: KGYS, City Security Management System; MOBESE, Mobile Electronic System Integration.

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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Areas	Ulus Atatürk Statue Junction	Ulus metro exit	Ulus Osmanlı Junction	Talatpaşa Blv. Opera junction	TCDD station junction	Hipodrom st. Karabekir st. Junc.	Tandoğan junction	Celal bayar bıvd.	Rüzgarlı st. istanbul st entry	Rüzgarlı st Çankırı st. Entry	Ulus itfaiye square	Talatpaşa blvd - gençlik park	İstanbul st. k. Karabekir st. Junc.	C. Bayar blvd K. Karabekir st.junc.	Ulus sports complex entry	AKM entry	Atatürk Blvd. Telekom entrv	Atatürk Blvd Talatpaşa Blvd	Rüzgarlı St. Mid. exit	Büyükşehir building front.
ny	85	70	50	20	75	10	80	10	65	60	65	30	35	40	50	55	65	40	35	20
ty	85	65	90	70	60	65	70	60	55	50	65	50	55	60	30	40	45	45	25	55
gc	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	1	0
ydb	4	2	3	3	3	3	3	4	2	2	2	3	3	3	1	1	1	3	1	0
bg	3	1	2	1	2	1	1	1	1	1	1	1	1	1	3	3	2	1	1	3
ayb	3	3	3	2	3	3	3	2	3	3	3	3	3	3	3	3	3	3	3	3
ak	90	80	75	70	80	50	60	20	45	50	65	30	45	60	50	50	20	45	10	65
kb	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
hb	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1

Table 1. Location data representing gene structure of candidate placement points.

MOBESE. With the system, public order and security services for the region, traffic flow and congestion control, detection of violation of rules and surveillance of large areas are provided (Ekinci, 2011; Obuz, 2009).

MOBESE, considering its benefits, became a critical part of city management. MOBESE application is costly and complex, sensitive to change due to direct connection with human factor and is affected by nature and weather conditions. Before application, it is imperative to make a very good analysis of area and execute with a plan that will provide the maximum benefit (Ekinci, 2011).

Purpose of the application is defined as generally lowering the setup costs of the system while maximizing the obtained benefit (Çakar, 2009). With the model constructed in the study, it is aimed to find a placement model for KGYS in Ankara city center using genetic algorithm method (Temel, 2009). Structure of the application includes assumptions, system setup parameters and constraints (Sag, 2008).

# MOBESE PLACEMENT OPTIMIZATION WITHIN ANKARA BY USING GENETIC ALGORITHMS

In a planned MOBESE or a MOBESE with a revised plan of placement, parameters determining install conditions and values belonging to placement points show a related property. For this reason, changes among parameters can be modeled mathematically.

### Modelling

In the problem, chromosome structure consists of hybrid valued genes. This structure is due to the flexible

structure of genetic algorithm, in other words everything being unplanned and unscheduled (Gökay and Çağatan, 2002; Paki et al., 2002). In a chromosome formed to represent a possible placement point, genes are coded including following information. 1<sup>st</sup> gene: Population density information (ny); 2<sup>nd</sup> gene: Traffic density information (ty); 3rd gene: Input-output information (gc); 4<sup>th</sup> gene: Road state (boulevard, street, area, junction) information (ydb); 5th gene: Environment-building security information (bg); 6<sup>th</sup> gene: Infrastructure information (ayb); 7<sup>th</sup> gene: Region weight coefficient (ak); 8<sup>th</sup> gene: Red light violation point information (kb); 9th gene: Speed limit violation information (hb). In a problem consisting of 9 pieces of information, position data of cameras are [ng, ty, gc, bcka, bg, ayb, ak, kb, hb]. Example chromosome structure islows: [65,6,0,1,0,1,25,1,0].

The main purpose in the study is determining possible placement points (chromosomes) in the city (population). For this reason, first population containing N chromosomes (20 in application) which will be the possible solution of placement problem is constructed according to the data in the Table 1.

### Genetic algorithm's implementation steps

Which member of candidate points cluster will be subjected to placement process will be answered in the solution of the problem. Chromosome representing 1<sup>st</sup> candidate point in the implementation area from Table 1 is constructed. Other chromosome structures are constructed similarly:

*K*<sub>1</sub>=[ 85 85 0 4 3 3 90 1 0]

After population individuals are constructed, process of

finding the best individual can start. For every  $k_i$ , i  $\in$  [1,100], chromosome  $f(k_i)$  suitability value is calculated using the formula:

$$f(k) = \frac{\sum_{i=1}^{n} f(x_i)}{100}$$

For  $k_1 = [85 85 0 4 3 3 90 1 0] f(k_1) = \frac{\sum_{i=1}^{n} f(x_i)}{100} = (85+85+0+4+3+3+90+1+0)/100=2.71$ 

Every individual in the population is subjected to the same process. As  $f_{\text{max}} = 2.71$ , chromosome representing the optimum placement point in 1<sup>st</sup> generation is  $k_1$  chromosome.

Selection strategy using roulette wheel is used. Firstly, to find the total suitability value of population  $K = \sum_{i=1}^{0} f(k_i)$  formula is used:  $\sum_{i=1}^{0} f(k_i) = 2.71 + 2.22 + 2.24 + 2.18 + 1.66 + 1.32 + 2.18 + 0.98 + 1.72 + 1.67 + 2 + 11.7 + 1.39 + 1.67 + 1.38 + 1.53 + 1.36 + 1.37 + 0.76 + 1.5 = 33.01$ 

After this process, roulette wheel is designed using the calculations of the probabilities of selection of chromosomes in next generation. Selection probabilities of individuals are calculated cumulatively (Coşkun, 2006).

$$p(x_i) = \frac{f(k_i)}{K}$$
  $p_1 = \frac{k_1}{K} = 2.71/33.01 = 0.0820$   $q_1 = 0.0820$ 

determining selection After intervals for each chromosome, 20 numbers are determined randomly for each chromosome in [0,1] interval. Roulette wheel is spun 20 times, and the number area produced in each step (number that comes when the roulette wheel is spun) selects the individual that is represented by that area (Table 1). As a result of this selection, despite chromosomes with high suitability value having a higher probability of selection, chance of selection for individuals with lower suitability exists. Cumulative probabilities of being selected as belonging to all the chromosomes are added together (Table 2).

1<sup>st</sup> population of the 2<sup>nd</sup> generation formed as a result of selection is constructed as follows:

$$K_1 = K_{1(old)} = [85\ 85\ 0\ 4\ 3\ 3\ 90\ 1\ 0]$$
  
 $K_2 = K_{20(old)} = [20\ 55\ 0\ 3\ 3\ 3\ 65\ 0\ 1]$ 

Process following the formation of new population is crossing for forming chromosomes with better suitability values than chromosomes from the previous population. It is not necessary to apply crossing to every individual in the population. A crossing ratio is determined for some individuals of population to pass to next population without being subjected to crossing. In the study, considering the size of the population, values defined by Shaffer et. al. (1989) for crossing are used (Erişen, 2011). Crossing ratio is selected as 0.75. A random number is produced for every individual in the population in the interval [0,1]. If this number is smaller than crossing ratio, individual is subjected to crossing. If the number is larger, crossing is not applied:

 $r_1 = 0.012, r_2 = 0.982, r_3 = 0.156, r_4 = 0.659, r_5 = 0.397,$  $r_6 = 0.165....r_{20} = 0.834$ 

Chromosome numbers to be crossed are determined as follows. Crossing ratio is multiplied with the number of individuals in the population. As crossing will be applied between even numbers, if the result is odd, one is subtracted to round to even.

In the application, crossing ratio is  $(p_c)$  0.75, chromosome size in the population is  $(p_b)$  20, therefore \*  $p_c = p_b 20^* 0.75 = 15$ , 15-1=14 chromosomes will be subjected to crossing.

In order to subject individuals to crossing, a random crossing point is needed to be determined. In the chromosome, genes after the crossing point are substituted mutually. Two new off springs are created as a result (Tozan, 2007).

Randomly determined numbers for each chromosome previously are compared to  $p_c$ , If  $r_i < p_c$ , chromosome represented by this number is selected for crossing. Otherwise chromosome is not selected for crossing.

As  $r_1 < p_c$  0.012<0.75 1<sup>st</sup> individual is selected for crossing

As  $r_2 > p_c$  0.982>0.75 2<sup>nd</sup> individual is not selected for crossing.

After the individuals who will be subjected to crossing are determined, crossing point is determined randomly:

 $\begin{array}{l} K_1 \mbox{ and } K_3 \mbox{ are crossed after randomly selected 3^{rd} gene} \\ K_1 = [\underline{85\ 85\ 0\ 4\ 3\ 3\ 90\ 1\ 0}] \longrightarrow K_1 = [50\ 90\ 0\ 4\ 3\ 3\ 90\ 1\ 0] \\ K_3 = [\underline{50\ 90\ 0\ 3\ 2\ 3\ 75\ 1\ 0}] \longrightarrow K_3 = [\underline{85\ 85\ 0\ 3\ 2\ 3\ 75\ 1\ 0}] \\ K_4 \mbox{ and } K_5 \mbox{ are crossed after randomly selected 3^{rd} gene} \\ K_4 = [\underline{30\ 50\ 0\ 3\ 1\ 3\ 30\ 0\ 0}] \longrightarrow K_4 = [\underline{80\ 70\ 0\ 3\ 1\ 3\ 30\ 0\ 0}] \\ K_5 = [\underline{80\ 70\ 0\ 3\ 1\ 3\ 60\ 1\ 0}] \longrightarrow K_5 = [\underline{30\ 50\ 0\ 3\ 1\ 3\ 60\ 1\ 0}] \\ \text{New population formed as a result of crossing is as follows.} \end{array}$ 

 $K_1 = [50\ 90\ 0\ 4\ 3\ 3\ 90\ 1\ 0]\ K_2 = [20\ 55\ 0\ 3\ 3\ 3\ 65\ 0\ 1]$ 

Chromosomes	Suitability functions (F)	Selection probability (p)	Consecutive total selection probability(q)	Interval		
1	2.71	0.082	0.082	0-0.082		
2	2.22	0.0672	0.1492	0.82-0.1492		
3	2.24	0.0678	0.217	0.1492-0.217		
4	2.18	0.0502	0.2672	0.217-0.2672		
5	1.66	0.066	0.3332	0.2672-0.3332		
6	1.32	0.0399	0.3731	0.3332-0.3731		
7	2.18	0.066	0.4391	0.3731-0.4391		
8	0.98	0.0296	0.4687	0.4391-0.4687		
9	1.72	0.0521	0.5208	0.4687-0.5208		
10	1.67	0.0505	0.5713	0.5208-0.5713		
11	2.0	0.0605	0.6318	0.5713-0.6318		
12	1.17	0.0354	0.6672	0.6318-0.6672		
13	1.39	0.0421	0.7093	0.6672-0.7093		
14	1.67	0.0505	0.7598	0.7093-0.7598		
15	1.38	0.0418	0.8016	0.7598-0.8016		
16	1.53	0.0463	0.8479	0.8016-0.8479		
17	1.36	0.0411	0.8890	0.8479-0.8890		
18	1.37	0.0415	0.9305	0.8890-0.9305		
19	0.76	0.023	0.9535	0.9305-0.9535		
20	1.5	0.0454	1.0	0.9535-1.0		

Table 2. Selection probabilities of chromosomes.

<i>K</i> <sub>3</sub> = [85 85 0 3 2 3 75 1 0]	<i>K</i> <sub>4</sub> =[80 70 0 3 1 3 30 0 0]
<i>K</i> <sub>5</sub> =[30 50 0 3 1 3 60 1 0]	<i>K</i> <sub>6</sub> =[80 70 0 3 2 3 75 1
0]	
<i>K</i> <sub>7</sub> =[50 90 0 3 1 3 60 1 0]	K <sub>8</sub> =[35 25 1 1 1 3 10 0
0]	
K <sub>9</sub> =[80 70 0 3 1 3 45 0 0]	$K_{10}$ =[35 55 0 3 1 3 60 1
0]	
<i>K</i> <sub>11</sub> =[20 70 0 3 1 2 70 0 0]	<i>K</i> <sub>12</sub> =[50 30 1 1 3 3 50 0
0]	
<i>K</i> <sub>13</sub> =[20 70 0 3 1 2 70 0 0]	<i>K</i> <sub>14</sub> =[35 25 1 1 1 3 10 0
0]	
<i>K</i> <sub>15</sub> =[65 65 0 2 1 3 65 0 0]	<i>K</i> <sub>16</sub> =[65 65 0 2 1 3 65 0
0]	
<i>K</i> <sub>17</sub> =[65 55 0 3 1 3 50 0 0]	<i>K</i> <sub>18</sub> =[10 65 1 2 1 3 45 0
0]	
<i>K</i> <sub>19</sub> =[50 90 0 3 2 3 75 1 0]	<i>K</i> <sub>20</sub> =[55 40 1 1 3 3 50 0
0]	

To provide the genetic diversity in the newly formed population as a result of crossing, mutation is applied using a certain probability value. For the mutation, for each gene of each individual, 180 random numbers are generated (20(individual)\* 9 (gene)=180) in the interval [0-1]. ( $0 \le ri \le 1$ ,  $i \in [1, 180]$ )

Before the mutation process, following equation suggested by Bäck will be used to determine the mutation ratio:

$$\frac{1}{PopulationSize} \le P_{MutationRatio} \le \frac{1}{ChromosomeLength}$$

 $\frac{1}{20} \le P_{MutationRatio} \le \frac{1}{9}$  From this mutation ratio ( $P_m$ ) is determined as 0.05.

The subject to consider here is, due to the unique structure of the chromosome, genes belonging to chromosome are not in the same structure and properties. Because of this, each gene will be subjected to mutation with their own properties. Genes 1, 2 and 7 are valued between 0 and 100, while genes 3, 4, 5, 6, 8, 9 are valued with 1,0 code. Therefore, genes 1, 2 and 7 are substituted with values that round them to 100 while genes 3, 4, 5, 6, 8, 9 are evaluated with modifiers.

Due to the difficulty of the application, instead of this method, application of following method will yield better results (Bağış, 1996).

1. A random x number is generated between 0-9

2. If x value is 1,2 or 7, a random y number is generated between 0-100  $\,$ 

3. If x value is not 1, 2 or 7, and current value is 0, y is generated as 1, if current value is 1, y is generated as 0 4. Gene values on chromosome is compared to this y

value.

5. If the generated y number is the same as the  $x^{th}$  gene value of the chromosome, a different y value is generated.

6. If the x<sup>th</sup> gene value in the chromosome is different than y value, gene in the x position in the chromosome is found.

7. Y value is substituted in the place of this found value

8. Apply these steps to all chromosomes in the population.

As a result of mutation, chromosomes with changed genes are substituted with the old ones, forming the new population (Civril, 2009). New population formed as a result of mutation of population is as follows:

 $K_1 = [50 \ 90 \ 0 \ 4 \ 3 \ 3 \ 90 \ 1 \ 0] \quad x=2, \ y=56 \longrightarrow K_1 = [50 \ 56 \ 0 \ 4 \ 3 \ 3 \ 90 \ 1 \ 0]$ 

 $K_2$  = [20 55 0 3 3 3 65 0 1] x=1, y=98  $\rightarrow K_2$  = [98 55 0 3 3 3 65 0 1]

Suitability value of the new population is calculated again. For  $k_1 = [50 \ 56 \ 0 \ 4 \ 3 \ 3 \ 90 \ 1 \ 0] \quad f(k_1) = (50+56+0+4+3+3+90+1+0)/100=2.11$ 

For  $k_2 = [98\ 55\ 0\ 3\ 3\ 3\ 65\ 0\ 1]$   $f(k_2) = (98+55+0+3+3+3+65+0+1)/100=2.28$ 

For  $k_{20}$ =[55 40 1 1 1 3 50 0 0]  $f(k_{20})$ =(55+40+1+1+1+3+50+0+0)/100=1.51

As  $f_{\text{max}}$  =2.55 chromosome representing the optimum

placement point in  $2^{nd}$  generation is  $k_3$  chromosome.

If the generation number determined at the beginning of the application is not completed, all steps are exercised again from step 2.

 $f_{tmax}$  values found as a result of every t generation are compared with each other. As a result of the comparison, chromosome giving the highest suitability value is giving the optimum placement plan. In the application, at the end of 2<sup>nd</sup> generation 3<sup>rd</sup> chromosome represents the best placement point.

Ulus Osmanlı Junction (3<sup>rd</sup> placement point in Table 1), represented with chromosome.  $K_3 = [85\ 85\ 0\ 3\ 2\ 3\ 75\ 1]$ 

1] represents the first point that needs placement. From the genes of the chromosome:

1st gene: 85, the area has a high population density

2<sup>nd</sup> gene: 85, the area has a high vehicle density

3<sup>rd</sup> gene: 0, the area is not an input-output point.

4<sup>th</sup> gene: 3, the area is a boulevard

5<sup>th</sup> gene: 2, area is in 2<sup>nd</sup> degree zone with respect to environmental safety

 $6^{\text{th}}$  gene: 3, area is a  $3^{\text{rd}}$  degree zone with respect to infrastructure

- 7<sup>th</sup> gene: 75, area weight coefficient is high
- 8<sup>th</sup> gene: 1, red light violation system is required

9<sup>th</sup> gene: 1, as it is a boulevard, speed limit violation system is required

### Conclusions

Application gives the optimum placement plan output in accordance with inputs belonging to candidate placement points. Output here represents the best result given by the candidate placement points. Output number will get higher as number of candidate application points in the city increase. Optimum placement point obtained as a result of the application is expected to improve depending on the number of iterations. In the example application, it is aimed to find 1 point which will yield the optimum result from 20 placement points in the city. In an application that will include the entire city, iteration number will get higher as output number gets higher.

As a result, designed application meets the expectations and gives the possibilities of application for bigger areas. Placement process done via the program includes placement number belonging to hardware, code, camera number, county and region information, placement purpose, hardware type and installation address.

### **Conflict of Interest**

The authors have not declared any conflict of interest.

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