Genetic Algorithm for Facility Layout Design with Unequal Departmental Areas and Different Geometric Shape Constraints

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Abstract

The objective of this research is to present a genetic algorithm-based model for facility layout problems with unequal departmental areas and different geometric shape constraints. Gene structures of the genetic algorithm are used to represent layout of departments. The algorithm involves deriving an initial assignment of departments to the given floor plan and then, possibly, improving the solution quality through genetic algorithm mechanisms (i.e., exchange parts of layout). Since genetic algorithm is parameter sensitive, the experiments indicate that crossover type, mutation type, mutation probability, and population size are the main parameters that designers need to consider while designing facility layout with genetic algorithm. Guidelines for such parameters are also given.

Keywords: Facility layout design, Genetic algorithm.

1. Introduction

Facility layout design involves the physical arrangement of a number of interacting facilities on a certain planar site [1]. A facility in this context means a physical entity used for facilitating the processing of any job. For instance, a work center, a machine tool, a department, a warehouse, a manufacturing cell, etc. No matter what types the facilities are, the common characteristic that is always a major concern in the design phase for all facilities is the area and shape occupied by the facility. Optimal design of the facility layout is one of the most critical issues that the designer has to solve in the early stages of the manufacturing system design.

While setting up a manufacturing system, the designer has to organize a floor plan layout for all facilities so that the travelling distance of personnel, paperwork (information), or material handling carriers between each pair of facilities is minimized. Several additional factors, some being conflicting, have to be taken into account to arrive at a satisfactory floor plan layout including area requirements, geometric constraints of each facility, traffic volume between facilities, etc. Very often, the designer has to tradeoff between conflicting factors to produce a feasible layout [2].

The facility layout problem is similar to the classical quadratic assignment problem (QAP) [3]. The objective function depends on the flow between the departments and their relative locations. The formulation of the total cost of assignment of the facility layout problem can be simply given by [4]:

$$\min Z = \sum_{i=1}^{m}\sum_{j=1}^{m} f_{ij} c_{ij} d_{ij} \qquad (1)$$

Where m denotes the number of departments, f_{ij} denotes the flow from department i to department j (expressed in number of unit loads moved per unit time), c_{ij} denotes the cost of moving a unit load one distance unit from department i to department j, and d_{ij} denotes the distance from department i to department j. Generally, the distance d_{ij} is generally measured rectilinearly between department centroids. In the final solution, each facility is assigned to a suitable site so that the total transportation cost (Z) is minimized without violating any imposed constraint, i.e.

each facility has to be assigned only once to a location on the floor plan and its area cannot be overlapped with one another.

It is known that QAP is one of the problems classified in the class of NP-complete problems [5]. As a result, no efficient algorithm to optimally solve the problem has been found yet. Large numbers of heuristics have been developed to obtain good and acceptable solutions [6]. Mainly, these heuristics can be classified into two categories, i.e., construction method and improvement method. In construction method, the solution is created by ordering all facilities according to some algorithm and then sequentially input them one-by-one into the floor plan. Once the facility is entered, its location on the floor plan will be fixed. In contrast, improvement method begins with an initial facility layout and tries to search for better quality of solutions by interchanging their locations. Despite their simplicity, both methods suffer when the constraints related to area requirements and geometric shapes are considered.

In this paper, the facility layout problem with unequal area requirements and different geometric shape constraints is addressed. Genetic algorithms (GAs) are employed as a solution procedure. The objective is to minimize total transportation cost while satisfying area and geometric constraints of each facility. In Section 2, an overview of GAs is presented. This is followed by a discussion on the experimental design used to test the efficiency of GAs. The experimental results are reported in Section 4. Finally, the conclusions of the paper are given in Section 5.

2. Genetic Algorithms

GAs are powerful stochastic search and optimization techniques based on the principles of evaluation theory [7]. They emulate the mechanism of natural selection and natural genetics. GAs begin with an initial set of solutions selected at random called *population*. In the given population, each individual, which is a solution to the problem and normally represented by a string of symbols, is called a *chromosome*. Each bit of the chromosome, being a part of the solution, is called a *gene*. Through successive iterations, called *generations*, the chromosomes evolve. Each chromosome in each generation is evaluated by some measures of its *fitness* (related to the objective function of the problem). New chromosomes for the next generation, called *offspring*, are formed from the current generation either by *crossover* operator (exchanging some particular parts of two chromosomes) or *mutation* operator (modifying a chromosome). A new generation is created by selecting some of the parents and offspring according to their fitness values. The fitter the chromosome, the higher the probability of being selected. In order to keep the size of population constant, some of the parents and offspring that have poor fitness values are discarded. After several successive iterations, the best chromosome emerges. This chromosome may represent the optimum solution or at least sub-optimal solution to the problem.

In order to employ GAs to search for the best solution of facility layout problems with unequal areas and different geometric shapes, the following steps are used.

Representation: The permutation of departments is employed as the way to encode the facility layout into a chromosome. For example, for 5-departments layout problems, one of the feasible chromosomes can be $v_k = [m^k_5, m^k_3, m^k_2, m^k_1, m^k_4]$, where m^k_i represents the i^{th} department of the k^{th} chromosome.

Physical arrangement: Once a chromosome is formed, it is ready for the physical placement of facilities into the given layout. It is essential that the placement procedure should generate a feasible layout with minimum computation. The placement procedure can be stated as follows:

1. *Divide the layout into bands or strips*. Each bandwidth is not necessarily equal so as to increase the diversity of the layout alternatives. These bandwidths are randomly generated. The sum of the bandwidths must be equal to the width of the floor plan. Also the number of bands is randomly generated.

$$\sum_{i=1}^{n} B_i = b \qquad (2)$$

Where:
B_i = Width of the i^{th} band.
n = Total number of the bands.
b = Width of the floor plan.

The random numbers generated for each bandwidth must satisfy the inequality constraint.

$$B_S \leq B_i \leq B_L \quad (3)$$

Where:
B_S = Smallest department width.
B_L = Largest department width.

2. *Lay off the departments into the bands.* The procedure is to lay off the facilities according to the sequence given by the chromosome into the bands. The facility is laid off from one end of the floor plan to the other, then the direction is reversed. The procedure continues until all the facilities are filled (See Figure 1 for 4- facility layout).

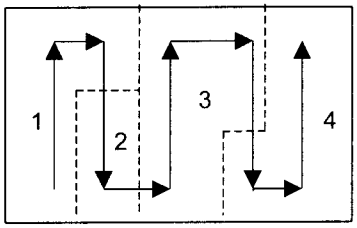

Figure 1. Facility placing procedure.

It can be seen that the shape of each facility is allowed to be a polygon, not being necessarily restricted to a rectangle. Having laid all facilities, feasibility checking of each department width is conducted against Equation (3). If there exists any constraint violation, the tentative layout is discarded and the placement procedure is restarted until a feasible solution is found.

Evaluation: Once all the departments are located on the floor plan, the total cost for the k^{th} chromosome is calculated as given in equation (1). Since the objective function has to be minimized, the fitness value of the chromosome has to reflect such relationship, i.e., the fitter chromosome the higher fitness value. As a result, the conversion is needed to transform the total cost of the k^{th} chromosome (Z_k) to the fitness value.

$$\text{eval}(v_k) = 1/Z_k \quad (4)$$

Where eval (v_k) is the fitness value of the k_{th} chromosome. The mechanism to reproduce chromosomes in the next generation is the roulette wheel method. Elitist strategy is also enforced within the roulette wheel selection to ensure that the best chromosome will be preserved in the next generation and overcome the stochastic sampling errors.

Crossover: Crossover is the main operation of GAs. Two chromosomes are randomly selected to generate offspring by exchanging the features of their chromosomes. Several crossover operators have been developed, such as partial-mapped crossover (PMX), order crossover (OX), cycle crossover (CX), position-based crossover (PBX), and order-based crossover (OBX). The details for each type of crossover operators can be stated as follows.

PMX begins by selecting two parents from the current population, selects two positions along the string of the parent at random, defines this portion of the string as *sub-string*, and calls the sub-strings of the two selected chromosomes as the *mapping sections*. Two sub-strings of the parents are then exchanged to produce proto-children (illegal children). Two mapping sections are matched to determine the *mapping relationship* between them. The legal offspring is created by utilizing the mapping relationship.

OX is very similar to PMX but using a different repairing procedure. It begins with selecting a substring from one parent at random and copies the substring into the corresponding positions of a proto-child. From the second parent, delete the numbers which already exist in the substring and place these numbers into the proto-child from left to right according to the order of the sequence to produce an offspring.

PBX begins with selecting a set of positions (generally not consecutive positions) from one parent at random and copies the substring into the corresponding positions of a proto-child. From the second parent, delete the numbers already exist in the substring and place these numbers into the proto-child from left to right according to the order of the sequence to produce an offspring.

OBX is a slight variation of PBX in which the order of genes in the selected position in one parent is imposed on the corresponding genes in the other parent.

CX determines the cycle defined by the corresponding positions of genes between parents and copies these genes in the cycle to an offspring with the corresponding positions of one parent. To determine the remaining genes for the offspring, those genes that are already in the cycle from the other parent are deleted. These remaining genes are placed into the unfixed positions of the offspring from left to right according to the order of sequence.

Mutation: Several types of mutation operators are used in this research, i.e. insertion, reciprocal exchange, and random sequence mutations. For insertion mutation, a gene is selected at random, taken off from the chromosome and then inserts it back in a random position. Reciprocal exchange mutation chooses two positions at random and then the genes on these positions are swapped. For random sequence mutation, a mutation point on the chromosome is selected at random. The genes to the left of the mutation point are kept frozen. In contrast, the sequence of the genes starting from the mutation point onward is rearranged randomly.

Stopping conditions: Two stopping conditions are employed to stop GAs from doing further iteration. First, if the number of iterations exceeds a predefined value, GAs stop the operation. On the other hand, if the value of objective function does not change within a given number of iterations, the mechanism of GAs is also stopped. Once stopped, the best value of the objective function is obtained.

3. Experimental Design

In order to study how several parameters effect the performance of GAs, the factors and their levels that are the main interest of this research are as follows:

- *Problem size (departments):* 6, 10, and 20 to represent small, medium, and big problem size respectively.
- *Crossover:* PMX, OX, CX, PBX, and OBX.
- *Mutation:* insertion, reciprocal exchange, and random sequence.
- *Population size:* 10, 15, and 20.
- p_c *(crossover probability):* 0.5, 0.7, and 0.9.
- p_m *(mutation probability):* 0.1, 0.2, and 0.3.

The total number of experiments is 3x5x3x3x3 = 405.

4. Results

From Figure 2, it can be seen that the objective function (minimizing) drops down rapidly during the beginning period of GAs manipulation and finally converge to a particular number after running GAs for a predefined amount of time or no more improvement can be achieved within the predefined number of iterations. The faster the convergent rate as well as the quality of solution, the better the characteristic of GAs. It is worth noting that GAs do not guarantee an optimal solution. However, from research experiences, GAs often provide a good and acceptable solution. Moreover, it is found that the final solution and the solutions at the beginning of the experiment is substantially different.

In the case of 6 departments, ANOVA [8] (Figure 3) shows that the factors that have significant impact on the solutions include population size, crossover types, mutation type, and mutation probability. It can be seen from Duncan's multiple-range tests that population size of 10; crossover type OX; mutation type insertion and reciprocal exchange; and probability of mutation of 0.3 are significantly different comparing with the other levels in the same factor (see Figure 4).

Similar to the previous case, ANOVA of the problems of 10 departments indicates that 4 factors have significant impact on the quality of solutions (Figure 5). These factors consist of population size, crossover type, mutation type, and mutation probability. Population size of 15; crossover type OBX; mutation type insertion and reciprocal exchange; and probabilities of mutation of 0.2 and 0.3 give significantly better performance than the others (Figure 6).

For the problem of 20 departments, only 2 factors show significant impact on the quality of solutions including crossover type and probability of mutation (Figure 7). Duncan's multiple range tests indicate that crossover type OX, PBX, PMX, and OBX; and probabilities of mutation of 0.3 and 0.2 outperform the other levels of the same factor (Figure 8).

From extensive experiments, it can be concluded that the factors that have significant effects on the quality of solution of GAs in solving facility layout problems are population size, crossover type, mutation type, and mutation probability. The factor that seems to have no significant impact on GAs' performance

is probability of crossover. It is worth noting that before the levels of probabilities of crossover and mutation were selected for conducting experiments, a number of pilot runs were carried out to identify appropriate solution space. Quality of solutions and fastness of convergence to the solutions are the main criteria for selecting appropriate levels of factors to conduct further experiments. Although significant differences cannot be notified while changing levels of crossover probabilities, it tends to be that this range of crossover probabilities is already acceptable.

From the experiments, guidelines for those who want to design facility layout with unequal departmental areas using GAs can be given as follows: crossover type OX; population size of 10 or 15; mutation probability of 0.2 or 0.3; and mutation type insertion or reciprocal exchange. Since GAs are parameter sensitive, in real facility design, one has to explore to find fitted parameters to the problem at hand. However, this guideline can be beneficial in terms of narrowing down the search space for solutions, especially while conducting rough-cut experiments. If optimal setting for the parameters of GAs is really needed, the response surface method [8] is worth considering.

5. Conclusions

The facility layout problem deals with searching for the most effective physical arrangement of facilities required to facilitate the production of products or services. This study has been conducted to utilize one of the artificial intelligence techniques known as GAs to solve this kind of problem. Since GAs are parameter sensitive, extensive experiments are carried out to find guidelines for setting such parameters. The parameters that tend to be significant and need proper setting include crossover type, population size, mutation type, and mutation probability. Hopefully the guideline provided in this research could help designers in finding an efficient facility layout, especially during the rough-cut design phase.

6. References

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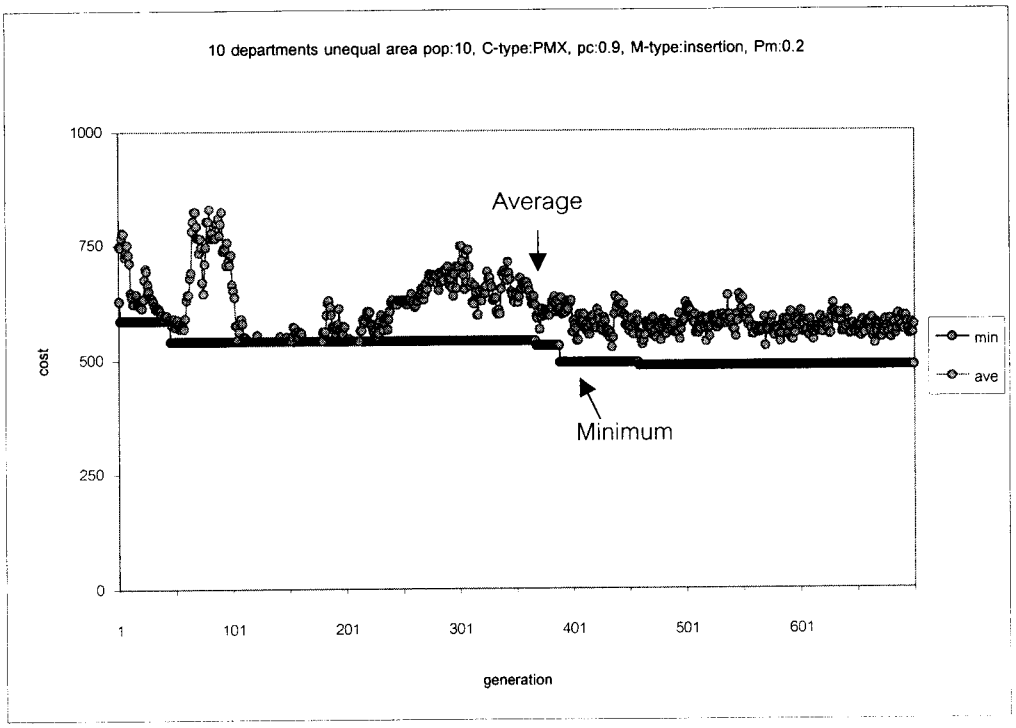

Figure 2. Plot between objective function and generation number.

Effect Test For 6 Departments

Source	DF	Sum of Squares	F Ratio	Prob > F
Pop	2	29878208	10.5272	< 0.0001
Ctype	4	79218965	13.9559	< 0.0001
Pc	2	6680507	2.3538	0.0963
Mtype	2	30211551	10.6447	< 0.0001
Pm	2	12125548	4.2723	0.0146
Pop* Ctype	8	11408949	1.0049	0.4316
Pop*Pc	4	8278653	1.4584	0.2141
Pop*Mtype	4	8424560	1.4841	0.2061
Pop*Pm	4	12086752	2.1293	0.0764
Ctype*Pc	8	12869971	1.1336	0.3393
Ctype*Mtype	8	12134895	1.0689	0.3840
Ctype*Pm	8	14042480	1.2369	0.2758
Pc*Mtype	4	1507257	0.2655	0.9000
Pc*Pm	4	4358809	0.7679	0.5466
Mtype*Pm	4	9088570	1.6011	0.1732
Pop*Ctype*Pc	16	18482415	0.8140	0.6699
Pop*Ctype*Mtype	16	12512101	0.5511	0.9186
Pop*Ctype*Pm	16	14073240	0.6198	0.8684
Pop*Pc*Mtype	8	3523085	0.3103	0.9620
Pop*Pc*Pm	8	3408711	0.3003	0.9657
Pop*Mtype*Pm	8	7082187	0.6238	0.7579
Ctype*Pm*Mtype	16	19244860	0.8476	0.6308
Ctype*Pc*Pm	16	44027692	1.9391	0.0160
Ctype*Mtype*Pm	16	19630327	0.8646	0.6110
Pc*Mtype*Pm	8	21250137	1.8718	0.0629
Pop*Ctype*Pc*Mtype	32	28525553	0.6282	0.9452
Pop*Ctype*Pc*Pm	32	35417266	0.7799	0.8017
Pop*Ctype*Mtype*Pm	32	38000976	0.8368	0.7235
Pop*Pc*Mtype*Pm	16	26370818	1.1614	0.2965
Ctype*Pc*Mtype*Pm	32	33479847	0.7373	0.8526
Pop*Ctype*Pc*Mtype*Pm	64	101883924	1.1218	0.2553

Figure 3. ANOVA for 6 departments.

Duncan's multiple range tests

Population size

Population size	15	20	10
Mean	19085.7	19315.4	19556.1
	•		
		•	

Crossover type

Crossover type	OX	PMX	Order-Base	Position-Base	CX
Mean	18786.8	19213	19420.4	19446.5	19728.9
	•				
		•	•	•	
			•	•	
				•	

Mutation Type

Mutation Type	Insertion	Reciprocal Exchange	Regen
Mean	19140.6296	19229.311	19587.3925
	•	•	
		•	

Pm

Pm	0.3	0.2	0.1
Mean	19163.1585	19332.1888	19461.9925
	•	•	
		•	•

Figure 4. Duncan' multiple range tests for 6 departments. (• = significant different)

Effect Test for 10 Departments

Source	DF	Sum of Squares	F Ratio	Prob > F
Pop	2	241909.2	1.6055	0.2021
Ctype	4	1228876.1	4.0780	0.0030
Pc	2	18780.3	0.1246	0.8828
Mtype	2	247536.2	1.6429	0.1947
Pm	2	3170717.1	21.0439	<0.0001
Pop* Ctype	8	334947.1	0.5558	0.8140
Pop*Pc	4	471708.7	1.5654	0.1827
Pop*Mtype	4	405835.6	1.3468	0.2519
Pop*Pm	4	409975.5	1.3605	0.2469
Ctype*Pc	8	358134.9	0.5942	0.7828
Ctype*Mtype	8	932809.5	1.5478	0.1389
Ctype*Pm	8	424871.5	0.7050	0.6872
Pc*Mtype	4	487048.5	1.6163	0.1693
Pc*Pm	4	1117485.5	3.7083	0.0056
Mtype*Pm	4	297906.4	0.9886	0.4135
Pop*Ctype*Pc	16	1824357.5	1.5135	0.0912
Pop*Ctype*Mtype	16	1052015.8	0.8428	0.6013
Pop*Ctype*Pm	16	1760265.5	1.4603	0.1109
Pop*Pc*Mtype	8	132442.6	0.2198	0.9873
Pop*Pc*Pm	8	1334367.7	2.2140	0.0256
Pop*Mtype*Pm	8	577776.8	0.9587	0.4680
Ctype*Pm*Mtype	16	1252451.7	1.0391	0.4138
Ctype*Pc*Pm	16	1942102.1	1.6112	0.0628
Ctype*Mtype*Pm	16	1160531.1	0.9628	0.4971
Pc*Mtype*Pm	8	825805.0	1.3702	0.2077
Pop*Ctype*Pc*Mtype	32	2612634.8	1.0837	0.3496
Pop*Ctype*Pc*Pm	32	2274253.8	0.9434	0.5588
Pop*Ctype*Mtype*Pm	32	259795.8	1.0701	0.3681
Pop*Pc*Mtype*Pm	16	1397993.0	1.1598	0.2979
Ctype*Pc*Mtype*Pm	32	2829205.4	1.1736	0.2410
Pop*Ctype*Pc*Mtype*Pm	64	3822566.8	0.7928	0.8725

Figure 5. ANOVA for 10 departments.

Duncan's multiple range tests

Population size

Population size	15	20	10
Mean	534.004	540.241	542.804
	•		
		•	•

Crossover type

Crossover type	Order-Base	Position-Base	PMX	OX	CX
Mean	531.864	537.704	538.623	540.444	546.444
	•	•	•		
		•	•	•	
			•	•	
				•	•

Mutation Type

Mutation Type	Insertion	Reciprocal Exchange	Regen
Mean	537.137	537.207	542.704
	•	•	
		•	

Pm

Pm	0.2	0.3	0.1
Mean	534.504	536.574	545.97
	•	•	
		•	

Figure 6. Duncan's multiple range tests for 10 departments. (• = significant different)

Effect Test for 20 Departments

Source	DF	Sum of Squares	F Ratio	Prob > F
Pop	2	11061.847	6.2689	0.0021
Ctype	4	17859.970	5.0607	0.0005
Pc	2	563.588	0.3194	0.7268
Mtype	2	5508.180	3.1216	0.0452
Pm	2	20165.514	11.4280	<0.0001
Pop* Ctype	8	5864.437	0.8309	0.5757
Pop*Pc	4	3463.901	0.9819	0.4174
Pop*Mtype	4	5124.109	1.4519	0.2161
Pop*Pm	4	10329.220	2.9268	0.0209
Ctype*Pc	8	9194.252	1.3026	0.2403
Ctype*Mtype	8	4223.733	0.5984	0.7793
Ctype*Pm	8	5499.400	0.7791	0.6213
Pc*Mtype	4	7544.412	2.1378	0.0754
Pc*Pm	4	2254.479	0.8388	0.6351
Mtype*Pm	4	2058.264	0.5832	0.6750
Pop*Ctype*Pc	16	882.963	0.6293	0.8605
Pop*Ctype*Mtype	16	1596.348	1.1311	0.3234
Pop*Ctype*Pm	16	8903.126	0.6307	0.8593
Pop*Pc*Mtype	8	3564.121	0.5050	0.8536
Pop*Pc*Pm	8	992.343	1.3035	0.2399
Pop*Mtype*Pm	8	3048.558	0.4319	0.9018
Ctype*Pm*Mtype	16	13748.378	0.9739	0.4846
Ctype*Pc*Pm	16	7759.089	0.5496	0.9195
Ctype*Mtype*Pm	16	12934.230	0.9162	0.5505
Pc*Mtype*Pm	8	3076.054	0.4358	0.8994
Pop*Ctype*Pc*Mtype	32	19692.985	0.6975	0.8928
Pop*Ctype*Pc*Pm	32	20149.496	0.7137	0.8773
Pop*Ctype*Mtype*Pm	32	23221.689	0.8225	0.7741
Pop*Pc*Mtype*Pm	16	5408.301	0.3831	0.9859
Ctype*Pc*Mtype*Pm	32	22446.748	0.7951	0.7820
Pop*Ctype*Pc*Mtype*Pm	64	50727.156	0.8984	0.6947

Figure 7. ANOVA for 20 departments.

Duncan's multiple range tests

Crossover type

Crossover type	OX	Position-Base	PMX	Order-Base	CX
Mean	5577.14	5591.9	5598.51	5620.56	5687.91
	•	•	•	•	
		•	•	•	
			•	•	
				•	

Pm

Pm	0.3	0.2	0.1
Mean	5568.28	5573.72	570363
	•	•	
		•	

Figure 8. Duncan's multiple range tests for 20 departments. (• = significant different)