Assiut Univ. J. of Mathematics and Computer Science *Printed ISSN 1687-4897*
47(2), pp42- 57 (2018)

MIXED VARIABLE OPTIMIZATION MODEL FOR MEDICAL WASTE REVERSE LOGISTICS NETWORKS USING HYBRID CELLULAR GENETIC ALGORITHM

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Received: 17/4/2018 **Accepted:** 24/6/2018 **Available Online:** 20/12/2018

The medical waste reverse logistics networks are an attractive topic as the possible public health dangers and ecological ventures for burning a large quantity of medical waste. Reverse logistics networks structures were created for reducing medical waste produced from hospitals for recovery. In this research, a Mixed Variable Optimization (MVO) model is presented for minimizing costs of medical waste reverse logistics networks. The total costs for reverse logistics contain stable cost of opening the gathering stations and treating stations, shipped cost and processing cost, finally a schedule is proposed of flows of medical waste in the network. A hybrid Cellular Genetic Algorithm (CGA) is used for solving the MVO model to be (CGAMV). Pattern search method (PSM) is added to the CGAMV, to be (*$CGAMV^P$*) to make more intensification on the best solutions in proposed grid. The grid structure and small neighborhood make fast convergence and exploration during genetic algorithm operators. The performance of the *$CGAMV^P$* algorithm by the presented model is examined on a numerical experiment and it is found promising.

Keywords: cellular genetic algorithm, medical waste, mixed integer programming, reverse logistics networks.

1. INTRODUCTION

In the past little years, on a global basis, there has been a growing in public care about the conducting of healthcare waste. Industrialists have to gather the medical waste and monitoring its recovery or disposal. Medical waste recovery, which comprises reusing, repairing and materials recycling, requests a chiefly designed reverse logistics network for gathering the medical waste efficaciously [17]. In Egypt, generation of medical waste has rapidly increased meantime the past decade. Medical waste must be managed with concern as the possibility destined and risky materials in it. Here reverse logistics is indicated to as the procedure of logistics management involved in planning, managing, and controlling the influx of medical waste for reuse or disposal of

waste. Jang [12] presented an oversight of the management trainings of medical waste, concerning generation, structuring, segregation, transportation, and elimination. Cheng [5] evaluated the quantities of medical waste and inspires that big hospitals are the main origin of medical waste. Conrardy [6] checked medical waste management, dominating legislation, treatment and disposal method, highlighting that an rising in unfavorable environmental impacts, concludes that better education of healthcare workers is key for efficacious waste management at healthcare instruments. Komilis [13] calculated the dangerous medical waste production rates using data from health-care facilities, indicating to the cargoes of the dangerous medical wastes which were orderly transmitted to the medical waste incinerator. Chen [4] investigated the gathering of the bottom dust produced from the solid waste crematory used for medical waste disposal. Consequently, the efficient design of a medical waste cure network is essential of the challenging issues in the recently field of reverse logistics. Garibaldi [9] designed waste-handling records with artificial patient waste to ensure sufficient sterilization and illuminated that the significant role of waste bundling in felicitous sterilization. Mantzaras [15] developed a model for minimizing the cost of a collection, transfer, process and disposal system for medical waste and calculates the optimum locations of the treatment and transfer facilities, their plan capacities and their optimum transmit trajectory.

Cellular genetic algorithm (CGA) is a type of (GA) which is an efficient random search algorithm and it is a class of the applicable metaheuristics. The major advantage of metaheuristics is a balance for finding a good solution (the global optimum) in a mild run time. GA works on a set of population, applying some stochastic operators (called genetic operators, e.g., selection, crossover (recombination), and mutation) [16]. CGA is a GA with dispersed population in which exchanges between individuals are restricted to closely neighbors. The main idea of this method is to permit the population of a specific structure clarified as a connected diagram, in which each individual interacts with his nearest neighbors. Individuals are mapped in a toroidal mesh, using this topology does not limit the region of the achieved solutions [1]. In it, the boundary solutions of the grid are connected to the individuals located on the opposite borders in the identical row/column. The attained effect is a toroidal grid, so that all the individuals have precisely the same number of neighbors. There are six common neighborhood structures for every individual called L5, L9, C9, C13, C21 and C25 presented in [1,8]. In CGA, cells can be renewed either

asynchronously or synchronously [7]. There exist four types for sequentially updating the cells of a CGA: fixed line sweep (FLS), fixed random sweep (FRS), new random sweep (NRS), and uniform choice (UC) [1].

In the current work, the grid structure of $CGAMV^P$ method helps to get fast convergence. The selected chromosome with its small neighborhood makes exploration through genetic algorithm operators. The considered neighborhood in $CGAMV^P$ method interest in making more intensification for every chromosome in population and also it tries to make some diversification to cover all parts in the search space. $CGAMV^P$ method tries to solve the presented model [18] and propose a schedule of flows of medical waste reverse logistic network for the opening gathering stations and treating stations.

The rest of present paper is arranged as follows: Section 2 defines the problem, and in section 3 shows the model structure. Section 4 proposes a mixed variable optimization model of medical waste reverse logistics network. Section 5 describes the $CGAMV^P$ method with their components in details for solving the model. A numerical experiment is offered in Section 6. The computational results of *CGAMV P* method, comparison and scheduling of flows of the network are showed in Section 7. Finally, Section 8 concludes the paper and future work.

2. Problem definition

In this study, the medical waste reverse logistics network is clarified in Figure1. The hospitals and manufactories have been stable. The position problem of gathering stations and treating stations is illustrated, including stable cost, shipped cost and processing cost. In this network, there are G gathering stations, and T treating stations. Medical waste is shipped from hospitals to gathering stations. Through some separating and collection in the gathering stations, the waste is again shipped from gathering stations to treating stations, where it will be completely antiseptic, disjointed, remanufactured or disposed. Finally, the reused medical items were transported to the manufactory. Regarding the nation wanted for these waste treating facilities as few as possible. The medical waste reverse logistics network design containing four classes: hospitals, gathering stations, treating stations and manufactory.

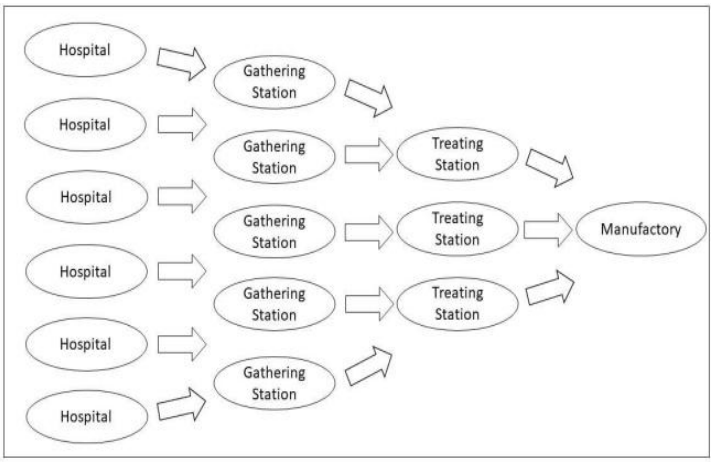

Figure 1: Medical waste reverse logistics network

The medical waste reverse logistics network problem can be discussed as: offered the potential position and the capacities of the gathering stations and treating stations, the whole quantities of every type of the medical waste produced by any hospital, the cost bodies for stable, shipping and other processing costs attached to the medical waste, the model design must find out which possible gathering stations and treating stations must be opened and how the medical waste transferred so that reverse logistics network can obtain the minimum whole costs. Finally, a schedule of flows of medical waste reverse logistic network for the opening gathering stations and treating stations is proposed.

3. Model structure

3.1 Control Variables

Control Variables were used:

X_{hgk}: quantities transported from hospital h to gathering station g for waste k;

Y_{gtk}: quantities transported from gathering station g to treating station t for waste k;

F_{tk}: quantities transported from treating station t to the manufactory for waste k;

$$J_g = \begin{cases} 1, & ,if\ gathering\ station\ g\ is\ open; \\ 0, & otherwise; \end{cases}$$

$$R_t = \begin{cases} 1, & ,if\ treating\ stationt\ is\ open; \\ 0, & otherwise; \end{cases}$$

3.2 Parameters

Parameters were used:

H: the number of hospitals where the medical waste are created;

$G = \{1,2,\ldots,G\}$, series of gathering stations;

$T = \{1,2,\dots,T\}$, series of treating stations;
K: the number of the medical waste kinds;
$G_{\max}$: the maximum number of possible gathering stations;
$T_{\max}$: the maximum number of possible treating stations;
Q_{hk}: the quantity from hospital h of medical waste k ;
G_g^s: the stable costs of structure or capacity expansion of gathering station g;
T_t^s: the stable costs of structure or capacity expansion of treating station t;
F^s: the stable costs of capacity expansion of the manufactory;
G_{gk}^p: the unit processing cost in gathering station g of medical waste k ;
T_{tk}^p: the unit processing cost in treating station t of medical waste k ;
F_k^p: the unit processing cost of medical waste k in the manufactory;
G_{gk}^d: the unit shipped cost of medical waste k from hospital h to gathering station g;
T_{tk}^d: the unit shipped cost of medical waste k from gathering station g to treating station t;
F_{tk}^d: the unit shipped cost of medical waste k from treating station t to the manufactory ;
G_{gk}^c: the maximum capacity of gathering station g for medical waste k;
T_{tk}^c: the maximum capacity of treating station t for medical waste k;
G_g^c: the maximum capacity of gathering station g;
T_t^c: the maximum capacity of treating station t;
λ_k: the discarding rate of medical waste k in gathering stations;
η_k: the discarding rate of medical waste k in treating stations;

4. Mathematical model ([18])

$$\text{Minimize } f(X,Y,F,J,R) = \sum_{g=1}^{G} G_g^s J_g + \sum_{t=1}^{T} T_t^s R_t + F^s + \sum_{h=1}^{H}\sum_{g=1}^{G}\sum_{k=1}^{K}\left(G_{gk}^d + G_{gk}^p(1-\lambda_k)\right)X_{hgk} + \sum_{g=1}^{G}\sum_{t=1}^{T}\sum_{k=1}^{K}\left(T_{tk}^d + T_{tk}^p(1-\eta_k)\right)Y_{gtk} + \sum_{t=1}^{T}\sum_{k=1}^{K}\left(F_{tk}^d + F_k^p\right)F_{tk} \quad (4.1)$$

subject to:

$$\sum_{g=1}^{G} X_{hgk} = Q_{hk}(h = 1,\dots,H; k = 1,\dots,K) \quad (4.2)$$

$$(1-\lambda_k)\sum_{h=1}^{H} X_{hgk} = \sum_{t=1}^{T} Y_{gtk}(g = 1,\dots,G; k = 1,\dots,K) \quad (4.3)$$

$$(1-\eta_k)\sum_{g=1}^{G}\sum_{t=1}^{T} Y_{gtk} = \sum_{t=1}^{T} F_{tk}(k=1,\ldots,K) \quad (4.4)$$

$$\sum_{h=1}^{H}\sum_{k=1}^{K} X_{hgk} \le G_g^c J_g(g=1,\ldots,G) \quad (4.5)$$

$$\sum_{g=1}^{G}\sum_{k=1}^{K} Y_{gtk} \le T_t^c R_t(t=1,\ldots,T) \quad (4.6)$$

$$\sum_{h=1}^{H} X_{hgk} \le G_{gk}^c J_g(g=1,\ldots,G; k=1,\ldots,K) \quad (4.7)$$

$$\sum_{g=1}^{G} Y_{gtk} \le T_{tk}^c R_t(t=1,\ldots,T; k=1,\ldots,K) \quad (4.8)$$

$$\sum_{g=1}^{G} J_g \le G_{\max} \quad (4.9)$$

$$\sum_{t=1}^{T} R_t \le T_{\max} \quad (4.10)$$

$$X_{hgk}, Y_{gtk}, F_{tk} \ge 0 \quad (4.11)$$

$$J_g \in \{0,1\}; R_t \in \{0,1\} \quad (4.12)$$

- The objective function 4.1 minimizes whole reverse logistics costs consisted of stable, shipped and processing costs for opening stations.
- Constraints 4.2 to 4.4 involve the equilibrium of medical waste in hospitals, gathering stations, treating stations and the manufactory, respectively.
- Constraint 4.5 includes that the whole amount of waste transported to each gathering station cannot skipped the capacity of the gathering station *g* keeping them.
- Constraint 4.6 includes that the whole quantity of waste transported to each treating center cannot skipped the capacity of the station *t* keeping them.
- Constraint 4.7 includes that the quantity of waste *k transported* to each gathering station cannot skipped the capacity of the station keeping it.
- Constraint 4.8 includes that the quantity of waste *k transported* to each treating station cannot skipped the capacity of the station keeping it.
- Constraints 4.9 and 4.10 restrict the number of the opening gathering stations and treating stations.
- Constraint 4.11 confirms that the non-negativity of control variables X_{hgk}, Y_{gtk} and F_{tk}.
- Constraint 4.12 confirms that the binary of control variables J_g and R_T.

5. Solution approach: Cellular Genetic Algorithm

Cellular Genetic Algorithm for Mixed Variable Optimization (CGAMV) is implemented as randomly generated chromosomes (individuals) to map on a 2-D toroidal grid (obtained by wrapping the columns and rows around them- selves). Focusing on a type of asynchronous FLS cellular genetic algorithm to update the cells which lies in sequentially updating the individuals of the population row by row. The selected individual and its neighbors defined as small population P, in which the genetic factors (selection, crossover and mutation) are applied that make exploration in every selected individual. The update of the grid is very important aspect in this search. The selected individual is updated by the best chromosome in P after GA operators. Therefore, the diversification process is added to cover the most space in the search region. Finally, a pattern search is added to CGAMV method to be $CGAMV^{P}$ to get more intensification on the best solutions. The proposed method is illustrated as follows:

5.1 Initialization

Chromosomes (Individuals) in initial population are created by uniform distributed inside the search region bounded by [**l**, **u**], representing a good solutions. Obviously, X_{hgk}, Y_{gtk}, F_{tk} are continuous value variables while J_g and R_t are binary value variables. Each chromosome initialized is based on one dimensional vector which contains continuous variables, representing quantity transported from hospital *h* to gathering station *g*, from gathering station *g* to treating station *t* and from treating station *t* to the manufactory for waste *k* and binary variables, related to gathering stations and treating stations. The chromosome contains six hospitals, five gathering stations, three treating stations three and one manufactory. Thus, each chromosome is represented as a (6×5+5×3+3×1+5+3) vector, where (6×5) genes represent the medical waste from six hospitals to five gathering stations; (5×3) genes represent the medical waste from five gathering stations to three treating stations; (3×1) genes represent the medical waste from three treat- ing stations to manufactory; (5) genes represent whether the gathering station is opened(=1) or closed(=0); (3) genes represent whether the treating station is opened (=1) or closed(=0). See the representation of a chromosome in Figure 2.

X_{111}	...	X_{652}	Y_{111}	...	Y_{532}	F_{11}	...	F_{32}	...	G_1	...	G_5	T_1	...	T_3

Figure 2: A representation chromosome scheme

5.2 Evaluation

This evaluation procedure is used for comparing one solution with others in the population. In this paper, penalty method [14] is used. For example, if $f(\mathbf{x}, \mathbf{y})$ is the old objective function, $\phi_i(x, y)$ is the inequality constraints, and $\psi_j(x, y)$ is the equality constraints. The general formulation of the penalty function is

$$\eta(x,y) = f(x,y) \pm [\sum_{i=1}^{m} u_i \times A_i + \sum_{j=1}^{p} v_j \times B_j]$$

Where $\eta(\mathbf{x}, \mathbf{y})$ is the new objective function, u_i and v_j called penalty factors, A_i and B_i are called constraint violation function, and defined below:

$$A_i = max[0, \phi_i(x, y)]^{\kappa},$$

$$B_j = |\psi_j(x, y)|^{\sigma},$$

Where κ and σ are normally 1 or 2.

5.3 Mapping on the grid

Individuals (chromosomes) are mapped on 2-D toroidal grid from best to worst. In the case of a population of size μ arranged in a toroidal grid of size $\sqrt{\mu} \times \sqrt{\mu}$ (assuming μ odd) [10]. An chromosome (individual) represented as $z = (X_{111}, \ldots, X_{652}, Y_{111}, \ldots, Y_{532}, G_1, \ldots, G_5, T_1, \ldots, T_3)$ mapped on the grid as position (z) is the pair of coordinates (i, j) in the two-dimensional grid.

5.4 Neighborhood

In CGA, every individual select some of neighborhoods with various methods. In our methods, the neighborhoods are selected by linear5 (L5) process. The neighborhood is the 4 nearest individuals standing for North, East, West, and South as clarified in Figure3. The considered individual with its neighborhood became a small population P. The genetic factors are applied to this P.

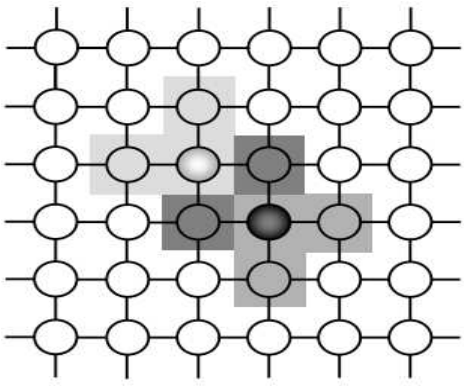

Figure 3: The L5 neighborhood

5.5 Selection

The selection operator is consumed to improve the population by giving the high-quality solutions. The selection procedure creates a med population, say $P^{'}$ from the current P. For the population size μ, the probability is calculated as

$$p_i = \frac{1}{\mu}(\zeta_{\max} - (\zeta_{\max} - \zeta_{\min})\frac{i-1}{\mu-1}) \quad i = 1, \ldots, \mu, \qquad (5.1)$$

where $\zeta_{\max} + \zeta_{\min} = 2$ and $1 \leq \zeta_{\max} \leq 2$. The linear ranking selection mechanism [2,3] is utilized to select the individuals in $P^{'}$ under the following procedure:

Procedure 5.1 *Linear Ranking Selection*

1. Set $s_0 = 0$.
2. Set $s_i = s_{i-1} + p_i$ for all i = 1, ..., μ, see equation5.1.
3. For all i = 1, ..., μdo step 4,5.
4. Generate a random number $\gamma \in [0, s_i[$.
5. Copy P_l in P'_i where$\leq s_{l-1} \leq \gamma \; s_l$.
6. return.

5.6 Crossover

Crossover is the major cellular genetic operator. A two point crossover [11] occurs between the two selected parents to produce two offsprings $\mathbf{o}^1$ and $\mathbf{o}^2$ under the following:

Procedure 5.2 *Two Point Crossover* ($\mathbf{p}^1$, $\mathbf{p}^2$, $\mathbf{o}^1$, $\mathbf{o}^2$)

Let n_x the number of continuous variables, n_y the number of discrete variables and $n = n_x + n_y$

1. Generate an integer random number $\gamma \in (1, n_x)$.
2. Let $\mathbf{p}^1 = (\mathbf{x}^1, \mathbf{y}^1)$ and $\mathbf{p}^2 = (\mathbf{x}^2, \mathbf{y}^2)$.
3. Calculate the recombined offspring $\mathbf{o}^1 = (\mathbf{r}^1, \mathbf{s}^1)$ and $\mathbf{o}^2 = (\mathbf{r}^2, \mathbf{s}^2)$, where

$$\mathbf{o}^1(1{:}n_x) = \mathbf{p}^1(1{:}\gamma) + \mathbf{p}^2(\gamma + 1{:}n_x),$$
$$\mathbf{o}^2(1{:}n_x) = \mathbf{p}^2(1{:}\gamma) + \mathbf{p}^1(\gamma + 1{:}n_x).$$

4. Generate an integer random number $\lambda \in (1, n_y)$.

5. Calculate the recombined offspring

$$\mathbf{o}^1(n_x+1:n) = \mathbf{p}^1(n_x+1:\lambda) + \mathbf{p}^2(\lambda+1:n),$$
$$\mathbf{o}^2(n_x+1:n) = \mathbf{p}^2(n_x+1:\lambda) + \mathbf{p}^2(\lambda+1:n).$$

6. return.

5.7 Mutation

This operator exchanges the value of the selected gene from a uniform distribution with the upper and lower bounds for this gene. For every gene in each chromosome (individual) in the med population $P^{'}$, a random number is generated in the interval (0, 1). If the generated number is lower than the mutation probability p_m, then the chromosome will be mutated. Let the numbers of the selected gene and chromosome are λ and θ, respectively. Then, the mutated offspring **z** is computed among the following:

Procedure 5.3 *Uniform Mutation*

1. If the selected gene λ is continues, update $\mathbf{z}^\theta$ by setting $x_\lambda^\theta = l_{x_\lambda} + \gamma(u_{x_\lambda} - l_{x_\lambda})$.

2. If the selected gene λ is integer, update $\mathbf{z}^\theta$ by setting $y_\lambda^\theta = l_{y_\lambda} + \gamma(u_{y_\lambda} - l_{y_\lambda})$, where $\gamma \in (0,1)$.

5.8 Replacement (Update the grid)

Our current individual is updated by the best offspring (solution) in the small population P after the GA operators (selection, recombination and mutation process).

5.9 Pattern search

Some elite offsprings of the generation are improved by adding pattern search schemes. Specially, some reformed versions of the PSM are invoked to deal with the present model. The inputs and parameters of PSM are reset to contain both continuous and integer settings. Some modification is added on pattern search method to decrease the rate of cost function. Modified pattern search use the set *D* in distinct way.

$$D = \{(\pm 1)^h e_1, \dots, (\pm 1)^h e_n\},$$

where *h* is random number $h \in \{1, 2\}$, therefore, modified pattern search generate only $n + 1$ points at every iteration.

Procedure 5.4 *Pattern Search Process*

1. Select an initial solution $\mathbf{x}_0$, select a positive spanning directions D, select a step size $\Delta_0 > 0$ and set the counter number $k := 0$.

2. Compute the grid $W_k = \{x: x = x^k \pm \Delta_k dz,\ d \in D,\ z \in Z_+^{|D|}\}$, get an improved point from W_k. If an improvement is achieved go to Step 4.

3. Choose the search direction set $D_k \subset D$ to compute the poll set $P_k = \{x: x = x^k \pm \Delta_k d,\ d \in D_k\}$,. Evaluate the cost function at all points in P_k.

4. If an improved point obtained in Step 2 or 3, set $\mathbf{x}^{k+1}$ equal to this improved point, and set $\Delta_{k+1} \geq \Delta_k$. Otherwise, set $\mathbf{x}^{k+1} := \mathbf{x}^k$, and $\Delta_{k+1} < \Delta_k$.

5. If the termination conditions are satisfied, then stop. Otherwise, set $k := k + 1$, and go to Step 2

5.10 CGAMV ^{P} Algorithm

The previous components for the *CGAMV* ^{P} are shown in Algorithm 5.1.

Algorithm 5.1 *CGAMV P* Algorithm Generate initial population(gpa.pop); Evaluation(fitness function) Mapping gpa.pop on the grid;

while Stop Condition **do**
for chromosome □ gpa.popsize **do**
neighbors □ Calculate Neighborhood(gpa, position(chromosome));
parents □ Selection(neighbors, chromosome);
offspring □ Crossover(gpa.p_c, parents);
offspring □ Mutation(gpa.p_m, offspring);
Replacement (position(chromosome),best offspring);
end for
Intensification □ Local search(best solution); Termination condition rule
end while

6 Numerical experiment

For describing the model, the model is applied using a numerical experiment. In this experiment, six hospitals, five gathering stations *G*1, *G*2, *G*3, *G*4, *G*5, three treating stations *T* 1, *T* 2, *T* 3 and one manufactory are used.

- Two classes of medical waste *I* and *II* (for example sharp waste and tissues waste) created from each hospitals see Table 1.
- Table 2 shows the stable cost of manufactory, gathering stations and

treating stations.

- The processing cost and capacity of gathering stations are exhibited in Table 3 and Table 4.
- The processing cost and capacity of treating stations are displayed in Table 5 and Table 6.
- The processing cost of manufactory shows in Table 7.
- The discarding rates of medical waste in gathering stations and treating stations are the same see Table 8.
- The maximum capacity of gathering and treating stations are exhibited in Table 9.

The shipped cost attached to the quantity of medical waste is shown Table 10 – 12.

Table 1: Quantity of medical waste from hospitals T(Ton)

Hospitals	WasteI	WasteII
1	45	20
2	70	40
3	95	75
4	60	45
5	80	55
6	55	20

Table 2: Stable cost (Pound,Pound/Ton, Ton)

Manufactory	1	50000
Gathering stations	1	8500
	2	10000
	3	15000
	4	12000
	5	10000
Treating stations	1	4000
	2	45000
	3	50000

Table 3: Processing Cost of gathering stations(Pound,Pound/Ton, Ton)

Gathering stations	WasteI	WasteII
1	7	3
2	5	3
3	5	1.5
4	6	2.5
5	4	3

Table 4: Capacity of gathering stations(Pound,Pound/Ton, Ton)

Gathering stations	WasteI	WasteII
1	100	80
2	150	120
3	150	150
4	130	150
5	120	100

Table 5: Processing Cost of treating stations(Pound,Pound/Ton, Ton)

Treating stations	WasteI	WasteII
1	9	7
2	7	5
3	5	4

Table 6: Capacity of treating stations(Pound,Pound/Ton, Ton)

Treating stations	WasteI	WasteII
1	6	1
2	3	5
3	5	7

Table 7: Processing Cost of manufactory(Pound,Pound/Ton, Ton)

Manufactory	WasteI	WasteII
1	8	6

Table 8: Discarding rates in gathering stations and treating stations

Discarding rates	WasteI	WasteII
α, β	0.8	0.7

Table 9: Maximum capacity (Pound,Pound/Ton, Ton)

Gathering stations	1	160
	2	260
	3	280
	4	260
	5	200
Treating stations	1	300
	2	400
	3	500

Table 10: Shipped cost from treating stations to the manufactory (Pound)

Treating stations	WasteI	WasteII
1	6	1
2	3	5
3	5	7

Table 11: Shipped cost from hospitals to gathering stations (Pound)

Hospitals	Waste	Gathering stations				
		1	2	3	4	5
1	I	5	10	8	7	6.5
	II	7	9	10	10	13
2	I	3	5	4	5	10
	II	8	8.5	3	6	6.5
3	I	6	4	5	3	9
	II	10	8.5	6	5	7
4	I	7	1	10	12	6
	II	12	11	8	9	10
5	I	4	3	6	9	5
	II	5.5	8	7	10	8
6	I	3	9	7	6	10
	II	8	12	8	9	10

Table 12: Shipped cost from gathering stations to treating stations (Pound)

Gathering stations	Waste	Treating stations		
		1	2	3
1	I	4	5	2
	II	6	7	5
2	I	6.5	5	7
	II	7	8	5
3	I	6.5	4	5.5
	II	8	6.5	5
4	I	7.5	3	8
	II	10	8	8
5	I	5	4	4
	II	5	7	6

5 Computational Results

The *CGAMV* ^{P} method is programmed in MATLAB. In this Section, a discussion of the parameters setting and the efficiency analysis of the *CGAMV* ^{P} algorithm as the following descriptions:

5.1 Parameters Setting

The *CGAMV* ^{P} parameters are setting as Table13 which discussed to cover the description of *CGAMV* ^{P} algorithm stated in the previous section. Assume P_{size} is the population size, N_i is the digit of pattern search iterations and N_g is the number of generations.

Table 13: Parameters used for the CGAMV^{P}

P_{size}	15×15 (225 Individuals)
Neighborhood	L5
Selection	Linear ranking
Crossover	Tow point
Cross. Prob	0.9
Mutation	Uniform
Mutation. Prob	0.05
N_i for every best solution	20
Termination Condition	N_g exceeds 500

6.1 Efficiency Analysis

In this section, the performance of *CGAMV* ^{P} method is discussed on the numerical experiment, which are shown in the previous section. The properties of this experiment is the type of NP-hard problems. The numerical results are discussed through 1 independent run. Shi [18] tries to find the solution of this problem but, he didn't mention the limitation of the search space so, it is not fair to compare with himself. On the other hand, we try to assume the limitation of the space to find near his solution and we can get the value of the fitness function value 139870. We try to make the value of our model as real problem so, the results are taken when using high limitation, then we get the fitness function value as 214730 and a schedule of the potential gathering stations 2, 3, 5 and treating stations 1, 2 are elected for the flows of the medical waste network is obtained.

7 Conclusion and Future Works

In this research, the medical waste reverse logistics network structure is discussed, created from the hospitals to manufactories. A mixed variable optimization model is presented for minimizing the total costs include stable cost of opening the gathering stations and treating stations, shipped cost and processing cost. A hybrid cellular genetic algo- rithm with pattern search has been used to get an a good solution with high promising to manipulate mixed variable optimization model. A scheduling of flows of the network is proposed of the opening gathering stations and treating stations. The selection procedure in the grid of $CGAMV^{P}$ method make more intensification on every chromosome and $CGAMV^{P}$ tries to cover the search space by diversification. The computational results for the numerical experi- ment are shown promising of the proposed method. In the future work, the qualification of the medical waste reverse logistics network inclusive real-data will discussed.

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