

# A hybrid genetic algorithm that optimizes capacitated vehicle routing problems

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## Abstract

This study primarily focuses on solving a capacitated vehicle routing problem (CVRP) by applying a novel hybrid genetic algorithm (HGA) capable of practical use for manufacturers. The proposed HGA has three stages. First, the nearest addition method (NAM) was incorporated into sweep algorithm (SA) that simultaneously accounts for axial and radius relationships among distribution points with the depot to generate a well-structured initial chromosome population, rather than adopting either the NAM OR SA alone. Second, response surface methodology (RSM) was employed to optimize crossover probability and mutation probability via systematic experiments. Finally, an improved sweep algorithm was incorporated into the GA, producing a stir over gene permutations in chromosomes that enhance the exploration diversity of the GA, thereby avoiding convergence in a limited region, and enhancing the search capability of the GA in approaching a close-to-optimal solution. Furthermore, an elitism conservation strategy holding superior chromosomes to replace inferior chromosomes was also performed. As the proposed HGA is primarily used to solve practical problem, benchmark problems with fewer than 100 distribution points from an Internet website were utilized to confirm the effectiveness of the proposed HGA. A real case regarding the mission of local active distribution from armed forces in Taiwan details the analytical process and demonstrates the practicability of the proposed HGA to optimize the CVRP.

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## 1. Introduction

The efficiency of distribution networks in a logistics system determines the speed of responses to rapidly changing market demands in this era of economic globalization, worldwide sourcing and mass customization. Furthermore, the increasingly effective radio frequency identification system has led manufactures to pay much attention to the issue of distribution networks to improve marketplace competitiveness. To obtain a business scale and satisfy various customer requirements, manufacturers typically increase the number of distribution points, which increases the complexity of distribution network operation. Therefore, effectively resolving vehicle route problems (VRPs)

in a distribution network in a logistics system improves the capability of a distribution network, thereby enhancing market competitiveness – an essential issue for contemporary business.

The VRP is, mathematically, a combinatorial optimization problem. Lawrence and Bruce (1981) proved that this problem type is non-deterministic polynomial-time (NP)-hard. Namely, the polynomial equation model of the VRP cannot be directly established to determine its optimal solution, and solving time for the VRP grows exponentially with the increase in distribution points, such that even the fastest computers are incapable of performing exhaustive computations required to determine an optimal solution. Hence, numerous studies have developed metaheuristic algorithms, such as genetic algorithms (GAs), ant colony systems and particle swarm optimization, to obtain a close-to-optimal solution for the VRP. Metaheuristic algorithms

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have three impediments to efficiently solving complex optimization problems, these algorithms become trapped in local optimum, leading to a limited cycle, and cannot escape from a specific search region. These three impediments must be overcome to effectively optimize complex problems when applying metaheuristic algorithms (Battiti & Tecchiolli, 1994). Some superior metaheuristic algorithms have recently been developed, and GAs have been shown to be capable of solving VRPs (Baker & Ayechew, 2003). The search mechanism in the GA corresponds to chromosome evolution, comprising reproduction, crossover, and mutation during imitated breeding process. Typically, determining search direction solely relies on probability settings regarding chromosome mutation and crossover for generating offspring during the breeding process. Additionally, as is well known, the structure of the initial chromosome population (namely, initial solution population) significantly impacts the resolution capability of the GA. Essentially, the initial structured chromosome population in the form of gene permutations is markedly better than that generated randomly (Baker & Ayechew, 2003). Because a GA and conventional heuristics are complementary, a hybrid approach typically outperforms using a GA or conventional heuristics alone. Numerous successful applications strongly favor such a hybrid approach (Chen, Pan Jason, & Lin, 2008). In a hybrid approach, a GA primarily performs global exploration in a population, whereas heuristics mainly focus on local exploitation of chromosomes. Some heuristic algorithms, such as sweep algorithms (SAs) (Gillett & Miller, 1974) and nearest addition method (NAM) (Bentley, 1992), which are well known and practical, have been employed to generate an initial population. The SA is based on the axial clustering relationship among distribution points relative to a depot, whereas the NAM accounts for radius clustering relationships among distribution points relative to a depot.

Baker and Ayechew (2003) applied an SA to generate an initial structured population for a GA. A hybrid heuristic, which incorporates a neighborhood search into a GA, has been developed to solve the VRP. The solution capability obtained by Baker and Ayechew (2003) were further compared with those obtained via a tabu search and simulated annealing techniques, thereby demonstrating the superiority of the GA. Baker and Ayechew (2003) also indicated that although development of modern heuristics has resulted in considerable progress, the quest for improved performance continues. The GA technique is widely used when solving practical VRPs in business. Despite the superiority of a GA, its application has some limitations. For example, until now, no systematic methods exist for optimizing GA parameter settings, including crossover probability, mutation probability and size of chromosomes. Consequently, improved GAs have shifted toward breeding (Battiti & Tecchiolli, 1994; Angelov, 2001).

This study solves a capacitated VRP (CVRP) using a proposed a hybrid GA (HGA) that can be used by manufacturers. The HGA has three stages. This study first incorporated

NAM into an SA to account simultaneously for axial and radius relationships among distribution points relative to a depot to generate a well-structured initial chromosome population. Second, this study utilized response surface methodology (RSM) (Montgomery, 2005) to optimize crossover probability and mutation probability through systematic experiments prior to employing the GA. A response surface model for the distance of a close-to-optimal route on crossover probability and mutation probability based on experimental data was established to determine the optimal probability settings for the two parameters. Finally, an improved SA was incorporated into the mutation process within the GA to produce a stir over gene permutations in chromosomes. This procedure enhances the exploration diversity of a GA, thus averting convergence in a limited region during the evolution process, and improves the search ability of a GA in approaching a close-to-optimal solution. Additionally, an elitism conservation strategy that replaces inferior chromosomes with superior chromosomes was performed during the GA evolution process. Because the proposed HGA is constructed to solve a practical problem, benchmark problems with fewer than 100 distribution points obtained from an Internet website were employed to verify the effectiveness of the proposed HGA. A real case, regarding the mission of a local active distribution task for the armed forces in Taiwan, presents the details of the analytical process and demonstrates the practicality of the proposed HGA in optimizing the CVRP.

## 2. Literature review

The basic VRP consists of a number of customers, each requiring a specific weight of goods to be delivered. Vehicles with capacity constraints when delivering the required goods are dispatched from a single depot to demand points (namely, customers) and then return to the depot; the number of vehicles is not a constraint. Only one vehicle visits each customer. The general VRP comprises an assignment problem, traveling salesman problem and vehicle-path problem. Based on practical requirements, various extensions of the basic VRP involve such problems such as the capacitated vehicle problem, vehicle routing problem with a time window, the VRP with backhauls, and the VRP with pickup and delivery. For details of the VRP, refer to Toth and Vigo (2002). As the complexity of the solution for the VRP is NP-hard, solution time exponentially increases as the number of distribution points increases. The mathematical programming technique can only be adopted to solve VRPs with small numbers of distribution points. With a large number of distribution points, even the fastest computer is incapable of performing the exhaustive computations required to determine an optimal solution. In 1986, Glover proposed the novel idea of global heuristics, thereafter studies on searching global optimum using metaheuristic algorithms, such as GAs, tabu search, neural network, simulated annealing, and an ant colony algorithm, to optimize

complex problems have been continuously developed. Baker and Ayechev (2003) demonstrated that the GA can solve the VRP, and competes with the performance of tabu search and simulated annealing. Genetic algorithms focus on conversion of genes through genetic evolution, thereby solving complex optimization problems. Accordingly, offspring are bred based on chromosome evolution using operators incorporated into GA reproduction, mutation, and crossover to form a search mechanism. This search mechanism, corresponding to offspring breeding, is guided by probability. Goldberg (1989) summarized the attributes of GAs as follows:

- (1) Genetic algorithm calculations are based on coded parameters, rather than the parameter values.
- (2) Genetic algorithms possess highly parallel search capability, avoiding becoming trapped in a local optimum.
- (3) Genetic algorithms have no complex mathematical formulas – only the fitness function must be calculated.
- (4) Genetic algorithms have no specific rules for guiding the search direction for an optimum, rather, a random search mechanism uses the probability rule.

Because GAs and conventional heuristics are complementary, a hybrid approach frequently outperforms either method used independently. Numerous successful applications strongly favor a hybrid approach (Chen et al., 2008). In this hybrid approach, the GA globally explores the population, while heuristics mainly focus on local exploitation of chromosomes. Runwei, Mitsuo, and Yasuhiro (1999) suggested that a hybrid approach can be applied in various ways. For example, incorporating heuristics into initialization generates a well-structured initial population and elitism is adopted; incorporation of a local search into the GA breeding process improves offspring. In practical applications, the form of the hybrid approach strongly depends on the optimized problem type. Baker and Ayechev (2003) indicated that the structure of the initial chromosome population in a GA significantly affects its resolution capability. Some studies developed an initial structured chromosome population to improve GA capability. For example, the SA (Gillett & Miller, 1974) and NAM (Bentley, 1992) consider axial and radius clustering relationships among distribution points relative to a depot to establish the initial structured chromosome population for the GA. Additionally, the probability settings for GA parameters are a determinant of resolution efficiency. Schaffer, Caruana, Eshelman, and Das (1989) suggested that the optimal probability setting for crossover is 0.75–0.95. Greffentette (1986) and Schaffer et al. (1989) revealed that the optimal probability setting for mutation is 0.005; however, the exact setting solely relies on the attributes of optimized problems, an essential issue when employing GAs (Chen et al., 2008). Shieh and May (2001) addressed the vehicle capacity constraint when conducting clustering analysis

of distribution points to form an initial structured solution, thereby optimizing the VRP using a GA. Prins (2004) developed a hybrid GA to solve a VRP and indicated that conventional heuristics can form a well-structured initial solution for metaheuristic algorithms to accelerate convergence. Baker and Ayechev (2003) employed the SA to generate an initial chromosome population. The NAM was then incorporated to the GA breeding process to improve offspring. Computational results were further compared with those obtained by tabu search and simulated annealing, and elucidated the capability of optimizing the VRP for the GA. Additionally, Baker and Ayechev (2003) indicated that although the development of modern heuristics has led to considerable progress, the quest for improved performance continues. The GA technique is widely utilized when solving practical VRPs in business.

According to these studies, the structure of the initial chromosomes in a GA and parameter settings involving crossover probability and mutation probability significantly affect the resolution capability of a GA. However, these parameter settings depend on VRP attributes, including the number of distribution points and their corresponding demands, depot location among distribution points, and degree to which distribution points are clustered. Accordingly, the parameter setting for the GA strongly relies on the attributes of VRPs. However, no systematic methods exist for determining GA parameter settings, and the study regarding the initial structured population still needs to be improved. Therefore, this study developed a HGA to optimize the CVRP for practical use. The proposed HGA incorporates NAM into SA to establish a well-structured initial chromosome population, thereby accelerating the speed at which a close-to-optimal solution for the CVRP is obtained. An improved SA is embedded into the GA mutation process and enhances the HGA search mechanism. Additionally, the RSM is adopted to establish a response surface model for the distance of a close-to-optimal route on crossover probability and mutation probability. The optimal parameter settings are determined based on the established response surface model to avoid the conventional trial-and-error method, which is very inefficient.

### 3. Problem statement and research scope

The solution for the CVRP determines a set of delivery routes that satisfy the requirements of distribution points, and obtains minimum total cost. In practice, minimizing total cost is equivalent to total distance traveled for the number of vehicles. The vehicles with capacity constraints delivering required goods are dispatched from a single depot to distribution points, and then return to the depot. The numbers of vehicles are unconstrained. Only one vehicle is allowed to visit each customer (namely, a distribution point). The mathematical model of the CVRP can be expressed as

$$\text{Minimize } \sum_{i=1}^n \sum_{j=1}^n \text{dist}_{ij} x_{ij} \quad (1)$$

$$\sum_{i=1}^n q_i y_{ik} \leq Q, \quad k = 1, \dots, m \quad (2)$$

$$\sum_{i,j \in S} x_{ij} \leq |S| - 1, \quad S \subseteq \{2, \dots, n\} \quad (3)$$

$$\sum_{k=1}^m y_{ik} = \begin{cases} m, & i = 1 \\ 1, & i = 2, \dots, n \end{cases} \quad (4)$$

$$\sum_{i=1}^n x_{ij} = \sum_{i=1}^n x_{ji} = \begin{cases} m, & j = 1 \\ 1, & j = 2, \dots, n \end{cases} \quad (5)$$

$$x_{ij} \in \{0, 1\}, \quad i = 1, \dots, n; \quad j = 1, \dots, n \quad (6)$$

$$y_{ik} \in \{0, 1\}, \quad i = 1, \dots, n; \quad k = 1, \dots, m \quad (7)$$

where  $\text{dist}_{ij}$  represents the distance from the  $i$ th distribution point to the  $j$ th distribution point;  $x_{ij}$  is the assignment condition of distance from the  $i$ th distribution point to the  $j$ th distribution point;  $x_{ij} = 1$  is the assignment, and  $x_{ij} = 0$  is not an assignment;  $y_{ik}$  represents the condition of the  $i$ th distribution point serviced by the  $k$ th truck;  $y_{ik} = 1$  indicates that the  $i$ th distribution point is serviced by the  $k$ th truck;  $y_{ik} = 0$  indicates that the  $i$ th distribution point is not serviced by the  $k$ th truck;  $q_i$  is the requirement of the  $i$ th distribution point;  $Q$  is the maximum capacity of vehicles.

Toth and Vigo (2002) suggested that although solution capability of metaheuristic algorithms is superior to conventional heuristics, metaheuristic algorithms generally take longer than conventional heuristics. For VRPs, the solution obtained via conventional heuristics generally falls between 2% and 10% above the best-known value. Practically, heuristics must balance solution quality and solution time. Therefore, given this requirement, this study developed a novel HGA to optimize the CVRP to obtain a solution within 5% above the best-known value for international benchmark problems. Since this study focuses on practical cases, the CVRPs with fewer than 100 distribution points obtained from international websites are utilized to demonstrate the practicality of the proposed HGA. To confirm the utility of the proposed optimization procedure, various properties of CVRPs – number of distribution points, pattern of distribution points (namely, clustered or randomly distributed around the depot), and depot location relative to the distribution points – were analyzed.

#### 4. The proposed hybrid genetic algorithm

Typically, the starting point for any GA corresponds to each solution for a population member. The starting point is in the form of a chromosome string. Individual positions within chromosomes are referred to as genes. Each individual gene corresponds to each distribution point in the CVRP. Restated, given  $n$  customers, the chromosome for an individual solution has a string of length  $n$ . Each chro-

sosome consists of a string of decimal numbers (namely, genes), rather than a binary representation, representing different distribution points. Consequently, the proposed HGA optimizes the CVRP, which includes the following three stages, each with several steps.

##### 4.1. Stage 1: generate the initial structured chromosome population

To create a well-structured initial chromosomes population, this study considers simultaneously the axial and radius clustering relationships among distribution points relative to the depot by combining NAM and SA to generate the initial structured chromosome population in the GA – NAM barely accounts for axial magnitude, while SA accounts for radius magnitude only. The expectation in incorporating NAM and SA is that it can produce better initial structured population than adopt only NAM or SA. The stage 1 includes the following five steps:

*Step 1:* Calculate the  $X$  and  $Y$  coordinates of all distribution points

The  $X$  and  $Y$  coordinates of all distribution points relative to the depot are calculated as follows:

$$\begin{cases} X_i = x_i - x_0 \\ Y_i = y_i - y_0 \end{cases} \quad (8)$$

where  $(X_i, Y_i)$  is the  $x$  and  $y$  coordinates of the  $i$ th distribution point relative to the depot,  $(x_0, y_0)$  is the coordinate of the depot, and  $(x_i, y_i)$  is original coordinates of  $x$  and  $y$  for the  $i$ th distribution point.

*Step 2:* Calculate the polar angles of distribution points

The  $X$  and  $Y$  coordinates of all distribution points are converted to polar angles using the following formulas:

$$\theta_i = \begin{cases} \tan^{-1} \frac{Y_i}{X_i}, & X_i > 0, \quad Y_i > 0 \\ \pi + \tan^{-1} \frac{Y_i}{X_i}, & X_i < 0 \\ 2\pi + \tan^{-1} \frac{Y_i}{X_i}, & X_i > 0, \quad Y_i < 0 \end{cases} \quad (9)$$

where  $\theta_i$  represents the polar angle of the  $i$ th distribution point.

*Step 3:* Sort the distribution points in ascending order of the polar angles

According to  $\theta_i$  obtained from Step 2, the distribution points are sorted in ascending order of the polar angles as follows:

$$\theta_j < \theta_{j+1} \quad (10)$$

where  $\theta_j$  represents the  $j$ th distribution point after sorting,  $j = 1, \dots, n$ , and  $n$  is the number of distribution points.

*Step 4:* Generate the structured chromosomes population

The gene (namely, distribution points) permutations within chromosomes are determined based on the sorted  $\theta_j$ . Therefore, given  $n$  distribution points, a total of  $n$  chromosomes with genes permutation, each starting at individual distribution points, are obtained. The gene permutations within chromosomes are then partitioned into



several segments under the capacity constraints of vehicles. The gene permutations within segments form a specific vehicle route. The partition of gene permutations within chromosomes can be expressed as

$$\sum_{j=r_{k-1}+1}^{r_k} q_j \leq Q < \sum_{j=r_{k-1}+1}^{r_{k+1}} q_j, \quad j = 1, \dots, n, \quad k = 1, \dots, m \quad (11)$$

where  $Q$  represents the vehicle capacity constraint,  $q_j$  is the demand of the  $j$ th distribution point,  $k$  is number of vehicles,  $r_k$  is the last distribution point after sorting (Step 3) regarding the  $k$ th vehicle, and  $r_0 = 0$ .

#### Step 5: Strengthen the chromosome structures

The gene permutations representing individual routes for each vehicle are improved using the NAM, which strengthens the structure of chromosomes. Restated, the nearest neighbor point within each vehicle is connected, starting at the depot. Consequently, a well-structured initial population can be generated.

### 4.2. Stage 2: determine the optimal GA parameter settings

Conventionally, setting GA parameters relies on a trial-and-error procedure. However, this procedure cannot determine optimal GA parameter settings and consumes considerable time consumed, which is extremely ineffective. This study employed the RSM to conduct systematic HGA experiments with various crossover and mutation probabilities. The close-to-optimal solutions for the CVRP during experiments were recorded. Accordingly, a response surface model of close-to-optimal solutions obtained by the HGA on crossover and mutation probabilities was established to determine the optimal combination of these two parameters. Stage 2 includes the following four steps.

#### Step 1: Plan the RSM experiments for the CVRP

The faced center cube central composite design (FCCD) from the RSM was adopted to plan experiments in which crossover probability and mutation probability are two experimental factors. In total, 13 experimental points involving 4 factorial points, 4 faced axial points, and 5 center points were designed. For further details of the central composite design, refer to Schaffer et al. (1989).

#### Step 2: Conduct RSM experiments and record experimental observations

The 13 planned FCCD experiments are conducted with various crossover and mutation probabilities, and the close-to-optimal solutions for the CVRP under experiment are recorded.

#### Step 3: Establish the response surface model of distance for the CVRP route

The response surface model for distance of a CVRP route on crossover probability and mutation probability is established based on experimental observations. The lack-of-fit test is utilized to determine the appropriateness of the model. Normally,  $p$  value of lack of fit test greater than  $\alpha = 0.05$  indicates no sufficient evidence to show that

the fitted model is inappropriate. That is, the fitted model is appropriate at the significance level of  $\alpha = 0.05$ . If a quadratic model is appropriate, the model can be expressed as follows:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 + \beta_{11} x_1^2 + \beta_{22} x_2^2 + \varepsilon \quad (12)$$

where  $y$  represents the distance of a CVRP route;  $x_1$  and  $x_2$  are the linear effects of crossover probability and mutation probability on the distance of a CVRP route, respectively;  $x_1 x_2$  indicates the interaction effects of crossover probability and mutation probability on the distance of a CVRP route;  $x_1^2$  and  $x_2^2$  are the quadratic effects of crossover probability and mutation probability on the distance of a CVRP route, respectively;  $\beta_0$ ,  $\beta_j$ ,  $\beta_{ij}$ , and  $\beta_{jj}$  are regression parameters;  $\varepsilon$  is a random error term.

#### Step 4: Determine the optimal combination of crossover probability and mutation probability

The optimal combination of crossover probability and mutation probability is determined based on the established response surface model obtained by Step 3. Accordingly, chromosome evolution through breeding is imitated.

### 4.3. Stage 3: conduct chromosome evolution to enhance GA solution capability

Because a well-structured chromosome population, which possesses a superior capability for exploitation in a local search, is generated in the first stage, the capability of diversified exploration should further improve solution capability for the proposed HGA in optimizing the CVRP. Except for standard operations, such as reproduction, crossover and mutation, for chromosome evolution within the GA, an improved SA incorporated into the mutation process was developed to diversify the structure of offspring, thereby improving fitness values. Stage 3 has the following six steps:

#### Step 1: Reproduce the initial chromosome population

The 10% of chromosomes with superior fitness values are recorded and denoted as parents A for use in subsequent steps prior to conducting reproductive procedure. The conventional roulette-wheel selection scheme is employed for reproductive and elimination procedures; the number of chromosome is the same as the initial population.

#### Step 2: Apply the crossover procedure to chromosomes

The linear-order-crossover method was applied as the crossover procedure to generate offspring. To produce excellent offspring in follow-up generations, 10% of chromosomes with inferior fitness values resulted from crossover procedure are replaced by parents A from Step 1.

#### Step 3: Determine whether to perform the stirring mechanism

If the difference between the best fitness value for each generation and the recorded best fitness value is  $< 0.0001$  for 100 successive generations, then the stirring mechanism is applied; otherwise, skip to Step 4-b. Applying this mechanism can expand the exploration region for the GA;

otherwise, skip to Step 4-a, which is the mutation procedure conducted in stage 2.

*Step 4-a:* Apply the mutation procedure to chromosomes

The mutation procedure is applied based on mutation probability resulting from stage 2.

*Step 4-b:* Apply the stirring mechanism

The stirring mechanism using the improved SA was employed to diversify the exploration region of the GA and improve individual routes. The improved SA has the following steps:

*Step 4-b-1:* Perform insertion action of genes to improve routes

Initially, the genes within an individual route (namely, a vehicle route) is stirred using the pure SA. Then, for the first two and last two genes in individual routes, the following criteria are applied to determine whether to perform the insertion action to the improve fitness value of a GA.

$$\overline{P_{0,0}P_{2,2}} < \overline{P_{0,0}P_{1,1}} \quad (13)$$

$$\overline{P_{0,0}P_{n-1,n-1}} < \overline{P_{0,0}P_{n,n}} \quad (14)$$

where  $P_{i,j}$ ,  $i, j \in \{1, 2, \dots, n\}$ . If  $n$  points are included within an individual route, represents a gene at the  $i$ th position for performing the pure SA, and the  $j$ th position after performing insertion action in stirring mechanism.  $P_{0,0}$  is the depot. If Eq. (13) is fulfilled and the stirring mechanism improved the fitness value, then insert genes  $P_{2,2}$  before the first gene (namely, point  $P_{1,1}$ ). If Eq. (14) is fulfilled and the stirring mechanism improved the fitness value, then insert the gene (namely, point  $P_{n-1,n-1}$ ) after the last gene (namely, point  $P_{n,n}$ ).

Except for the first two and last two genes, the genes within individual routes are stirred using the following criteria:

$$\overline{P_{0,0}P_{i,d}} < \overline{P_{0,0}P_{k_1,1}} \quad (15)$$

$$\overline{P_{0,0}P_{i,d}} < \overline{P_{0,0}P_{k_2,n}} \quad (16)$$

where  $P_{i,d}$  represents a gene at the  $i$ th position for performing the pure SA and the  $j$ th position after performing the insertion action in the stirring mechanism,  $d \in \{3, 4, \dots, n-2\}$ ;  $P_{k_1,1}$  indicates a gene at the  $k_1$ th position for performing the pure SA and the first position after performing the insertion action in the stirring mechanism,  $k_1 \in \{1, 2, \dots, n-2\}$ ;  $P_{k_2,n}$  is, simultaneously, a gene at the  $k_2$ th position for performing the pure SA and the first position after performing the insertion action in the stirring mechanism,  $k_2 \in \{3, 4, \dots, n\}$ . If Eq. (15) is satisfied only and the stirring mechanism improved the fitness value, then insert the gene (namely, point  $P_{i,d}$ ) before the first gene (namely, point  $P_{k_1,1}$ ). If Eq. (16) is fulfilled only and the stirring mechanism improved the fitness value, then insert the gene (namely,  $P_{i,d}$ ) after the last gene (namely,  $P_{k_1,n}$ ). If both Eqs. (15) and (16) are satisfied and the stirring mechanism improved the fitness values, the insertion action with the best fitness value is selected for the stirring mechanism.

*Step 4-b-2:* Apply mutation to chromosomes

Before applying mutation to chromosomes, the 10% of chromosomes with the best fitness values, denoted as parents A, are initially reserved and prepared for elitism policy in the following steps. Simple mutation is then applied to new offspring, in which two genes are selected at random and their values exchanged. The 10% of chromosomes with inferior fitness values resulting from mutation are replaced by parents A.

The example of 7 points in a vehicle elucidated the insertion action within the stirring mechanism. When performing Step 4-b-1, a route is initially obtained by applying the pure SA (Fig. 1). According to criteria, Eqs. (13) and (14), the second gene (namely, point  $P_{2,2}$ ) is inserted before the first gene (namely, point  $P_{1,1}$ ), and the notations  $P_{2,2}$  and  $P_{1,1}$  are modified to  $P_{2,1}$  and  $P_{1,2}$ , respectively. Fig. 2 presents the route after performing the insertion action. According to criteria, Eqs. (15) and (16), the genes – except for the first two points and the last two points – are sequentially determined to assess whether to perform the insertion action. Fig. 3 shows the final route improved by performing Step 4-b-1.

*Step 5:* Determine whether to replace the elitism

If the fitness value during each generation surpasses a recorded best fitness value (namely, the elitism), the elitism is replaced by the champion; otherwise, the worst fitness value in each generation in Step 4 is replaced by the elitism.

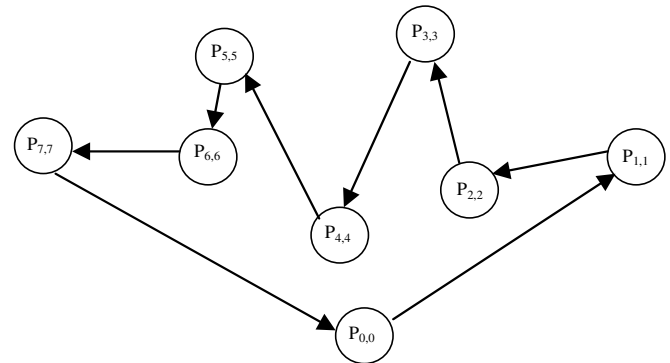


Fig. 1. The route obtained by the pure SA.

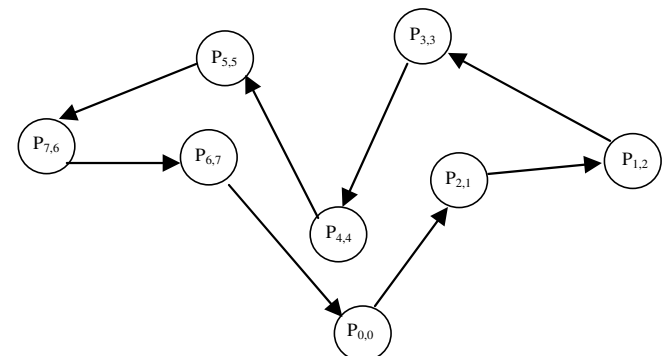


Fig. 2. Routes after performing the insertion action.

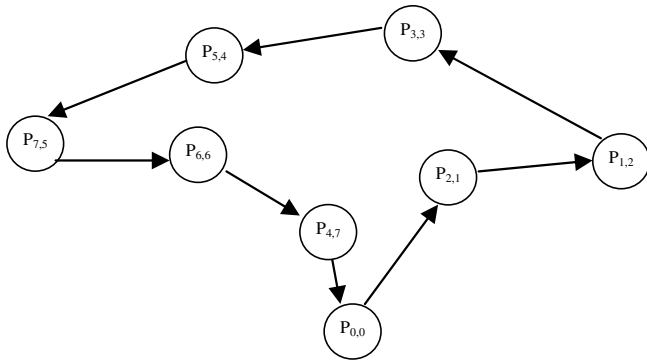


Fig. 3. Final route improved by via Step 4-b-1.

**Step 6: Terminate the HGA**

The proposed HGA is terminated whenever the following conditions are satisfied.

- (1) The change to the fitness values is  $<0.0001$  in 1000 successive generations, enabling a reduction in average CPU time.
- (2) The maximum of 10,000 generations is reached.

Fig. 4 displays the flow chart for stage 3, and Fig. 5 displays the structure of the proposed HGA.

**5. Verification of the proposed HGA**

Benchmark problems obtained from international VRP websites (<http://neo.lcc.uma.es/radi-aeb/WebVRP/>) were

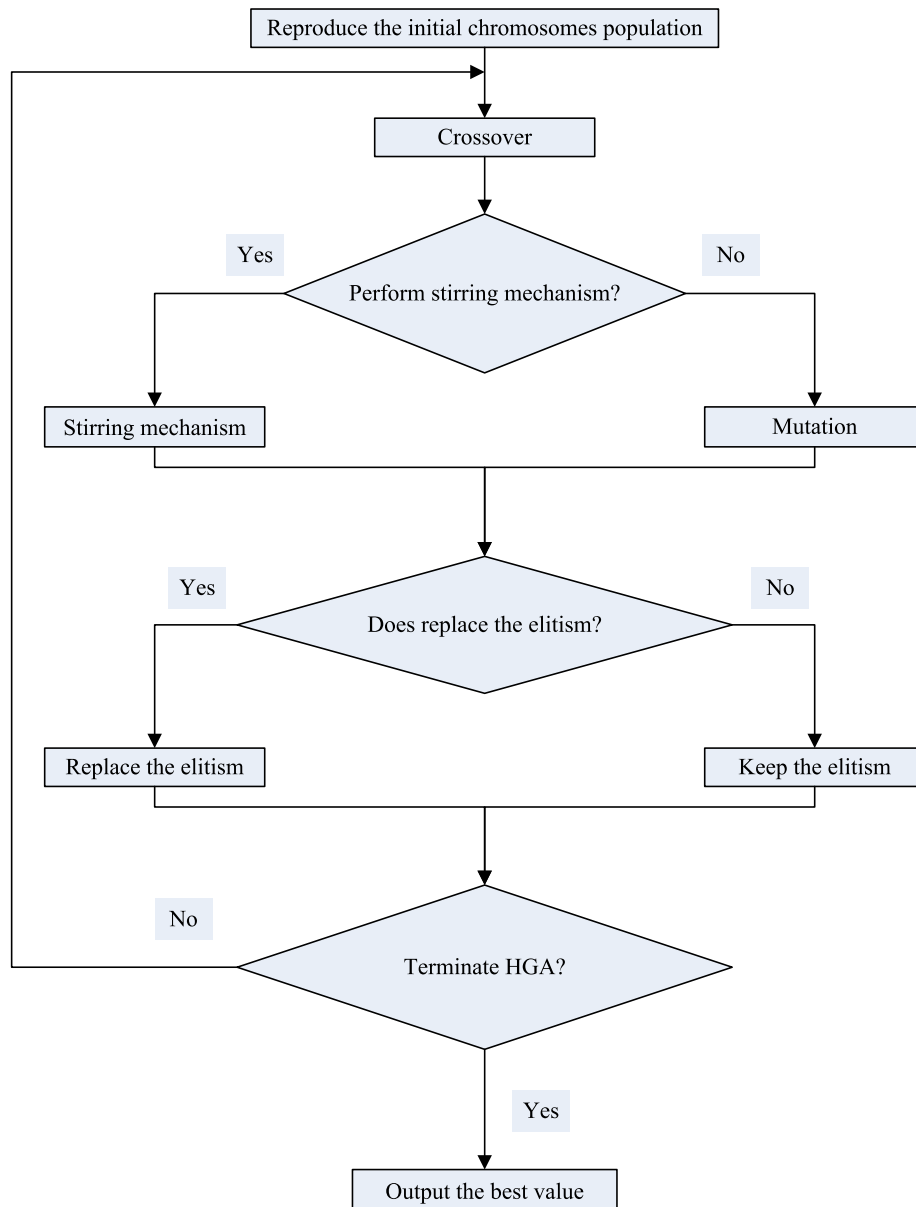


Fig. 4. Flow chart for stage 3.

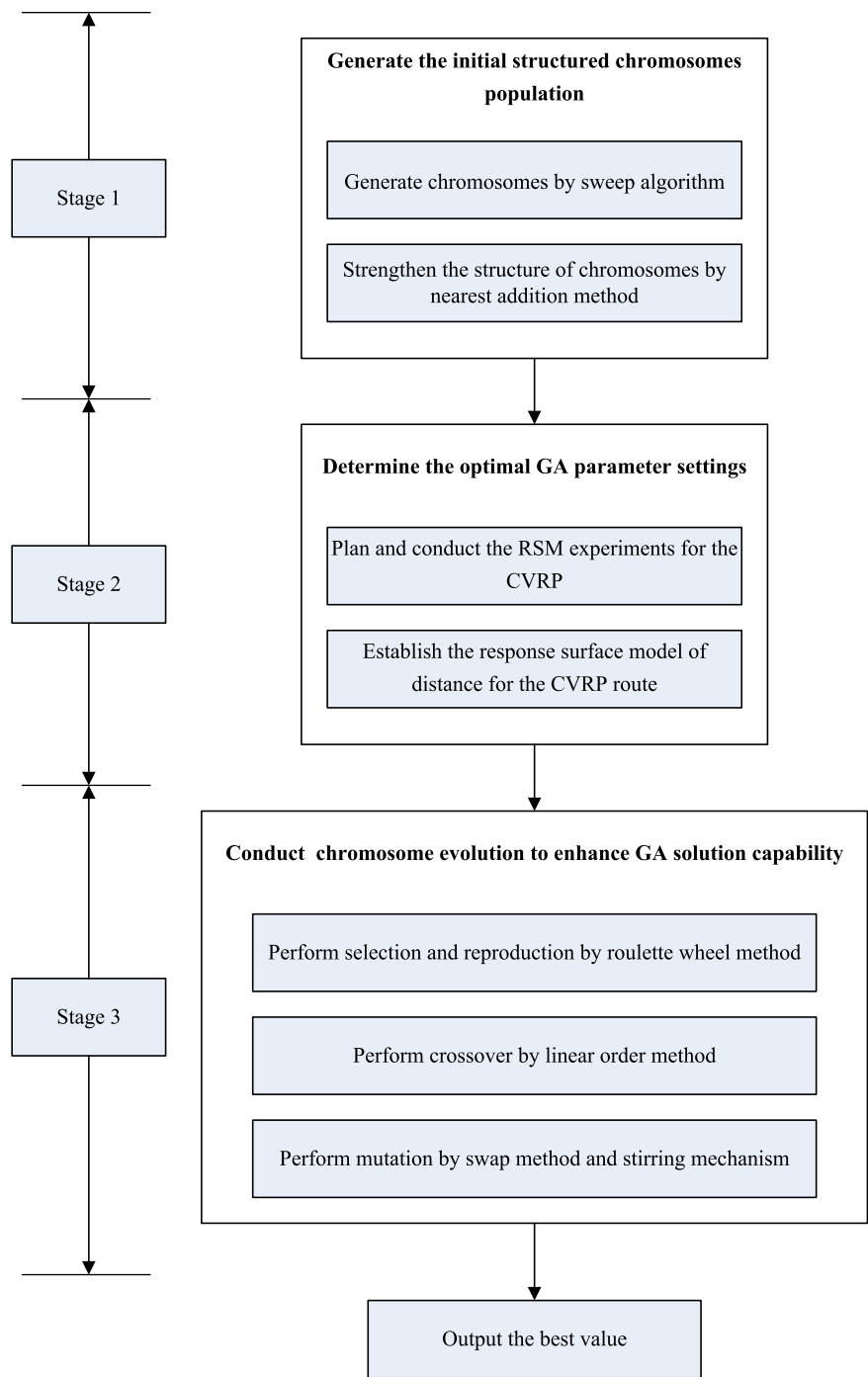


Fig. 5. Structure of the proposed HGA.

adopted to evaluate and verify the proposed HGA and optimize the CVRP. The E-n51-k3 problem details the solving process stage by stage as follows:

5.1. Stage 1: generate the initial structured chromosome population

Chromosome genes are generated using Eqs. (8)–(11). The gene permutations of each chromosome are then improved using the NAM in step 5. Since there are 50 dis-

tribution points in the E-n51-k3 problem, 50 initial chromosomes comprise the initial structured chromosome population in the GA. Table 1

Table 1 Factors levels		
Factors	Low level	High level
Crossover probability	0	1
Mutation probability	0	1



## 5.2. Stage 2: determine the optimal GA parameter settings

### Step 1: Plan the RSM experiments for the CVRP

The crossover and mutation probabilities are set as two designed factors of RSM experiments for the CVRP. Table 2 shows the allocation of the factors levels. The FCCD is utilized to produce the designed points. In total, 13 designed points are generated using the experimental design software DESIGN EXPERT.

### Step 2: Conduct RSM experiments and record experimental observations

Experimental observations, distance of the CVRP route, obtained by the proposed HGA are recorded. Table 3 shows the RSM experiments and corresponding distance of the CVRP route.

### Step 3: Establish the response surface model of distance for the CVRP route

The lack-of-fit test reveals that a quadratic response model was appropriate ( $p > 0.05$ ). The fitted model is as follows.

The coefficient of determinant for this model is  $R^2 = 0.9663$ . Table 3 presents the analysis of variance (ANOVA) spell out unless it is common terminology to use the acronym table.

Table 2  
Designed experiments and route distance

Experimental points	Crossover probability	Mutation probability	Route distance
1	0.5	0.5	537.54
2	1	0.5	536.14
3	1	1	524.61
4	0.5	0.5	536.14
5	0.5	1	524.81
6	0	0	579.09
7	0	1	528.92
8	0.5	0.5	536.14
9	0.5	0.5	524.81
10	1	0	579.09
11	0.5	0	579.09
12	0.5	0.5	524.61
13	0	0.5	539.32

Table 3  
ANOVA table for CVRP route distance

Source	Sum of squares	DF	Mean square	F value	P value
Model	5433.19	5	1086.64	40.17	< 0.0001
A (crossover probability)	9.35	1	9.35	0.35	0.5751
B (mutation probability)	4209.79	1	4209.79	155.61	< 0.0001
A2	34.11	1	34.11	1.26	0.2985
B2	868.63	1	868.63	32.11	0.0008
AB	4.64	1	4.64	0.17	0.6910
Residual	189.38	7	27.05		
Lack of fit	18.21	3	6.07	0.14	0.9297
Pure error	171.16	4	42.79		
Cor total	5622.57	12			

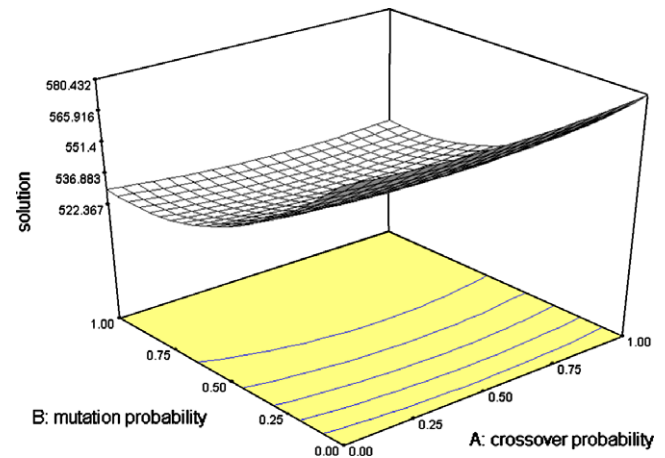


Fig. 6. Response surface diagram of the CVRP solution for the E-n51-k3 problem.

According to ANOVA results, both the linear and quadratic effects of mutation probability on the CVRP solution are significant. However, crossover probability does not significantly affect the CVRP solution and neither does the interaction between crossover probability and mutation probability. Fig. 6 presents the response surface diagram of the CVRP solution on crossover probability and mutation probability. Based on the response surface diagram, the various crossover and mutation probabilities can be further explored.

Step 4: Determine the optimal combination of crossover probability and mutation probability. Via mathematical programming, the combined optimal crossover and mutation probabilities are 0.98 and 0.75, respectively. This optimal setting is then substituted into GA breeding process within the HGA to efficiently approach the close-to-optimal CVRP solution.

## 5.3. Stage 3: apply evolution to chromosomes to enhance GA solution capability

The initial structured chromosome population is enhanced through imitated evolution via the proposed HGA, in which the improved SA and elitism policy are incorporated given a crossover probability of 0.65 and mutation probability of 0.88. This study conducted 30 replication experiments under optimal parameter settings. Thirty solutions for CVRP route distance were obtained. Table 4 lists these solutions.

The optimal distance of the CVRP route is 524.61 (Table 4). This computational result surpasses the best known value of 524.944. The coefficient of variation (CV) – standard deviation divided by the mean – for the 30 CVRP solutions is 0.41%. This computational finding confirms that the proposed HGA has high reproducibility for solving the CVRP problem E-n51-k3. Restated, the proposed HGA is robust in solving the CVRP. This study further optimized another 9 benchmark problems using the

Table 4  
The CVRP solutions under optimal crossover and mutation settings

Run	CVRP solution	Run	CVRP solution	Run	CVRP solution
1	524.61	11	524.61	21	524.81
2	524.61	12	524.61	22	524.61
3	524.61	13	524.61	23	524.61
4	524.61	14	524.61	24	526.17
5	524.61	15	524.81	25	524.81
6	524.61	16	524.61	26	524.61
7	526.37	17	524.61	27	524.61
8	524.61	18	536.37	28	524.61
9	524.61	19	524.61	29	524.61
10	524.81	20	524.61	30	524.81

same three-stage procedures. The deviation percentage between the solved close-to-optimal solution and best-known value was derived to evaluate the solution capability of the proposed HGA. Table 5 summarizes these calculations, and Appendix 1 displays the optimized route for each problem.

According to optimization results for over 10 benchmark problems, the feasibility and effectiveness of the proposed HGA in optimizing the CVRP are as follows:

- (1) The optimal combination of GA crossover and mutation is markedly affected by the search mechanism embedded in the GA. Furthermore, the characteristics of the CVRP, including the number of distribution points and corresponding demands, depot location relative to distribution points, also significantly affect the optimal combination of GA crossover and mutation. Using RSM can efficiently determine the optimal combination of crossover and mutation probabilities and be adopted for different search mechanisms embedded in the GA. Analyzing the crossover and mutation combination (Table 5) determined that all optimal mutation probabilities were  $>0.70$ , and mutation probability was larger than crossover probability for the E-n51-k5 and E-n76-k8 problems. Therefore, we conclude that the proposed HGA has high mutation probability, and is capable of extensively diversifying GA exploration. This experimental result meets with the expectation that

a extensive diversity of chromosomes enhance exploration capability of the GA and is complementary to a well-structured initial population.

- (2) Optimization results for the E-n30-k3 problem with 29 distribution points and the E-n30-k3 problem with 50 distribution points both exceed the current best-known value.
- (3) Although the E-n33-k4 problem has fewer distribution points than the E-n51-k5 problem, its depot is located outside demand points; thus the difficulty in solving the E-n33-k4 problem is greater than that for the E-n51-k5 problem. However, the optimization result obtained by this study was  $<0.78\%$  of the best-known value. This computational finding demonstrates the effectiveness of the proposed HGA in optimizing the CVRP.
- (4) The E-n101-k8 and E-n101-k14 problems, each with 100 distribution points, have the same demands and only differ in vehicle capacity constraints. Because vehicle capacity in the E-n101-k14 problem is less than that in the E-n101-k8 problem, larger feasible solutions are generated compared with those for the E-n101k problem. The complexity of the E-n101-k14 problem is significantly larger than that of the E-n101-k8 problem. Accordingly, the computational result for the E-n101-k14 problem is inferior to the E-n101-k8 problem.

This study efficiently solved CVRPs with fewer than 100 distribution points. Therefore, we conclude that the proposed HGA optimized the CVRP.

## 6. A real application for the armed forces

The proposed HGA was employed to optimize a case of transportation route from the armed forces. The current route is determined based on managerial experience and operational criteria. The maximum truck capacity is 5000 units. Currently, 22 transportation routes are served by 24 trucks assigned to deliver the demands of 70 transportation points. Appendix 2 presents the coordinates of 70 transportation points and the corresponding demands.

Table 5  
Summary of calculations for benchmark problems

Problems number	Crossover probability	Mutation probability	CV of CVRP solution (%)	CVRP solution	Best known value	Deviation percentage (%)
E-n23-k3	1.00	0.74	0.32	568.56	568.563	0.00
E-n30-k3	0.98	0.75	0.00	508.14	538.958	-5.72
E-n33-k4	1.00	0.85	0.85	845.24	838.721	0.78
E-n51-k5	0.65	0.88	0.41	524.61	524.944	-0.06
E-n76-k7	0.74	0.70	0.84	701.28	687.603	1.99
E-n76-k8	0.62	0.73	0.73	750.48	735	2.11
E-n76-k10	1.00	0.85	0.73	853.05	832	2.53
E-n76-k14	1.00	0.76	0.67	1057.70	1032	2.49
E-n101-k8	0.88	0.77	1.13	847.50	817	3.73
E-n101-k14	1.00	0.81	0.66	1121.30	1077	4.11

Table 6  
The route, corresponding distance and loading rate for each truck

Route number	Route	Loading rate (%)	Transportation distance (km)
1	1 → 4 → 64 → 63 → 1	79.14	35.2
2	1 → 47 → 48 → 42 → 49 → 46 → 1	15.52	43.6
3	1 → 6 → 65 → 5 → 41 → 1	26.58	50.1
4	1 → 38 → 36 → 1	95.22	58.6
	1 → 37 → 62 → 1	75.70	28.2
	1 → 35 → 24 → 34 → 1	84.70	80.1
5	1 → 50 → 1	5.78	76.2
6	1 → 55 → 54 → 53 → 57 → 1	16.62	77.1
7	1 → 25 → 1	3.04	44.6
8	1 → 20 → 71 → 56 → 69 → 21 → 19 → 18 → 52 → 22 → 1	70.86	83.3
9	1 → 26 → 27 → 30 → 29 → 28 → 1	38.82	22.4
10	1 → 33 → 32 → 70 → 1	37.38	18.1
11	1 → 39 → 58 → 59 → 61 → 11 → 68 → 1	14.84	42.2
12	1 → 67 → 66 → 1	17.58	127.3
13	1 → 60 → 51 → 44 → 1	44.74	134.0
14	1 → 43 → 1	3.62	148.2
15	1 → 40 → 10 → 12 → 13 → 1	50.68	34.6
16	1 → 45 → 1	6.02	46.2
17	1 → 7 → 1	2.50	39.6
18	1 → 9 → 8 → 31 → 1	32.66	43.4
19	1 → 14 → 1	54.66	53.0
20	1 → 15 → 16 → 1	16.14	49.3
21	1 → 23 → 2 → 3 → 1	19.32	43.9
22	1 → 17 → 1	10.14	33.6

Table 6 presents the current 24 trucks routes. Fig. 7 displays the route diagram, in which transportation distances indicates actual travel distances. In total, 24 trucks are needed; the third route requires 3 trucks (Table 5). Furthermore, the loading rates for trucks 1, 4, 8, 15, and 19 are <50%, and the loading rates for trucks 5, 7, 14, 16, and 17 are <10%. Average loading rate is 34.26%. Vehicle availability is very low. Total delivery distance is 1450.5 km. Further analyzing the transportation points finds out that 4 points deviate significantly from the other clustered points, and the logistics center is located outside the transportation points. In summary, the current route is extremely ineffective, largely reducing the availability of resources such as facilities and human resources.

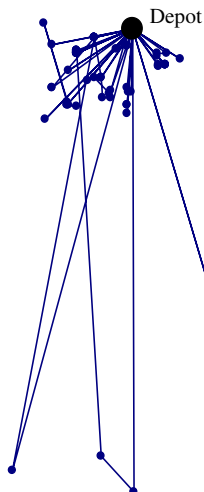


Fig. 7. Diagram of transportation routes.

This real case was analyzed using the proposed HGA, in a stage-by-stage manner, as follows.

#### 6.1. Stage 1: generate the initial structured chromosome population

As there are 70 distribution points, 70 chromosomes are produced as the initial population.

#### 6.2. Stage 2: determine the optimal combination of crossover and mutation probabilities

The quadratic response model of route distance on crossover and mutation probabilities for this case is deter-

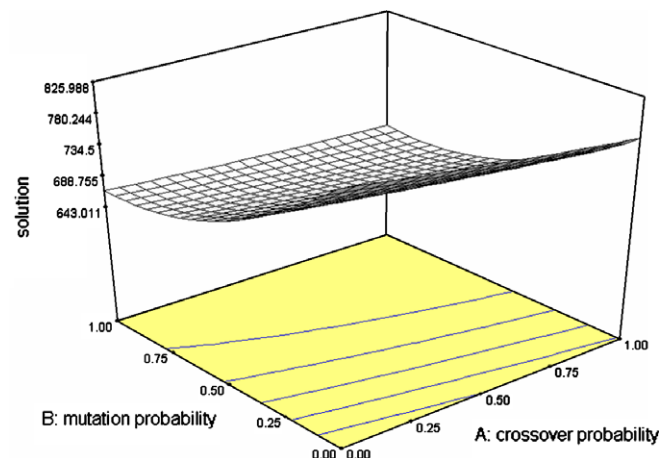


Fig. 8. Response surface diagram of the CVRP for the armed forces case.

Table 7  
Optimal routes of an armed forces case

Trucks number	Routes	Loading rate (%)	Transportation distance
1	1 → 29 → 66 → 26 → 53 → 62 → 45 → 39 → 60 → 58 → 61 → 68 → 59 → 40 → 10 → 64 → 63 → 11 → 1	99.98	59.5
2	1 → 27 → 28 → 30 → 31 → 46 → 49 → 48 → 47 → 65 → 42 → 6 → 41 → 5 → 9 → 8 → 1	93.14	69.3
3	1 → 32 → 69 → 56 → 57 → 21 → 19 → 18 → 20 → 71 → 70 → 1	97.16	48.1
4	1 → 24 → 50 → 67 → 51 → 44 → 43 → 7 → 1	84.22	231.9
5	1 → 23 → 3 → 2 → 16 → 15 → 14 → 33 → 1	94.30	56.0
6	1 → 25 → 54 → 55 → 34 → 38 → 37 → 1	97.66	66.8
7	1 → 17 → 12 → 35 → 13 → 1	93.08	41.0
8	1 → 36 → 22 → 52 → 1	94.76	59.6
9	1 → 4 → 1	67.96	2.6

Table 8  
Comparisons between the current routes and optimization routes for HGA

	Current routes	Optimization routes for HGA	Improvement	Improvement rate (%)
Trucks required	24	9	15	62.50
Average loading rate (%)	34.26	91.36	57.10	57.10
Loading variance	0.2889	0.0983	0.1906	65.99
Total transportation distance (km)	1450.5	634.8	815.7	56.24

mined. The coefficient of determination is  $R^2 = 0.9639$ . This model is as follows:

$$\hat{y} = 825.99 - 66.71x_1 - 338.84x_2 + 36.50x_1x_2 + 9.76x_1^2 + 176.56x_2^2$$

where  $\hat{y}$  represents the predicted route distance, and  $x_1$  and  $x_2$  are the crossover probability and mutation probability, respectively. Fig. 8 displays the response surface diagram. The optimal crossover and mutation probabilities are 1.00 and 0.85, respectively.

### 6.3. Stage 3: conduct evolution of chromosomes to enhance GA solution capability

The initial GA population with 70 chromosomes resulting from stage 1 is improved using the proposed HGA. The close-to-optimal solution obtained was 634.8 km. Table 7 lists the optimized routes for this case.

The number of optimized routes is reduced to 9 from the current 24 routes (Table 8). Truck average loading rate is increased to 91.36% from 34.26%, an increase of 57.1%. The total transportation distance is reduced to 634.8 km from 1450.5 km, a reduction of 56.24%. This case demonstrates that the proposed HGA reduces the number of trucks and human resources required to transport goods and materials and improves truck loading rate. Therefore, transportation distance is markedly reduced, improving the effectiveness of transportation compared with current operations.

## 7. Conclusion

Metaheuristic algorithms have been applied to solve complex optimization problems in which GAs are extensively employed to solve the combinatorial optimization problems. The search mechanism embedded in the GA focuses on the breeding process in evolution on crossover and mutation operators that are applied using probability setting to approach a close-to-optimal solution. Because GA and conventional heuristics are complementary, a hybrid approach frequently outperforms the application of either method alone. Furthermore, past studies have verified that crossover and mutation operators in a GA affect to its solution capability and the construction of the initial GA population. This study constructs the initial GA population by embedding the NAM into an SA to form a well-structured initial GA population. The superior offspring can be bred via evolution. Furthermore, the FCCD experiment was conducted to establish a response surface model for distances of CVRP routes on crossover and mutation probabilities. The optimal combination of crossover and mutation probabilities was determined to enhance the capability of the GA to search for a close-to-optimal solution. Additionally, the elitism policy, applied during the GA breeding process, was used to replace inferior chromosomes with superior chromosomes. The effectiveness and practicality of the proposed HGA was verified via international benchmark problems. Finally, the proposed HGA was employed to solve a real logistics transportation problem. In summary, the proposed HGA has the following benefits:

- (1) Generating the initial GA population considers the axial and radius relationships relative to the logistics center, simultaneously to obtain a well-structured chromosome population, thus strengthening the capability of locally exploited chromosomes.
- (2) Using RSM, a systematic methodology, considerably reduces the time required to identify GA parameter settings compared with the conventional trial-and-error method. The optimal combination of crossover and mutation probabilities is thus obtained.
- (3) The improved SA combined with the elitism policy improves the exploration capability of the GA, and

avoids premature and rapid convergence to a limited region.

- (4) The proposed HGA was proved capable of solving international benchmark problems. Addition-

ally, a case problem of logistics transportation was optimized using the proposed HGA. Therefore, the proposed HGA is practical and sound.

## Appendix 1

The routes of benchmark problems from the proposed HGA

Number of route	Route															
Problem number	E-n23-k3															
1	1	19	20	21	23	18	15	16	17	4	3	2	7	12	13	1
2	1	8	10	9	6	5	22	1								
3	1	11	14	1												
Problem number	E-n30-k3															
1	1	21	4	5	6	2	7	25	26	30	28	29	27	20	1	
2	1	19	24	11	12	13	9	15	10	18	8	14	17	16	1	
3	1	3	23	1												
4	1	22	1													
Problem number	E-n33-k4															
1	1	12	19	20	22	21	23	24	25	26	18	14	1			
2	1	4	3	13	33	11	10	9	8	7	6	5	1			
3	1	31	32	15	16	2	1									
4	1	30	29	17	28	27	1									
Problem number	E-n51-k5															
1	1	47	6	50	11	40	34	46	16	45	38	13	1			
2	1	9	27	32	29	4	37	36	21	23	2	33	1			
3	1	12	3	30	22	17	51	35	31	10	39	1				
4	1	19	14	42	41	20	43	18	5	48	1					
5	1	28	49	24	8	44	25	26	15	7	1					
Problem number	E-n76-k7															
1	1	18	52	17	64	24	57	50	25	19	51	33	45	4	1	
2	1	31	49	48	37	71	61	72	70	22	62	29	75	76	1	
3	1	7	34	74	2	44	42	43	65	23	63	3	69	1		
4	1	47	9	20	55	14	58	16	21	38	6	30	46	1		
5	1	27	13	73	59	11	32	56	26	10	40	41	1			
6	1	8	36	54	15	60	12	67	66	39	1					
7	1	5	28	53	35	68	1									
Problem number	E-n76-k8															
1	1	46	30	6	38	21	71	61	72	70	37	48	49	1		
2	1	76	52	17	64	24	57	50	25	4	45	18	1			
3	1	7	34	74	2	44	42	43	65	23	63	1				
4	1	47	9	20	55	14	58	16	28	53	35	1				
5	1	13	40	10	26	56	19	51	33	41	1					
6	1	12	67	66	39	11	32	73	59	1						
7	1	69	3	29	62	22	75	31	5	1						
8	1	68	36	15	60	54	8	27	1							
Problem number	E-n76-k10															
1	1	75	22	48	37	70	72	61	71	21	30	1				
2	1	52	17	64	24	57	50	25	4	18	1					
3	1	74	2	44	42	43	65	23	62	69	1					
4	1	31	49	6	38	16	58	14	47	1						

(continued on next page)



## Appendix 1 (continued)

Number of route	Route																
5	1	9	55	20	60	15	54	36	1								
6	1	45	51	19	56	26	33	41	1								
7	1	59	11	32	10	40	73	13	1								
8	1	8	12	67	66	39	27	1									
9	1	7	34	63	29	3	76	1									
10	1	5	46	28	53	35	68	1									
Problem number	E-n76-k14																
1	1	37	70	72	61	71	21	38	30	1							
2	1	44	42	43	65	23	62	1									
3	1	17	50	25	57	24	64	1									
4	1	46	6	16	58	14	28	1									
5	1	33	26	56	19	4	52	1									
6	1	75	22	48	49	31	1										
7	1	34	2	74	63	29	1										
8	1	59	39	11	32	73	1										
9	1	47	9	20	55	53	1										
10	1	8	12	67	66	1											
11	1	27	13	41	18	1											
12	1	36	15	60	54	1											
13	1	40	10	51	45	1											
14	1	7	3	69	76	1											
15	1	5	35	68	1												
Problem number	E-n101-k8																
1	1	28	70	2	71	31	21	67	33	91	64	11	63	89	32	1	
2	1	53	8	83	49	20	12	65	50	37	48	47	9	84	19	1	
3	1	77	78	4	80	79	35	36	66	72	10	52	82	34	51	1	
4	1	29	13	81	69	30	25	55	56	26	40	5	41	54	1		
5	1	7	97	100	94	62	17	87	18	46	85	6	61	90	1		
6	1	27	22	73	76	57	68	24	42	23	75	74	59	1			
7	1	60	99	86	92	45	39	15	101	38	93	95	1				
8	1	14	96	98	88	43	44	16	58	3	1						
Problem number	E-n101-k14																
1	1	97	100	6	85	18	46	84	61	90	1						
2	1	53	8	20	50	65	12	63	89	1							
3	1	28	70	71	33	91	64	11	32	1							
4	1	77	79	35	36	10	82	34	51	1							
5	1	14	88	43	44	16	58	3	59	1							
6	1	54	41	74	42	23	75	73	22	1							
7	1	31	21	67	66	72	52	2	1								
8	1	83	49	48	37	47	9	19	1								
9	1	94	92	45	39	15	101	98	1								
10	1	69	81	25	30	80	4	78	1								
11	1	27	5	26	56	55	13	29	1								
12	1	95	60	99	38	93	96	1									
13	1	62	87	17	86	7	1										
14	1	76	24	68	40	57	1										

## Appendix 2

The coordinate and capacity of a real case

Transportation point	X coordinate	Y coordinate	Capacity
1	0.00	0.00	0
2	−5.02	−91.28	269
3	−0.92	−91.18	290
4	−0.70	−0.49	3398
5	32.97	−53.73	418
6	33.00	−53.40	583
7	60.79	−44.18	125
8	31.93	−35.98	394
9	31.92	−40.08	404
10	−69.61	−35.67	562
11	−69.63	−35.83	146
12	−69.63	−35.99	468
13	−69.62	−35.98	851
14	−6.13	−123.01	2733
15	−5.70	−111.27	443
16	−5.79	−111.38	364
17	−68.47	−33.85	507
18	−28.92	−93.67	705
19	−26.34	−100.93	95
20	−26.73	−90.64	523
21	−37.01	−101.04	179
22	−55.22	−75.87	425
23	−6.12	−85.62	407
24	−69.41	−113.60	1073
25	−80.26	−61.87	152
26	−47.75	−12.80	284
27	−47.80	−12.96	196
28	−47.81	−13.08	338
29	−47.84	−13.21	738
30	−47.86	−13.32	385
31	42.95	−35.28	835
32	−19.40	−30.21	1218
33	−6.18	−24.83	209
34	−80.94	−111.22	334
35	−80.35	−110.45	2828
36	−80.45	−110.16	4304
37	−80.82	−105.85	3564
38	−80.72	−110.28	457
39	−69.09	−32.66	83
40	−68.94	−32.67	653
41	33.06	−53.56	143
42	42.27	−52.16	343
43	154.49	−604.19	181
44	2.81	−674.84	1553
45	−99.78	−22.26	301
46	42.19	−52.18	85
47	42.17	−52.26	110
48	42.17	−52.32	121
49	42.16	−52.41	117
50	−108.61	−131.78	289

## Appendix 2 (continued)

Transportation point	X coordinate	Y coordinate	Capacity
51	−39.25	−623.61	174
52	−47.55	−70.30	9
53	−47.78	−12.51	366
54	−99.51	−85.35	150
55	−99.57	−85.10	226
56	−39.19	−71.40	513
57	−39.12	−71.34	89
58	−68.84	−32.70	81
59	−68.84	−32.60	145
60	−68.82	−32.54	510
61	−68.82	−32.43	150
62	−110.53	8.18	221
63	−69.73	−35.68	137
64	−69.75	−35.79	422
65	42.30	−52.30	185
66	−47.75	−12.67	63
67	−149.87	−644.14	816
68	−68.77	−32.71	137
69	−39.21	−71.47	548
70	−9.78	−21.99	442
71	−9.79	−22.07	546

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