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# Ant algorithm for modifying an inconsistent pairwise weighting matrix in an analytic hierarchy process

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**Abstract** One important issue in the analytic hierarchy process (AHP) is confirming the consistency of comparison matrix to verify the logical respondent opinion. As inconsistent comparison matrix cannot be used as reference to make decisions, this paper proposes a method using an ant algorithm to modify an inconsistent pairwise weight matrix to be consistent in AHP, called ANTAHP. This method employs the matrix element as the path in an ant colony optimization to construct the tour. By laying pheromone information on their path, the ants can find the optimal matrix (or tour), which satisfies the consistency and closer to the original judgment of the decision makers. The experimental results demonstrate that the proposed algorithm is able to make consistent matrices, as well as minimize the difference index.

**Keywords** Ant algorithm · Inconsistent matrix ·  
Pairwise weight matrix · Consistent ratio

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## 1 Introduction

Decision making is intensively performed in daily life and occurs most commonly in business activities where it involves multiple evaluation criteria for selecting the best policy. The analytic hierarchy process (AHP) is a basic multi-criteria decision making (MCDM), which concerns determining the significant criteria and then selecting the best strategy regarding the criteria analysis [4, 11, 16]. This technique is effective for quantitatively judging the importance level of each criterion indicated by its corresponding weight [24, 26]. However, there are some drawbacks of the AHP in measuring the weights importance of the decision criteria. Triantaphyllou and Mann [29] argued that the traditional AHP which proposes relative measurement of the various criteria is represented by a set value integers ( $\frac{1}{9}, \frac{1}{8}, \frac{1}{7}, \dots, 7, 8, 9$ ). In fact, some problems can be represented better by fuzzy sets in continuous values as opposed to discrete values. They revealed that this constraint causes high failure rates. Another study [19] found that it is hard to identify in-between members even it can easily classify the representative members in a fuzzy set. As a consequence of the above weaknesses, the inconsistency of pairwise weighting matrix (PWM) or comparison matrix on behalf of the decision maker's (DM) opinion often occurs especially for high number criteria. The simple illustration of inconsistency can be stated as follows. Suppose in the DM's opinion that *A* is better than *B*, and *B* is better than *C*. The consistent logic of the DM's opinion should be that *A* must be better than *C*. Contrarily, it would be inconsistent if the DM's opinion stated that *C* is better than *A*. Consistency of the PWM is revealed by the consistency ratio (CR). Saaty defined the threshold of the CR as being 0.1 [24]. The reason for choosing this threshold

1 satisfactory is described in [30]. As such, the method of modifying an inconsistent comparison matrix becomes an interesting issue. Generally, there are two ways for transforming inconsistent comparison matrices into consistent ones. (1) The value of the comparison matrix is changed by the reassessment process. This means that the opinion of the decision makers is asked again to obtain new matrix value; however, this method still does not guarantee that consistency is obtained. Therefore, the process will be repeated until the consistency is satisfied. (2) The original matrix is modified by particular method such that it meets the consistency threshold. Modifying the inconsistent matrix has received attention from researchers. There are some methods presented in solving inconsistency multiplicative preference [1, 3, 8, 12, 14, 15, 17, 20, 28, 31, 40] and fuzzy preference relations problem [5, 6, 22, 33–38].

In multiplicative preference, Siraj et al. [28] improved the consistency by detecting and removing intransitive in comparison matrices. Dong et al. [8] proposed the method, which has two purposes, the improving individual consistency measure and the consensus measure. Jose et al. [15] presented a model based on multilayer perceptron (MLP) neural networks to develop missing values in incomplete and improving its consistency as well. Ishizaka and Lusti [17] proposed an expert module that consists of some parts such as detecting rule transgressions, suggesting alternative and giving hints to continue the comparison process. One of the important steps in this module is comparison matrix, which has four types: principal diagonal, independent, transitive and comparisons. Daji et al. [12] modified the inconsistent comparison matrix by proposing the induced matrix to identify the elements, which lead the matrix to be inconsistent. Ultimately, they suggested altering the elements to obtain consistent matrix. Consequently, they did not change most of the elements matrix except for the parts suspected of rendering the matrix inconsistent. Jose and Lamata [1] presented an estimation method for a good random coefficient index (RI). They used a simpler function than Saaty to define the accepting or rejecting matrices, and also offered the levels of consistency to consider restrictive situations. Xu and Wei [40] developed a consistent matrix  $B$  by replacing the inconsistent matrix  $A$  with  $b_{ij} = a_{ij}^\alpha (W_i/W_j)^{1-\alpha}$ , where  $W = (W_1 \dots W_i \dots W_j \dots W_n)^T$  is the eigenvector  $A$ , and  $\alpha$  is a positive value closer 1.0. Cao et al. [3] extended Xu and Wei's method by decomposing the original matrix as a Hadamard product of a consistent matrix and a reciprocal deviation matrix. A modified matrix is built via a convex combination of the reciprocal deviation matrix and a zero deviation matrix.

The issues of consistency in fuzzy preference relation also have received attention from researchers. Xu et al. [35] proposed a revised approach by using linear programming

models to generate interval priority weights for additive interval fuzzy preference relations. Xu et al. [38] presented the method to fulfill the element, which is incomplete on fuzzy preference for group decision making based on additive transitive and accumulate the auxiliary value into a group auxiliary relation. This research was extended by Xu et al. [33], who deduced a function between the additive transitivity fuzzy preference and its corresponding priority vector. Xu et al. [34] proposed algorithm by eliminating the cycles of length 3 to  $n$  in the digraph of the incomplete reciprocal preference relation and convert it to one with ordinal consistency. Liu et al. [22] proposed a method to solve the incompleteness preference matrix and also repairing the inconsistency preference matrix. This method calculated minimal of the squared error to fulfill the missing value  $s$  and generated the consistency fuzzy preference such that the modified is the closest to the original one. Chen et al. [5] presented a method for group decision making using incomplete fuzzy preference based on additive consistency. Chicalana et al. [6] proposed a functional equation to model the cardinal consistency in the strength of preferences of reciprocal preference relations. Xia et al. [32] improved the consistency by using the geometric consistency index either complete or incomplete fuzzy preference.

Another important research trend is using an intelligent algorithm to modify an inconsistent matrix. Lin et al. [21] and Jose [7] used a genetic algorithm (GA) to obtain the consistent matrices. Yang et al. [39] combined particle swarm optimization (PSO) and Taguchi method to modify inconsistent matrices. The Taguchi method was incorporated into the procedure to reduce the number of experiments required for tuning the control parameters of PSO. Besides, considering CR must be less than 0.1. Lin et al. and Yang et al. also determined 2 further aspects. These aspects include (1) matrix distance between modified and original matrix comparison, called difference index ( $D_i$ ); and, (2) eigenvalues close to number comparison elements ( $\lambda_{\max} = n$ ). These two aspects were combined in the objective function to minimize the overall index ( $OI$ ).

From all the methods mentioned above, there is no special consideration to chase the lowest different matrix between the original (inconsistent) and modified (consistent) matrix. Although the GA [21] and PSO [39] methods reduce the difference index, it does not get the optimal difference index. We argue that the CR value does not need the lowest CR value. CR value is changed only to satisfy the standard threshold of CR (less than 0.1). We emphasize that the closer the matrix is to the original matrix, the more important it is, as long as the consistency matrix is acceptable.

To implement this idea, we use the concept of ant colony optimization (ACO) method, which is one of the



intelligent algorithms using swarm optimization. As we know, until now, there is no research using ACO to solve the inconsistent in pairwise comparison matrix. ACO has been widely used due to its top performance in solving various optimization problems, such as traveling salesman problem (TSP) [9, 10], clustering [27], vehicle routing problem (VRP) [13], data mining [23], shop scheduling [2] and so forth. Therefore, we use this ant algorithm to repair an inconsistent matrix to become consistent by modifying the discrete values to the continuous values. Although there are value changes, it will not change the judgment tendency of the decision maker. The proposed algorithm not only satisfies the consistent matrix, but also maintains the original matrix judgment by enhancing the minimal difference index.

However, we also prove AHPANT is very competitive with the other methods in same objective function on Yang et al. method [39] and same the maximum threshold of the difference between original and modified value on Xu, Wei and Cao et al. [3, 40].

The remainder of this paper is organized as follows: Sect. 2 gives a brief introduction to the inconsistency matrix problem in AHP. Section 3 provides a detailed description of the proposed algorithm, while performance evaluation of the proposed algorithm is presented in Sect. 4. Finally, conclusions are offered in Sect. 5.

## 2 Problem definition

AHP was proposed to derive the weight ratio for pair comparison in multilevel hierarchic structures [24]. These comparisons may be obtained by a real measurement scale, or subjective opinion that reflects the relative strength of the preference and feeling [26]. AHP can analyze multiple criteria to select the dominant strategy/alternative in the decision making process. To obtain the priority alternative, all decision problems are considered as a hierarchical structure. The first level indicates the goal for the specific decision problem, while in the second level, the goal is decomposed to several criteria and the lower levels can follow this principal and divide into other sub-criteria. Suppose matrix  $A$  denotes a PWM, so  $A$  can be depicted as Fig. 1.

The element  $a_{ij}$  on  $A$  represents comparing alternatives  $i$  and  $j$  with  $a_{ij} = 1/a_{ji}$ . In the study of [24], Saaty proposed 9-scale value (1, 2, 3, ..., 9) to reveal the judgment of

Fig. 1 Pairwise weighting matrix (PWM) of AHP

$$A = \begin{pmatrix} a_{1,1} & a_{1,2} & \cdots & a_{1,n} \\ a_{2,1} & a_{2,2} & \cdots & a_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ a_{n,1} & a_{n,2} & \cdots & a_{n,n} \end{pmatrix}$$

decision makers. Since AHP is represented as a comparison matrix, it will also automatically set the reverse judgment of the decision makers with 9-scale value  $(1, \frac{1}{2}, \frac{1}{3}, \dots, \frac{1}{9})$  as well. As described in introduction, this comparison matrix should satisfy the consistency value. It is because the decision cannot be taken based on judgments that results in such low consistency or inconsistency. In [25], consistency is defined as the intensities of relations among ideas or object based on a particular criterion justifying each other in some logical way. A PWM is said to be perfectly consistent if all the transitivity relationship are satisfied as described by Eq. (1):

$$a_{ij} = a_{ik} \cdot a_{kj}, \tag{1}$$

In fact, a perfect consistency matrix is hard to obtain due to discrete 9-value scale especially for high number of criteria. The consistency of a pairwise comparison is measured by the principle eigenvalue as described by Eq. (2).

$$AW = \lambda_{\max} W, \tag{2}$$

where  $\lambda_{\max}$ ,  $W$  are the largest eigenvalue and eigenvector of the matrix  $A$ , respectively. Saaty [24] proposed a consistency index (CI) as described by Eq. (3):

$$CI = \frac{\lambda_{\max} - n}{n - 1}, \tag{3}$$

while the consistency ratio (CR) is defined by Eq. (4):

$$CR = \frac{CI}{RI}, \tag{4}$$

where  $n$  is the number order criteria, and RI (random consistency index) is the average index of the randomly generated weights and must vary according to each matrix order. The value of RI for each matrix order is described in Table 1, where the pairwise is identified as consistent if CR is less than 0.1. Perfect consistency is obtained when the eigenvalue maximum is the same as the number criteria ( $\lambda_{\max} = n$ ).

## 3 Proposed method

### 3.1 Notations

To simplify the discussion, the next notations are used in the of the rest paper.

Table 1 Random consistency index (RI)

Number criteria	1	2	3	4	5	6	7	8	9	
		0	0	0.58	0.9	1.12	1.24	1.32	1.41	1.45

$A'$	is the matrix modified of matrix $A$ .
$D_i$	denotes the difference index. It can be obtained by sum of division lower triangular element of the original matrix and lower triangular of the modified matrix.
$n$	denotes size matrix $n \times n$ .
$G_A$	represents genotypes (row vectors comprising the lower triangular element) of matrix $A$ .
$g_{rs}$	is the element node of $G_A$ , where $r$ represents the index node, and $s$ is the index of the candidate node.
$g_{r's}$	denotes the element node of $G_A$ which its position after $g_{rs}$ , thus $r' = r + 1$ .
$g_{rs^*}$	represents the origin element in node $r$ .
$\psi$	is factor fraction; the element of each original data should be fractioned into some candidate with an interval factor fraction.
$\Delta(g_{rs} - g_{r's})$	is the distance from $g_{rs}$ to $g_{r's}$ .
$\eta$	is heuristic distance such that $\eta = 1/\Delta$
$\phi g_{rs}$	denotes the division node $g_{rs}$ and the original node $g_{r's}$ .
$P_{ij}^k$	is the probability of $k$ th ant from node $i$ to $j$ .
$N_k(i)$	represents the set of feasible candidates from the $k$ th ant from node $i$ .
$\tau(i, j)$	is the pheromone valued on edge $ij$ .

### 3.2 The objective function

There are two important aspects to determine the objective function in generating the modified PWM from the original. The first aspect is the consistency ratio rate. The perfect consistency is achieved if CR = 0, which happens when the maximum eigenvalue is the same as the number of criteria / size matrix ( $\lambda_{max} = n$ ). Due to a lower CR being more consistent, the first objective is to get minimized CR. However, CR is pursued only less than 0.1. The second aspect is to minimize the distance from the original and modified matrix. Modified matrices are kept closer to their original matrices in order to maintain the original judgment. There are several methods to measure the distance between two matrices such as the Hamming distance between two genotypes, the root mean square error, and the square distance. In this study, the difference index ( $D_i$ ) is used to measure the distance between two matrices. The reason  $D_i$  is preferred in this study is because, as Lin et al. [21] mentioned, using  $D_i$  reflects a more real difference between the same gene values in two genotypes.  $D_i$  is defined the second objective function as described in Eq. (5).

$$D_i = \frac{\Sigma(G_{A'}/G_A + G_A./G_{A'})}{n^2 - 1} - 1, \tag{5}$$

where  $G_{A'}$  and  $G_A$  are row vectors comprising the lower triangular elements of the substitute matrix  $A$  and of the original matrix  $A$ , respectively;  $\Sigma$  is a summation ; and  $.$  means the element-to-element division. A smaller  $D_i$  indicates that the two matrices are more similar, and  $D_i$  will be 0 if two matrices are same. The first objective function is employed when no one agent (ants) can satisfy the threshold of consistent ratio. The second objective as the final goal is employed when there is at least one agent that satisfies the threshold of consistent ratio. Therefore, it is important to emphasize that it is more optimal if  $D_i$  is less even its CR is bigger, but not exceed 0.1.

### 3.3 Encoding element PWM for ant algorithm

In ACO solving TSP, the tour is constructed by visiting one node (city) to other nodes and back again to the first node [9, 10]. Therefore, to firstly implement the ant algorithm to repair inconsistent PWMs, nodes can be set based on values of elements on the PWM matrix. Due to the value element of PWM being reciprocal ( $a_{ij} = 1/a_{ji}$ ), it can only encode the lower triangular elements of the matrix as nodes [39]. Take matrix  $A$  for example, whose order size ( $n = 4$ ) is described on Fig. 2a. The encoding of  $A$  can be assembled by picking row by row sequentially in the elements of the lower triangular matrix  $A$  which is represented as  $G_A$  as shown in Fig. 2b. The number of elements of  $G_A$  can then be determined ( $\frac{n^2-n}{2}$ ). Elements of  $G_A$  can be represented as the sequence of cities traveled in ACO. So in this sample, an ant will travel starting from node  $a_{21}$  and ending at node  $a_{43}$ .

When matrix  $A$  is identified as an inconsistent matrix, the sequence nodes which represents the ant's tour should be categorized as "inconsistent-tour". To obtain consistent matrix or "consistent-tour", the scale value of the each element original matrix should be changed to a new value. The new values are generated by fractioning from the original values into several candidate values.

The fractioned strategy to build the candidate value is adjusted as follows. First, if the original element has a scale

$$A = \begin{pmatrix} 1 & a_{12} & a_{13} & a_{14} \\ a_{21} & 1 & a_{23} & a_{24} \\ a_{31} & a_{32} & 1 & a_{34} \\ a_{41} & a_{42} & a_{43} & 1 \end{pmatrix} \tag{a}$$

$$G_A = a_{21} - a_{31} - a_{32} - a_{41} - a_{42} - a_{43} \tag{b}$$

Fig. 2 a Matrix  $A$  with  $n = 4$ , b Encoding of matrix  $A$

**Table 2** The original element fractioned into candidate elements with  $\psi = 0.2$

Origin element	Candidate element
1	1
2, 3, 4, 5, 6, 7, 8, 9	1.2, 1.4, 1.6, ..., 8.8, 9
$\frac{1}{2}, \frac{1}{3}, \frac{1}{4}, \frac{1}{5}, \frac{1}{6}, \frac{1}{7}, \frac{1}{8}, \frac{1}{9}$	$\frac{1}{1.2}, \frac{1}{1.4}, \frac{1}{1.6}, \dots, \frac{1}{8.8}, \frac{1}{9}$

$$A = \begin{pmatrix} 1.000 & 0.200 & 4.000 & 0.333 \\ 5.000 & 1.000 & 3.000 & 0.200 \\ 0.250 & 0.333 & 1.000 & 0.125 \\ 3.000 & 5.000 & 8.000 & 1.000 \end{pmatrix}$$

(a)

$$G_A = 5 - 0.25 - 0.333 - 3 - 5 - 8$$

(b)

**Fig. 3** a Matrix A with  $n = 4$ , b Encoding of matrix A

value of between 2 and 9, it should be fractioned into candidate value between 1 and 9. Otherwise, if the origin element has a scale value of between  $\frac{1}{9}$  and  $\frac{1}{2}$ , it should be fractioned into candidate values of between  $\frac{1}{9}$  and 1. This strategy guarantees that although fraction data changes the original value, it only changes the judgment weight without changing the judgment tendency. Second, if the original element is 1 (neutral), the data should not be fractioned and is performed to maintain the judgment neutrality. Third, each candidate value is built from the minimal to maximal based on the fraction factor ( $\psi$ ). Different values of  $\psi$  will set different numbers of candidate values. For example, if  $\psi = 0.2$  then the number of candidate values of each element will be 40 ( $=\frac{9-1}{0.2}$ ).

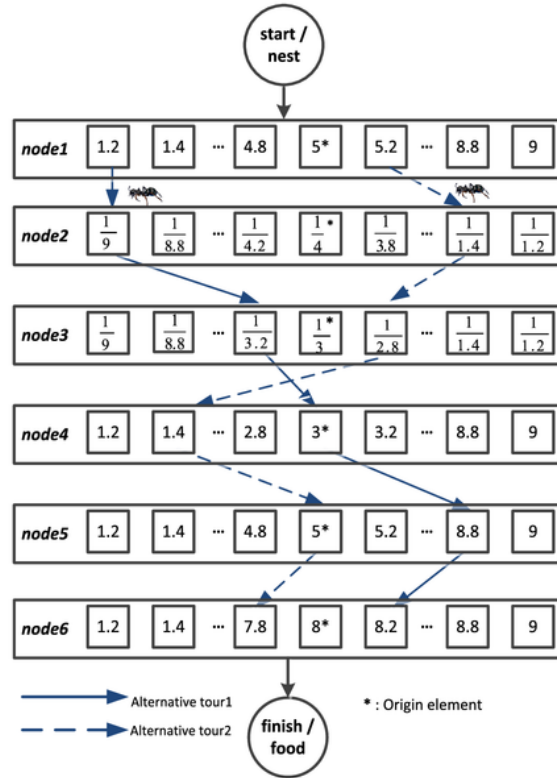
Suppose  $g_r$  is the original value on node  $r$  and  $n$  is the matrix size; thus,  $G_A$  can be described as Eq. (6)

$$G_A = g_1 - g_2 - g_3 - \dots - g_{\frac{n^2-n}{2}} \quad (6)$$

Each element of  $g_r$  is fractioned into several candidate elements  $g_{rs}$ . Value  $s$  indicates the index of candidate element. The candidate element can be produced by follow the role on Eq. (7).

$$g_{rs} = \begin{cases} g_{r,s-1} + \psi, & \text{if } 1 < g_r \leq 9 \\ \frac{1}{g_{r,s-1} + \psi}, & \text{if } \frac{1}{9} \leq g_r < 1 \end{cases} \quad (7)$$

where  $g_{r0} = 1; r = 1, 2, 3, \dots, \frac{n^2-n}{2}; s = 1, 2, 3, \dots, \frac{9-1}{\psi}$ . In this study,  $\psi$  is set at 0.2, the reason for which is described in Sect. 4. Table 2 shows the original element fractioned into some candidate element using  $\psi = 0.2$ . So, each original element (except when its value is 1) will have 40 candidates to substitute.



**Fig. 4** The candidate in each node from matrix on Fig. 3

The result of the fraction data for each element can become the candidate node to travel on the ant algorithm. The ant will move from the candidate in one node to the candidate in the next node to substitute the original value. However, it is possible that the ant may still choose the same candidate node with the original element. To more clearly illustrate, this sample shows how the ant builds the tour by using traveling elements of matrix PWM. Matrix A (size = 4) in Fig. 3 is encoded by picking the value of the lower triangular matrix A as described in Fig. 3b.

Clearly, the ant will travel 6 nodes to complete the tour. Ants start from the “nest” stage to search for food by traveling from nodes by nodes (from node1 to node6) and finish at the “food” stage as illustrated on Fig. 4. At each node, the ant can choose only one candidate node before continuing to the next node.

### 3.4 The heuristic distance

In ACO, there are two important variables to construct the tour: pheromone and distance. Ants prefer moving to cities, which are connected by edges with a high amount of pheromone and short edge (distance). So it is also



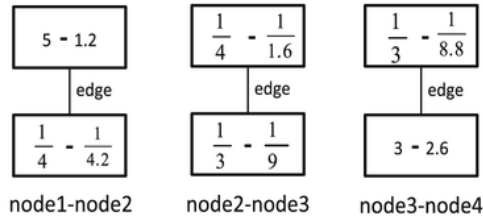
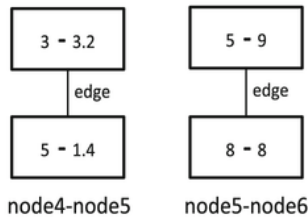


Fig. 5 The some sample edges of Fig. 4



important to define the distance term in this study. In this proposed method, each edge denotes the connection between two parts, which in turn represents two adjacent nodes. Each part consists of two candidate nodes in the same node. Yet, one of the two candidates must be the original node. Figure 5 depicts some sample edges from the illustration in Fig. 4 such as edge  $(5, 1.2 - \frac{1}{4}, \frac{1}{4.2})$  in *node1-node2*, edge  $(\frac{1}{4}, \frac{1}{1.6} - \frac{1}{3}, \frac{1}{9})$  in *node2-node3*, edge  $(\frac{1}{3}, \frac{1}{8.8} - 3, 2.6)$  in *node3-node4*, edge  $(3, 3.2 - 5, 1.4)$  in *node4-node5*, edge  $(5, 9 - 8, 8)$  in *node5-node6* and so forth.

The distance which represents the length of two nodes can be determined as follows. Let the candidate nodes in node  $r$  be  $g_{r1}, g_{r2}, \dots, g_{rs}, \dots, g_{r\frac{q-1}{\psi}}$ , and the candidate nodes in the following step  $r'$  be  $g_{r'1}, g_{r'2}, \dots, g_{r's'}, \dots, g_{r'\frac{q-1}{\psi}}$  where  $g_{rs}$  and  $g_{r's'}$  denote the original values for node  $r$  and  $r'$ , respectively, where  $r' = r + 1$ . Suppose  $s$  is the index candidate for node  $r$  such that  $s = \{1, 2, 3, \dots, \frac{q-1}{\psi}\}$ , while  $s'$  is the index candidate for node  $r'$  such that  $s' = \{1, 2, 3, \dots, \frac{q-1}{\psi}\}$ , so the distance  $g_{rs}$  and  $g_{r's'}$ , defined as  $\Delta(g_{rs} - g_{r's'})$  can be determined via Eqs. (8), (9) and (10):

$$\Delta(g_{rs} - g_{r's'}) = \phi g_{rs} + \phi g_{r's'}, \tag{8}$$

$$\phi g_{rs} = \begin{cases} \frac{g_{rs}}{g_{r's'}}, & \text{if } g_{rs} \geq g_{r's'} \\ \frac{g_{r's'}}{g_{rs}}, & \text{if } g_{rs} < g_{r's'} \end{cases} \tag{9}$$

```

Procedure for choosing the best ant
For each ants
  Perform the tour and get the  $D_i$  and CR
  if (CR < 0.1)
    The best ant ← The smallest  $D_i$ 
  else
    The best ant ← The smallest CR
  end if
End For
End
    
```

Fig. 6 Procedure for choosing the best ant

$$\phi g_{r's'} = \begin{cases} \frac{g_{r's'}}{g_{rs}}, & \text{if } g_{r's'} \geq g_{rs} \\ \frac{g_{rs}}{g_{r's'}}, & \text{if } g_{r's'} < g_{rs} \end{cases} \tag{10}$$

Equations (8), (9) and (10) show that if the candidate node is closer to the original node, the distance will be smaller. It also can be concluded that the smallest distance of the two candidate nodes  $g_{rs}$  and  $g_{r's'}$  is 2. This happens when the candidate nodes are the same as the original nodes either on node  $r$  or node  $r'$ . In this study, it is clear that the smaller distance indicates a smaller deviation of the scale of the DMs opinion. Due to smaller deviations being expected, the heuristic information value ( $\eta$ ) is revealed as inverse of the distance between two nodes.

### 3.5 Constructing the tour

To start constructing the tour in this method, each ant is firstly randomly placed in one of the candidate nodes on the first node (*node1*). Each ant chooses one of the candidate nodes of next nodes with a probability that is a function of the heuristic distance ( $\eta$ ) and the amount of pheromone ( $\tau$ ) on the connecting edge before continuing to the next node. Suppose that candidate nodes  $g_{rs}$  and  $g_{r's'}$  on Sect. 3.4 and are represented by  $i$  and  $j$ , respectively. While the  $k$ th ant is in candidate node  $i$ , the next candidate node  $j$  is selected from the feasible set,  $N_k(i)$ , according to the probability,  $P_{ij}^k$ , as described in Eq. (11):

$$P_{ij}^k = \frac{[\tau(i,j)]^\alpha \cdot [\eta(i,j)]^\beta}{\sum_{j \in N_k(i)} [\tau(i,j)]^\alpha \cdot [\eta(i,j)]^\beta}, \tag{11}$$

After all ants travel all nodes, the performance of the ants will be evaluated to conclude who the best ant is. To choose the best ant, there are two crucial issues to consider. The first issue is whether the ant can obtain a consistency ratio of less than 0.1. The second issue is if the ant can

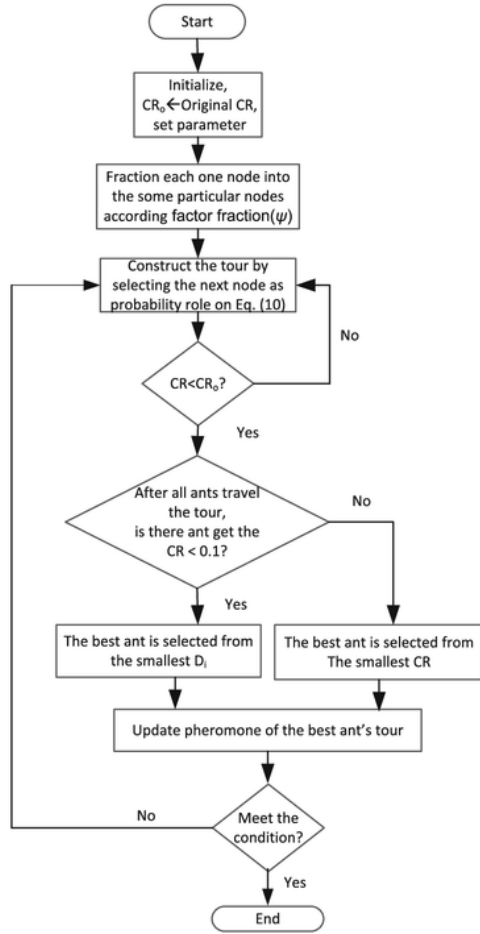


Fig. 7 Flowchart of the ANTAHP

acquire the minimal  $D_i$  between the original and modified PWM. The first issue has a higher priority than the second. Therefore, if there is only one ant that can obtain the consistent-tour, it can be judged as the best ant. If there is more than one ant that achieves a consistent-tour, then the ant which has the smallest  $D_i$  is indicated as the best ant. Nevertheless, if no ant achieved the consistent-tour, the smallest consistency ratio (CR) is chosen as the best ant. The edges of the tour of that the best ant traveled are updated by adding the pheromone. The procedure for choosing the best ant and updating its tour is depicted in Fig. 6.

The pheromone level is updated by applying the updating rule of Eqs. (12) and (13).

$$\tau(i, j) = (1 - \rho)\tau(i, j) + \rho\Delta\tau(i, j), \tag{12}$$

Table 3 Parameter setting of ANTAHP

Parameter	Symbol	Set value
Number ant	$M$	10
Iteration	$nc$	200 or 500 or 1,000
Degree pheromone	$\alpha$	1
Degree heuristic distance	$\beta$	2
Initial pheromone	$\tau_0$	$\frac{2}{n^2-n}$ , $n = \text{size matrix}$
Pheromone decay	$\rho$	0.1
Constant update	$Q$	0.001

Table 4 The dataset inconsistency PWMs

PWM	Value element PWM	CR
	Size $3 \times 3$	
PWM1	9-9-3a	0.116
PWM2	$\frac{1}{5}$ -5-5a	0.254
PWM3	7-7- $\frac{1}{5}$ a	0.255
PWM4	$5-\frac{1}{3}$ - $\frac{1}{5}$ a	0.117
PWM5	7-9- $\frac{1}{3}$ a	0.178
PWM6	9-7- $\frac{1}{7}$ a	0.282
	Size $4 \times 4$	
PWM7	$9-\frac{1}{5}$ - $\frac{1}{5}$ - $5-\frac{1}{2}$ 2b	0.172
PWM8	7-5- $\frac{1}{7}$ -3- $\frac{1}{4}$ -6	0.205
PWM9	$\frac{1}{5}$ -3-5- $\frac{1}{4}$ - $\frac{1}{2}$ -c	0.191
PWM10	5-7-3-5-4-3c	0.125
	Size $5 \times 5$	
PWM11	$3-\frac{1}{2}$ - $\frac{1}{7}$ -6-9-9-2-4-4-5	0.330
PWM12	$\frac{1}{3}$ -2-1-7-8-2- $\frac{1}{2}$ -7- $\frac{1}{2}$	0.307
PWM13	$\frac{1}{7}$ - $\frac{1}{6}$ - $\frac{1}{7}$ -4-3-3- $\frac{1}{2}$ -5-8-5	0.142
	Size $6 \times 6$	
PWM14	$\frac{1}{5}$ -1-5-3-7-1-7-3-7-3-3-5- $\frac{1}{5}$ - $\frac{1}{5}$ 5a	0.546
PWM15	$\frac{1}{5}$ -9-3-1-5- $\frac{1}{5}$ -5-5-5-7-3-3- $\frac{1}{3}$ -3-7a	0.381
	Size $7 \times 7$	
PWM16	7-3-9-1-2- $\frac{1}{5}$ -3- $\frac{1}{4}$ -2-3-4- $\frac{1}{3}$ -3-9- $\frac{1}{2}$ - $\frac{1}{7}$ - $\frac{1}{3}$ - $\frac{1}{4}$ - $\frac{1}{5}$	0.210
PWM17	$\frac{1}{9}$ -3- $\frac{1}{2}$ -9-3-1-9-4-2-1-9-3-1- $\frac{1}{2}$ -2-9- $\frac{1}{7}$ -3-2-3	0.357
	Size $8 \times 8$	
PWM18	$\frac{1}{5}$ -3- $\frac{1}{7}$ - $\frac{1}{5}$ - $\frac{1}{6}$ - $\frac{1}{3}$ -3- $\frac{1}{6}$ - $\frac{1}{3}$ -4-2-3-5- $\frac{1}{6}$ -7-5-5-4-7-5-8-6-6-2d	0.169
PWM19	$\frac{1}{2}$ -2- $\frac{1}{4}$ - $\frac{1}{2}$ -1- $\frac{1}{4}$ -2-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -2-4-1-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -e	0.105
	Size $9 \times 9$	
PWM20	$\frac{1}{2}$ -2- $\frac{1}{4}$ - $\frac{1}{2}$ -1- $\frac{1}{4}$ -2-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -2-4-1-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -3-4-7-6- $\frac{1}{6}$ -3- $\frac{1}{7}$ -2b	0.185

Data on <sup>a,b,c,d,e</sup> are picked from [12, 25, 39, 40] and [18], respectively



**Table 5**  $D_i$  in some PWMs on  $\psi_1 = 0.1, \psi_2 = 0.2, \psi_3 = 0.4$

PWM	Size	$D_i$					
		$\psi_1 = 0.1$		$\psi_2 = 0.2$		$\psi_3 = 0.4$	
		$D_i(\text{best})$	$D_i(\text{avg})$	$D_i(\text{best})$	$D_i(\text{avg})$	$D_i(\text{best})$	$D_i(\text{avg})$
PWM1	3x3	<b>0.0005</b>	<b>0.0011</b>	0.0007	0.0014	0.0010	0.0024
PWM7	4x4	0.0140	0.0174	<b>0.0110</b>	<b>0.0158</b>	0.0150	0.0190
PWM11	5x5	0.0790	0.0882	<b>0.0641</b>	<b>0.0736</b>	0.0732	0.0864
PWM14	6x6	0.1857	0.2019	<b>0.1690</b>	<b>0.1806</b>	0.1770	0.1962
PWM16	7x7	0.0768	0.0935	<b>0.0429</b>	<b>0.0652</b>	0.0650	0.0824
PWM18	8x8	0.0670	0.0961	<b>0.0101</b>	<b>0.0435</b>	0.0630	0.0700
PWM20	9x9	0.0512	0.0719	<b>0.0321</b>	<b>0.0342</b>	0.0617	0.0712

Bold values indicate the best solution

**Fig. 8** **a** Origin matrix PWM11. **b-d** are modified matrices of PWM11 after repairing with  $\psi_1 = 0.1, \psi_2 = 0.2, \psi_3 = 0.4$ , respectively

$$\begin{pmatrix} 1 & 0.333 & 2 & 0.167 & 0.500 \\ 3 & 1 & 7 & 0.111 & 0.250 \\ 0.500 & 0.143 & 1 & 0.111 & 0.250 \\ 6 & 9 & 9 & 1 & 0.200 \\ 2 & 4 & 4 & 5 & 1 \end{pmatrix} \quad \text{(a) CR} = 0.330$$

$$\begin{pmatrix} 1 & 0.385 & 2.000 & 0.175 & 0.263 \\ 2.600 & 1 & 4.400 & 0.167 & 0.244 \\ 0.500 & 0.227 & 1 & 0.120 & 0.122 \\ 5.700 & 6.000 & 8.300 & 1 & 0.312 \\ 3.800 & 4.100 & 8.200 & 3.200 & 1 \end{pmatrix} \quad \text{(b) CR} = 0.098, D_i = 0.0790, \psi = 0.1$$

$$\begin{pmatrix} 1 & 0.500 & 2.000 & 0.227 & 0.357 \\ 2.000 & 1 & 5.000 & 0.167 & 0.278 \\ 0.500 & 0.200 & 1 & 0.116 & 0.167 \\ 4.400 & 6.000 & 8.600 & 1 & 0.385 \\ 2.800 & 3.600 & 6.000 & 2.600 & 1 \end{pmatrix} \quad \text{(c) CR} = 0.099, D_i = 0.0641, \psi = 0.2$$

$$\begin{pmatrix} 1 & 0.333 & 2.200 & 0.161 & 0.263 \\ 3 & 1 & 5.800 & 0.185 & 0.294 \\ 0.453 & 0.172 & 1 & 0.111 & 0.152 \\ 6.200 & 5.400 & 9.000 & 1 & 0.385 \\ 3.800 & 3.400 & 6.600 & 2.600 & 1 \end{pmatrix} \quad \text{(d) CR} = 0.099, D_i = 0.0732, \psi = 0.4$$

$$\Delta\tau(i, j) = \begin{cases} \frac{Q * \tau_0}{CR_{best}} \text{ or } \frac{Q * \tau_0}{D_{i,best}} & \text{if } (i, j) \in \text{best tour} \\ 0 & \text{Otherwise} \end{cases} \quad (13)$$

where  $0 < \rho < 1$  is the pheromone decay parameter, and  $Q$  is constant.

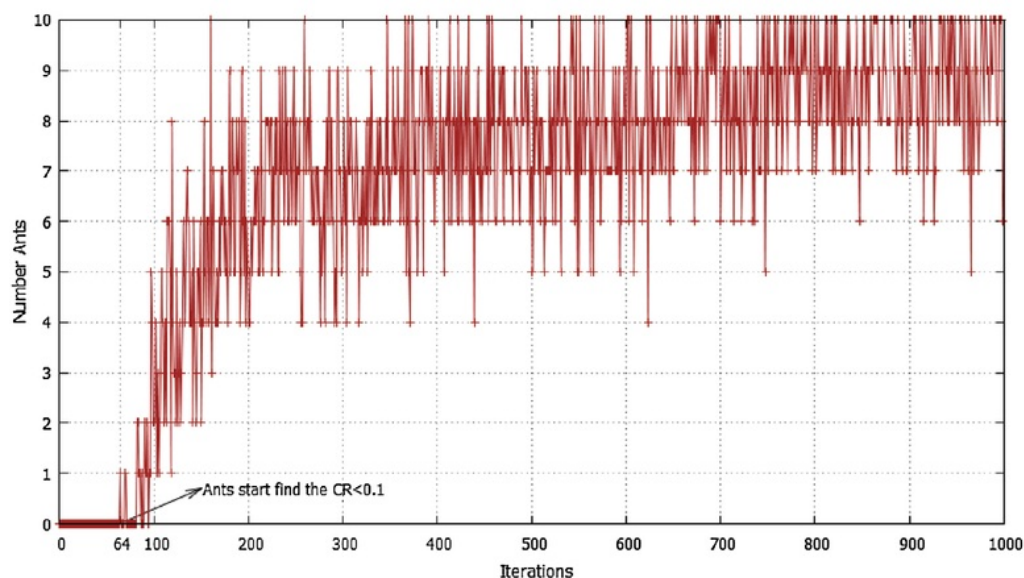
Due to there being two ways to get the best ant, there are also two functions to determine the updating pheromone. Function  $\frac{Q * \tau_0}{CR_{best}}$  is used when no ant can achieve a consistent-tour, while  $\frac{Q * \tau_0}{D_{i,best}}$  is employed when an ant can achieve a consistent-tour. The above procedure is performed iteratively with a set number of iterations or until the condition is met. In the beginning step/iteration, the impact of the heuristic value is more dominant, yet the impact of the value decreases gradually. This is because when adding iterations, the ants continue to lay the pheromone to the path, which is expected to be the good tour. This ensures that the pheromone will provide the effect rather than the heuristic distance value. The procedure of this proposed method, ANTAHP, is shown in the flowchart of Fig. 7.

### 4 Experimental result

In this section, we start with the parameter setting and analysis of parameter  $\psi$ . Then, we evaluate the performance of ANTHAP algorithm by using it to solve some inconsistent pairwise weighting matrices. At last, we evaluate it by comparing some other methods.

#### 4.1 Parameter setting and dataset

This algorithm uses the setting of various parameters as shown in Table 3. There are 20 dataset PWMs (shown in Table 4) with various matrix size. These datasets represent the lower triangular matrix of PWM, similar to Fig. 3b representing Fig. 3a. All of the datasets are inconsistent and need to be repaired. PWM1-PWM6, PWM14, PWM15 are picked from Yang et al. [39]. These PWMs are real data of decision maker opinion to assess the properness of the construction of a high-tech facility for a national research center located in northern Taiwan. PWM9, PWM10 are picked from Saaty [25]. PWM9 is one of matrix comparison to assess the extrinsic factors, which affect a firm's



**Fig. 9** The number of ants which get consistent-tour in each iteration (case:PWM16)

performance. The factors are economic, political, social and technological. PWM10 has to assess estimating the percentage of a company's sales affected by the energy crisis. PWM18 is taken from Xu and Wei [40]. Some of researchers also use this matrix to show the performance of their proposed method [12, 26]. Matrix PWM19 is introduced by Kwiesiele-wicz and Uden [18] in their research. This matrix is also used by Ergu et al. [12] to test their proposed method. PWM7 and PWM20 are picked from Ergu et al. [12]. We also add six inconsistent PWMs to show the performance of our proposed method. They are PWM8, PWM11-PWM13, PWM16, and PWM17.

In order to be efficient, all datasets are conducted five times with various iterations: small size matrix ( $3 \times 3$  and  $4 \times 4$ ), middle size matrix ( $5 \times 5$  and  $6 \times 6$ ), large size matrix ( $7 \times 7$ ,  $8 \times 8$  and  $9 \times 9$ ) consisted of 200, 500 and 1,000 iterations, respectively.

#### 4.2 Determining setting value of $\psi$

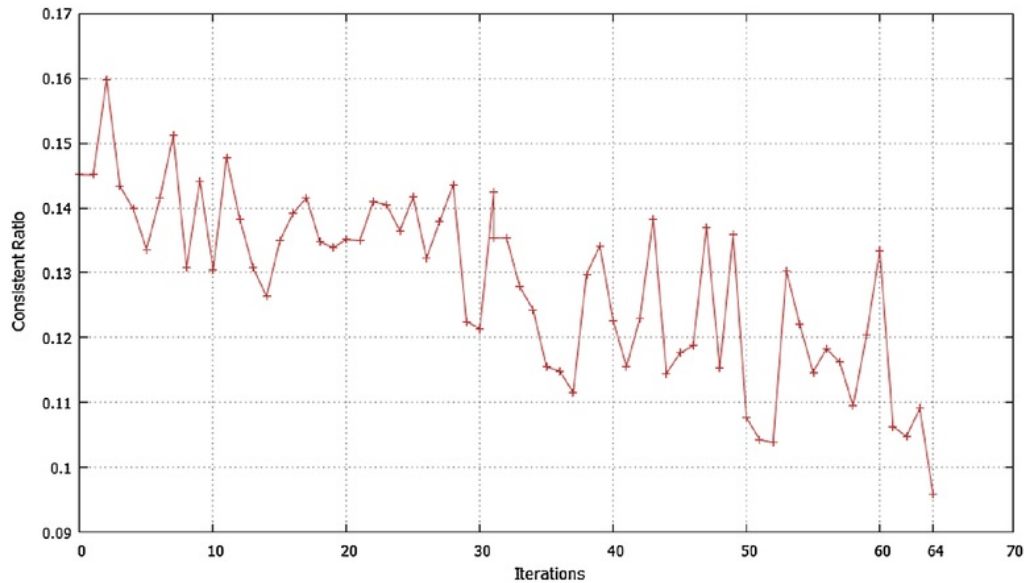
To obtain the optimal factor fraction setting ( $\psi$ ), the experiments were conducted with three various  $\psi$  ( $\psi_1 = 0.1, \psi_2 = 0.2, \psi_3 = 0.4$ ) for some datasets on various size. The different  $\psi$  will assign the different numbers of candidate data. Due to the scale of the original data from 1 to 9 or  $\frac{1}{9}$  to 1, there are therefore: 80, 40, 20 candidate data for  $\psi_1 = 0.1, \psi_2 = 0.2$ , and  $\psi_3 = 0.4$ , respectively. Table 5 shows the  $D_i$  for various PWMs of the three various  $\psi$ . From Table 5,  $D_i$  on PWM1 is minimal when  $\psi = 0.1$ . However, most PWMs (PWM7, PWM11,

PWM14, PWM16, PWM18 and PWM20) are minimal when  $\psi = 0.2$ . One of the samples from Table 5 is PWM11, which is depicted in Fig. 8. After repairing, PWM11 has  $CR = 0.330$  (Fig. 8a) and succeed as the consistent matrix with  $D_i = 0.0790$  (Fig. 8b), 0.0641 (Fig. 8c), 0.0732 (Fig. 8d) using  $\psi_1 = 0.1, \psi_2 = 0.2, \psi_3 = 0.4$ , respectively. These results yield one conclusion: when the factor fraction is set relatively too small ( $\psi = 0.1$ ), the candidate will increase. As a consequence, all candidates will have almost the same value. This makes it easy for the ant become trapped in particular range and less to explore the different value to obtain the best solution. This will yield many alternatives  $D_i$ s, which are not significantly different. Contrarily, when  $\psi$  is set relatively too large ( $\psi = 0.4$ ), the number candidates is few. As a result, the tours produced have different significant  $D_i$ s. This makes it more difficult to converge to the optimal  $D_i$ .

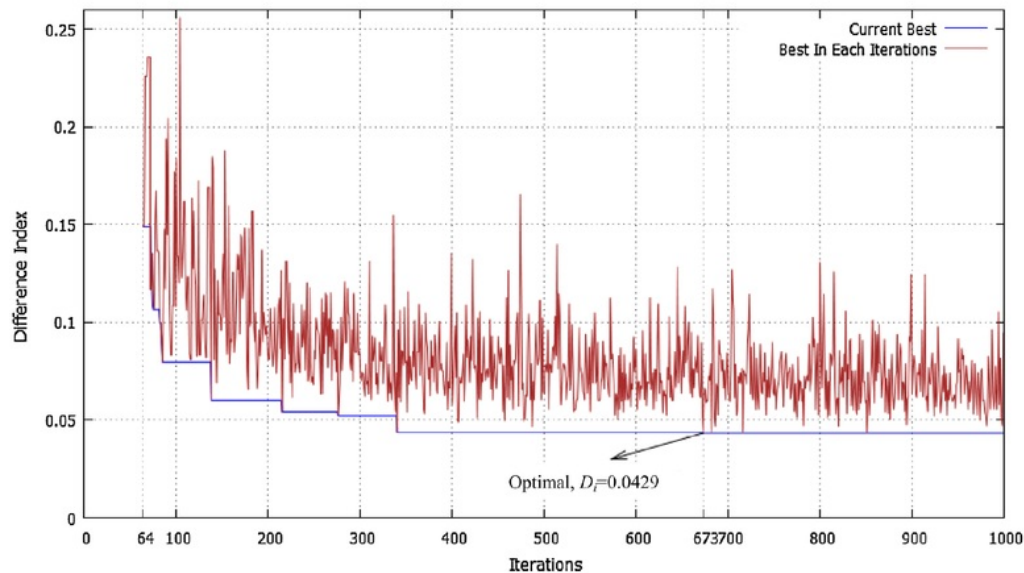
#### 4.3 Performance analysis of the ANTAHP

As aforementioned, the indicator of a good tour is getting both the smallest  $D_i$  and satisfying the consistency ratio. In fact, on beginning iterations, especially for the big size matrix, it is difficult for the ants to get the consistency matrix. The ant which fails to satisfy the consistent ratio cannot be used as the alternative modified matrix, even its  $D_i$  is low.

Consequently, the first focus in this algorithm is how an ant tends to choose its consistent-tour. This can be solved by updating the pheromone, which obtains the smallest consistent ratio. This update makes the edges which



**Fig. 10** The convergency history to get the consistent-tour (case:PWM16)



**Fig. 11** The convergency history to get the consistent-tour (case:PWM16)

generates the closest consistent matrix preferable in the next iterations. As a consequence, in next iteration, it is easier for the ant to get the consistent matrix. Figure 9 shows this phenomenon. This figure shows that no ant achieves the threshold of the consistent ratio below 0.1 on the 63rd of beginning iterations. Yet, with more iterations, the number of ants that can achieve a consistent matrix increases gradually. After 64th iteration, the ant starts to

find the tour which satisfies the threshold consistent ratio. Although in next iteration, there may sometimes still be the threshold not achieved, the number of ants gradually achieving a consistent-tour increases.

This indicates that the more the iterations, the more significant the contribution of the pheromone amount. Figure 10 shows the convergence of the ant's tour to obtain a consistent-tour. Due to the 64th iteration being the ants



**Table 6** The dataset PWMs after repaired by ANTAHP with  $\psi = 0.2$

PWM	Value element PWM	CR	$D_i$
Size 3 × 3			
PWM1	9-9-2.8	0.094	0.0007
PWM2	$\frac{1}{4}$ -6.4-4.4	0.099	0.0210
PWM3	8.4-5.8- $\frac{1}{4}$	0.099	0.0210
PWM4	4.8- $\frac{1}{3}$ - $\frac{1}{5.4}$	0.093	0.0011
PWM5	7.6-8- $\frac{1}{2.6}$	0.098	0.0067
PWM6	9-5.4- $\frac{1}{4.6}$	0.099	0.0410
Size 4 × 4			
PWM7	7.6- $\frac{1}{2.6}$ - $\frac{1}{5.8}$ -4- $\frac{1}{2}$ -2.2	0.096	0.0110
PWM8	8.8-3.8- $\frac{1}{6.2}$ -3.4- $\frac{1}{3.4}$ -4.2	0.099	0.0028
PWM9	$\frac{1}{4.2}$ -2.6-4.8- $\frac{1}{4}$ - $\frac{1}{1.4}$ - $\frac{1}{2.4}$	0.096	0.0180
PWM10	5-7-2.8-5.6-4-2.8	0.098	0.0018
Size 5 × 5			
PWM11	2- $\frac{1}{2.5}$ -4.4-6-8.6-2.8-3.6-6-2.6	0.099	0.0641
PWM12	$\frac{1}{3}$ - $\frac{1}{7.2}$ -1.2-1-5.6-7.4-1.2- $\frac{1}{1.2}$ -5.0- $\frac{1}{2}$	0.099	0.0510
PWM13	$\frac{1}{7}$ - $\frac{1}{5.2}$ - $\frac{1}{5.2}$ -2-3- $\frac{1}{2}$ -5-8-5	0.099	0.0140
Size 6 × 6			
PWM14	$\frac{1}{3.4}$ -1.4-4.2-2.6-7.4-1.4-7-6.8-3.8-1.6-2.8-6.2- $\frac{1}{1.6}$ - $\frac{1}{2.4}$ -1.8	0.094	0.1720
PWM15	$\frac{1}{5}$ - $\frac{1}{3.4}$ -3-1-3.6- $\frac{1}{2}$ -2.8-6.4-3.4-4-2.2-4.6- $\frac{1}{1.2}$ -3-1.6	0.098	0.1490
Size 7 × 7			
PWM16	3.8-4.4-8.8-1-1.6- $\frac{1}{5}$ - $\frac{1}{1.2}$ -2.2- $\frac{1}{3.2}$ -2.4-3.6-3.2- $\frac{1}{1.6}$ -2.4-7.4- $\frac{1}{4}$ - $\frac{1}{2.4}$ - $\frac{1}{8.4}$ - $\frac{1}{2.6}$ - $\frac{1}{4.4}$ - $\frac{1}{5.8}$	0.099	0.0429
PWM17	$\frac{1}{9}$ - $\frac{1}{5.2}$ -3.2- $\frac{1}{1.8}$ -9-2.4-1-9-3.8-1.6-1-9-3-1- $\frac{1}{1.6}$ -1.4-8.6- $\frac{1}{1.8}$ -2.8-1.2-2.4	0.099	0.0657
Size 8 × 8			
PWM18	$\frac{1}{4.2}$ -2.4-3- $\frac{1}{7.4}$ - $\frac{1}{4.4}$ - $\frac{1}{6.8}$ - $\frac{1}{5.8}$ - $\frac{1}{2.6}$ - $\frac{1}{3.4}$ -2.8- $\frac{1}{5.4}$ - $\frac{1}{2.4}$ - $\frac{1}{4.2}$ -3.4-1.8-2.4-4- $\frac{1}{4.4}$ -7-5-3-4-6-8-4.2-9-6-8-6-8-2	0.099	0.0101
PWM19	$\frac{1}{2}$ -2- $\frac{1}{2.8}$ - $\frac{1}{2}$ -1- $\frac{1}{4}$ -2-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -2-4-1-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$	0.099	4.6x10 <sup>-5</sup>
Size 9 × 9			
PWM20	$\frac{1}{2}$ -2- $\frac{1}{1.2}$ - $\frac{1}{2}$ -1- $\frac{1}{4}$ -2-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -2-4-1-4-1-4- $\frac{1}{2}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -1- $\frac{1}{4}$ -3-4-3.2-5- $\frac{1}{6}$ -3- $\frac{1}{7}$ -2	0.098	0.0321

obtaining a consistent-tour, this graph only shows iterations 1 to 64. After the ants achieve the consistent ratio threshold, the next focus is to get the minimal  $D_i$ . This is done by updating the pheromone on the edges of a tour ant which gets the least  $D_i$ . Figure 11 depicts the optimal  $D_i$  achieved from the 64th iteration until the 1000th iteration. The  $D_i$  of iteration 1 to 63 is ignored to determine the optimal  $D_i$  for

there is no ant that can achieve a consistent-tour. Figure 11 shows a large number of iterations, where  $D_i$  is minimal. Although the  $D_i$  fluctuates, in each iteration  $D_i$  each iteration gradually decreases (toward minimal). The best tour is achieved in the 673th iteration with  $D_i = 0.0429$ .

Table 6 presents the performance of ANTAHP repairing an inconsistent PWM matrix. This is found by implementing ANTAHP by choosing the best of the five experiments with 200, 500 or 1,000 iterations. ANTAHP succeeds in modifying the PWM matrix to be consistent and closer to the original matrix.

#### 4.4 Comparison with the other methods

We also compare our results with other methods. Yang et al. [39] combined PSO and the Taguchi methods and provided an example inconsistent matrix PWM as described in Fig. 12a with CR = 0.14. Differing from Yang et al., ANTAHP does not search for the lowest CR, but rather only satisfies the standard threshold of the consistency ratio. ANTAHP pursues the original opinion of the DM by searching for the closest matrix to the original PWM as long as the matrix is consistent.

Figure 12 demonstrates the comparison of the PSO + Taguchi method, which is proposed by Yang et al. and ANTAHP in an inconsistent matrix. Yang et al. repaired the PWM such that its CR = 0.0131, and  $D_i = 0.0691$  as shown in Fig. 12b. ANTAHP can also perform a repair such that CR = 0.099 and  $D_i = 0.0047$ . Tables 7 and 8 show another sample for evaluating the performance ANTAHP by comparing PSO + Taguchi method. The eight matrices (PWM1, PWM2, PWM3, PWM4, PWM5, PWM6, PWM14 and PWM15) were also selected from [39]. Each matrix is executed 30 times. The results demonstrate the performance of ANTAHP is emphasized to get the closer matrix than Yang et al. [39] proposed. It can be seen the ANTAHP of  $D_i$  is smaller than [39]. However, by chasing closer to the original matrix, it makes the consistency ratio be higher. Yet, it still can be categorized as consistent matrix. All standard deviation (SD) of the results are too small comparing Mean (less than 5%). The small deviation indicates that all of the data tend to be very close to the expected value. This study also conducted the Wilcoxon signed-rank test. This test is a nonparametric hypothesis test statistic to compare two related samples or repeated measurements on a single sample to assess whether their population mean ranks differ. It can be used as an alternative to the  $t$  test for dependent samples when the population have no normal distribution. The bound significant ( $\alpha$ ) is used less than 0.01. The *Asymp. Sig.* represents asymptotic significance.

**Table 7** Comparison  $D_i$  with PSO + Taguchi [39] and ANTAHP

	$D_i$ (PSO + T)				$D_i$ (ANTAHP)				$D_i$ (PSO + T) - $D_i$ (ANTAHP) Asymp. Sig. (2-tailed)
	Min	Max	Mean	SD	Min	Max	Mean	SD	
PWM1	0.0328	0.0366	0.0338	0.0014	0.0007	0.0022	0.0013	0.0018	0.000
PWM2	0.0640	0.0693	0.0663	0.0028	0.0210	0.0312	0.0265	0.0036	0.000
PWM3	0.0606	0.0672	0.0631	0.0031	0.0200	0.0321	0.0243	0.0023	0.000
PWM4	0.0299	0.0353	0.0322	0.0017	0.0011	0.0021	0.0017	0.0021	0.000
PWM5	0.0434	0.0489	0.0457	0.0021	0.0067	0.0094	0.0084	0.0032	0.000
PWM6	0.0776	0.0816	0.0791	0.0032	0.043	0.0721	0.0541	0.0016	0.000
PWM14	0.3577	0.4164	0.3786	0.0162	0.1720	0.2598	0.2092	0.0085	0.000
PWM15	0.4576	0.5325	0.4983	0.0213	0.1490	0.2079	0.1799	0.0133	0.000
Average	0.1404	0.1610	0.1496	0.0065	0.0517	0.0771	0.0632	0.0046	0.0000

**Table 8** Comparison CR with PSO + Taguchi [39] and ANTAHP

	CR (PSO + T)				CR (ANTAHP)				CR (PSO + T) - CR (ANTAHP) Asymp. Sig. (2-tailed)
	Min	Max	Mean	SD	Min	Max	Mean	SD	
PWM1	0.022	0.033	0.0267	0.0025	0.094	0.099	0.0963	0.0007	0.0000
PWM2	0.028	0.039	0.0351	0.0037	0.099	0.099	0.099	0.0000	0.0000
PWM3	0.033	0.042	0.0373	0.0033	0.099	0.099	0.099	0.0000	0.0000
PWM4	0.013	0.025	0.0182	0.0041	0.093	0.099	0.0952	0.0011	0.0000
PWM5	0.022	0.049	0.0313	0.0102	0.098	0.099	0.0987	0.0004	0.0000
PWM6	0.052	0.067	0.0578	0.0047	0.099	0.099	0.099	0.0000	0.0000
PWM14	0.019	0.029	0.0246	0.0029	0.094	0.099	0.0972	0.0008	0.0000
PWM15	0.023	0.035	0.0270	0.0044	0.098	0.099	0.0987	0.0005	0.0000
Average	0.0265	0.0399	0.0323	0.0045	0.097	0.099	0.0978	0.0004	0.0000

$$\begin{pmatrix} 1.000 & 0.200 & 0.143 & 3.000 \\ 5.000 & 1.000 & 0.200 & 7.000 \\ 7.000 & 5.000 & 1.000 & 7.000 \\ 0.333 & 0.143 & 0.143 & 1.000 \end{pmatrix}$$

(a) CR = 0.14  
W=(0.073, 0.254, 0.634, 0.038)<sup>T</sup>

$$\begin{pmatrix} 1.000 & \frac{1}{4.6} & \frac{1}{6.8} & 2.600 \\ 4.600 & 1.000 & \frac{1}{4.6} & 7.200 \\ 6.800 & 4.600 & 1.000 & 8.000 \\ \frac{1}{2.6} & \frac{1}{7.2} & \frac{1}{8} & 1.000 \end{pmatrix}$$

(c) CR = 0.099,  $D_i = 0.0047$   
W=(0.074, 0.253, 0.633, 0.039)<sup>T</sup>

$$\begin{pmatrix} 1.000 & 0.294 & 0.149 & 1.965 \\ 3.403 & 1.000 & 0.365 & 5.498 \\ 6.716 & 2.741 & 1.000 & 9.000 \\ 0.509 & 0.182 & 0.111 & 1.000 \end{pmatrix}$$

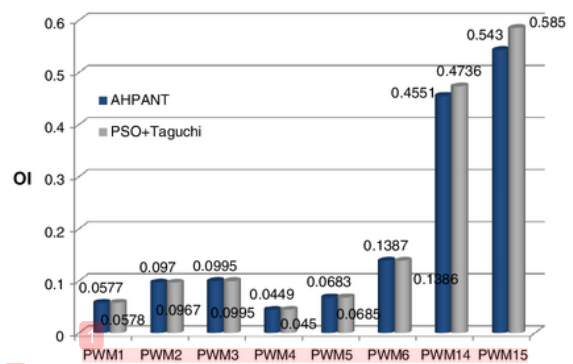
(b) CR = 0.0131,  $D_i = 0.0691$   
W=(0.088, 0.267, 0.593, 0.052)<sup>T</sup>

$$\begin{pmatrix} 1.000 & \frac{1}{3.4} & \frac{1}{6.8} & 2.000 \\ 3.400 & 1.000 & \frac{1}{2.8} & 5.4 \\ 6.800 & 2.800 & 1.000 & 9 \\ \frac{1}{2} & \frac{1}{5.4} & \frac{1}{9} & 1.000 \end{pmatrix}$$

(d) CR = 0.014,  $D_i = 0.0664$   
W=(0.088, 0.267, 0.593, 0.052)<sup>T</sup>

**Fig. 12** a Original matrix, b PSO + Taguchi, c ANTAHP, d ANTAHP with  $OI$  as objective function

If *Asymp. Sig.* <  $\alpha$ , it indicated that these two related samples are different significantly. In this study, value of *Asymp. Sig.* which defines the different data by PSO + Taguchi [39] and ANTAHP is 0.0000 (less than 0.01). It shows that the results by processing of the



**Fig. 13** Comparison with PSO + Taguchi [39] and ANTAHP with objective function  $OI$

ANTAHP and PSO + Taguchi [39] methods are different significantly.

However, to see the fair comparison of PSO + Taguchi and ANTAHP, the objective function of ANTAHP is adjusted to follow the PSO + Taguchi method. As

$$\begin{pmatrix} 1 & 5 & 3 & 7 & 6 & 6 & \frac{1}{4} & \frac{1}{4} \\ \frac{1}{5} & 1 & \frac{1}{3} & 5 & 3 & 3 & \frac{1}{5} & \frac{1}{5} \\ \frac{1}{3} & \frac{1}{5} & 1 & 6 & 3 & 4 & \frac{1}{6} & \frac{1}{6} \\ \frac{1}{7} & \frac{1}{3} & \frac{1}{6} & 1 & \frac{1}{3} & \frac{1}{4} & \frac{1}{7} & \frac{1}{7} \\ \frac{1}{6} & \frac{1}{3} & \frac{1}{4} & \frac{1}{3} & 1 & \frac{1}{2} & \frac{1}{6} & \frac{1}{6} \\ \frac{1}{6} & \frac{1}{3} & \frac{1}{4} & \frac{1}{2} & \frac{1}{2} & 1 & \frac{1}{6} & \frac{1}{6} \\ \frac{1}{4} & \frac{1}{5} & \frac{1}{6} & \frac{1}{7} & \frac{1}{6} & \frac{1}{6} & 1 & \frac{1}{4} \\ \frac{1}{4} & \frac{1}{5} & \frac{1}{6} & \frac{1}{7} & \frac{1}{6} & \frac{1}{6} & \frac{1}{4} & 1 \end{pmatrix}$$

(a) CR=0.169

$$W=(0.173, 0.054, 0.188, 0.018, 0.031, 0.036, 0.167, 0.333)^T$$

$$\begin{pmatrix} 1 & 4.524 & 2.339 & 7.523 & 5.888 & 5.686 & 0.425 & 0.292 \\ 0.221 & 1 & 0.326 & 4.516 & 2.671 & 2.580 & 0.222 & 0.147 \\ 0.427 & 3.067 & 1 & 6.749 & 3.460 & 4.188 & 4.155 & 0.249 \\ 0.1333 & 0.221 & 0.148 & 1 & 0.373 & 0.287 & 0.134 & 0.104 \\ 0.170 & 0.374 & 0.289 & 2.681 & 1 & 0.561 & 0.197 & 0.147 \\ 0.176 & 0.388 & 0.234 & 3.479 & 1.784 & 1 & 0.204 & 0.153 \\ 2.354 & 4.497 & 0.241 & 7.479 & 5.073 & 4.899 & 1 & 0.501 \\ 3.419 & 6.786 & 4.024 & 9.624 & 6.783 & 6.551 & 1.996 & 1 \end{pmatrix}$$

(b) CR=0.097,  $D_i=0.01022$ ,  $\delta=1.845$ ,  $\sigma=0.434$

$$W=(0.173, 0.056, 0.179, 0.018, 0.032, 0.038, 0.170, 0.335)^T$$

$$\begin{pmatrix} 1 & 4.4412 & 2.3682 & 7.6743 & 5.8559 & 5.6079 & 0.4201 & 0.2968 \\ 0.2252 & 1 & 0.3210 & 4.4224 & 2.6175 & 3.5392 & 0.2268 & 0.1486 \\ 0.4223 & 3.1151 & 1 & 6.9149 & 3.5351 & 4.2774 & 4.5105 & 0.2487 \\ 0.1303 & 0.2261 & 0.1446 & 1 & 0.3805 & 0.2927 & 0.1313 & 0.1030 \\ 0.1708 & 0.3820 & 0.2829 & 2.6278 & 1 & 0.5722 & 0.1960 & 0.1444 \\ 0.1783 & 0.3938 & 0.2338 & 3.4166 & 1.7478 & 1 & 0.2055 & 0.1494 \\ 2.3804 & 4.4099 & 0.2217 & 7.6136 & 5.1012 & 4.8661 & 1 & 0.5004 \\ 3.3689 & 6.7293 & 4.0215 & 9.7130 & 6.9235 & 6.6949 & 1.9984 & 1 \end{pmatrix}$$

(c) CR=0.098,  $D_i=0.01030$ ,  $\delta=1.713$ ,  $\sigma=0.448$

$$W=(0.173, 0.055, 0.185, 0.018, 0.032, 0.037, 0.168, 0.334)^T$$

$$\begin{pmatrix} 1 & 4.2 & 2.4 & 7.4 & 5.8 & 5.4 & \frac{1}{2.4} & \frac{1}{3.4} \\ \frac{1}{4.2} & 1 & \frac{1}{3} & 4.4 & 2.6 & 2.4 & \frac{1}{4} & \frac{1}{6.8} \\ \frac{1}{2.4} & \frac{1}{3} & 1 & 6.8 & 3.4 & 4.2 & 4.4 & \frac{1}{4.2} \\ \frac{1}{7.4} & \frac{1}{4.4} & \frac{1}{6.8} & 1 & \frac{1}{2.8} & \frac{1}{3.4} & \frac{1}{7} & \frac{1}{9} \\ \frac{1}{5.8} & \frac{1}{2.6} & \frac{1}{3.4} & \frac{1}{2.8} & 1 & \frac{1}{1.8} & \frac{1}{5} & \frac{1}{6.8} \\ \frac{1}{5.4} & \frac{1}{2.4} & \frac{1}{4.2} & \frac{1}{3.4} & \frac{1}{1.8} & 1 & \frac{1}{5} & \frac{1}{6.8} \\ 2.4 & 4 & \frac{1}{4.4} & 7 & 5 & 5 & 1 & \frac{1}{2} \\ 3.4 & 6.8 & 4.2 & 9 & 6.8 & 6.8 & 2 & 1 \end{pmatrix}$$

(d) CR=0.099,  $D_i=0.01013$ ,  $\delta=1.6$ ,  $\sigma=0.415$

$$W=(0.171, 0.056, 0.179, 0.019, 0.033, 0.038, 0.167, 0.338)^T$$

Fig. 14 a The inconsistent matrix (case: PWM18), b modified by Xu and Wei, c modified by Cao, d modified by ANTAHP

described on [39], the objective function is described as follows.

$$OI = D_i + (\lambda_{\max} - n), \tag{14}$$

where  $OI$  = overall index.

The modified matrix by PSO + Taguchi in Fig. 12c is found with  $D_i = 0.0691$ ,  $\lambda_{\max} - n = 0.0353$  and  $OI = 0.1044$ . ANTAHP generates the nonsimilar matrix with  $D_i = 0.0664$ ,  $\lambda_{\max} - n = 0.038$  and  $OI = 0.1044$ . Figure 13 shows the performance of ANTAHP with objective function as described on Eq. (14) and comparison with PSO + Taguchi. In small size matrix, the ANTAHP

and PSO + Taguchi are very competitive. Yet, in bigger-size matrix (PWM14 and PWM15), the ANTAHP can generate the smaller  $OI$ .

Another comparison involves the methods proposed by Xu and Wei [40] and Cao et al. [3]. Xu and Wei proposed two criteria to measure the closeness between the original matrix  $A$  and the modified matrix  $A'$  as described on Eqs. (15) and (16).

$$\delta = \max_{i,j} \{ | a'_{ij} - a_{ij} | \}, \tag{15}$$

$$\sigma = \sqrt{\frac{\sum_{i=1}^n \sum_{j=1}^n (a'_{ij} - a_{ij})^2}{n}}, \tag{16}$$

where  $A = [a_{ij}]$ ;  $A' = [a'_{ij}]$ ;  $i, j = 1, 2, \dots, n$ ;  $n$  = size matrix. Both of smaller  $\delta$  and  $\sigma$  indicate the two matrices are closer. When two matrices are exactly same,  $\delta$  and  $\sigma$  will be 0. Xu and Wei proposed that the maximum difference of the original and modified ( $\delta$ ) element matrix is 2 and  $\sigma$  is not more than 1. To make a fair comparison, ANTAHP is also adjusted such that the maximum  $\delta$  is 2. So the ant can choose the next node if the distance between their nodes is lower than 2.

To see the performance, we used the sample inconsistent matrix shown in Xu and Wei which was named PWM18 in this article. As shown in Fig. 14, all of the methods are very competitive, which can retain the weight of the original criteria very close to the original. The order of weight criteria was  $W_8 > W_3 > W_1 > W_7 > W_2 > W_6 > W_5 > W_4$ . This also shows that ANTAHP outperforms both methods in  $D_i$ . Two indicators ( $D_i, \sigma$ ) of modified matrix show ANTAHP achieve the smallest value as compared to both methods. Further, unlike the method employed by Xu and Wei, and Cao, ANTAHP preserves the origin range scale (maximum scale 9). To modify PWM18,  $a_{84}$  was changed to be 9.7130, 9.624, and 9 by Cao, Xu, and AHAPANT, respectively.

#### 4.5 Application of the proposed method

This proposed method can be applied on some applications in real-world problem to solve the inconsistency of judgment in AHP. In Sect. 4.1, this proposed method uses some matrices to repair in real-world problem such as decision for construction in Taiwan [39], factors affecting the performance firm, and impact energy crisis for a company sales [25]. The proposed method can be a smart tool to help taking decision in all problems when DMS construct the inconsistent judgment.

Besides the good performance as described on Sect. 4.4, another advantage of ANTAHP is that it can also generate more than one consistent matrix as an alternative to repair inconsistent matrix. Although this method demonstrates its good performance, the modified version of matrix generated exposes that the weight of each criteria is not changed



1 significantly. In fact, the set weight criteria are derived from the inconsistent judgment of decision makers, which cannot be used to take a decision. In some cases, sometimes, the original of opinion still needs to be retained. Therefore, the re-assessment to obtain new original judgment which satisfies consistency is still needed. The proposed method is hard to implement in that case. Moreover, in certain important cases, although the consistency of the comparison matrix is already generated, it still needs a committee to make the final decision [39].

## 5 Conclusion

This paper proposed a method, ANTAHP, using an ant algorithm to modify the inconsistent PWM to become consistent matrices by considering the minimal distance between the original matrix and its modified version. This method was inspired by ACO, which was successful in solving some optimization problems. Tour inconsistency represents elements of original matrix, which needs repair. With pheromone information on the edges, which is updated in each iteration, ants can find the optimal tour. In the beginning, the ants are instructed to find the consistent matrix, and lastly, each ant competes to find the shortest difference index, which preserves the original DM or experts opinions. The result of modifying twenty PWMs shows that the ANTAHP method is effective to repair the inconsistent matrices. These results also demonstrate that the proposed method can be relatively closer to the original matrix comparison than other methods. In the future, our focus will be to find which optimization problem in analytic heuristic process (AHP) can be solved effectively by ACO.

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