ESTIMATION OF MISSING ELEMENTS IN PAIRWISE COMPARISON MATRIX USING GENETIC ALGORITHM

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Abstract This paper concerns the incomplete pairwise comparison matrix produced from judgments of experts in the Analytic Hierarchy Process (AHP). In such situation, we have to estimate the missing elements with suitable values by ensuring the consistency of the pairwise matrix. Metaheuristics are powerful tool to solve optimization problems. Then, improved genetic algorithm (GA) is proposed to recover the missing judgments until a satisfactory level of consistency is reached. Experiment results are performed with incomplete pairwise matrices with different sizes showing the effectiveness of our algorithm.

1 Introduction

Analytic Hierarchy Process (AHP) is a very effective decision-analysis tool which was developed by T.L. Saaty in 970s [7]. This technique is used to numerous applications including forecasting, investment decisions and socio-economic planning issues [6].

In the AHP method, individual or group decision-making have to made all of the necessary pairwise comparisons, which require a significant amount of work, especially in realistic problem where the number of alternatives and criteria is often quite higher. Thus, due to time pressure arising from the need to complete all pairwise comparisons which must be made in the AHP method, in particular in group decision making, one suggests to allow the group to focus on the debate and not completely filling the pairwise comparison matrix. Thus, we are dealing with an incomplete pairwise comparison matrix [3].

The pairwise comparison matrix are made on ratio scale where the scale have a bounded value between 1 and 9 corresponding to a verbal description of the intensity of preference. However, the obtained matrix must be consistent which is not always the case. An index "consistency ratio" (CR) has been suggested by L.T. Saaty as a measure of the inconsistency of the judgments which have to be less than 0.1 to consider the matrix as acceptable.

Metaheuristic approaches are methods inspired by natural phenomena; among them, we find genetic algorithms (GAs) developed by Jean Holland [9]. GAs are inspired from the natural biological mechanisms of the theory of evolution, proposed by Charles Darwin [10] which have shown their effectiveness for various applications [11, 13]. It is an iterative process where a population of individuals constituting possible solutions will undergo different suitable genetic operators such as selection, crossing and mutation, allowing the creation of new population containing an approximate solution that will continue to improve from one iteration to another.

Several works have studied pairwise matrices and have proposed different methods whose objective is to complete the judgments and estimate the missing elements of the incomplete matrices [15, 16, 17, 18]. The purpose of this paper is to estimate the elements of a given incompete pairwise matrix as first step, and ensure that the obtained matrix is consistent. To this end, we propose an improved genetic algorithm, as a well khnown metaheuristic method, allowing the completion of the judgments by suitable values for the missing entries and improving the consistency of the matrix until a satisfactory level is reached.

The remaining parts of this paper are organized as follows. In the second section, we briefly describes the Analytic Hierarchy Process and the problem of incomplete pairwise comparison matrix. In section 3, we present a genetic approach to estimate the missing elements in incomplete pairwise matrix. In section 4, numerical results are performed with different size of

matrices showing the effectiveness and accuracy of the proposed method to recover the missing judgments by ensuring the consistency f the matrix.

2 Incomplete pairwise matrix in the AHP method

2.1 Overview of the AHP method

Analytical Hierarchy Process, which is a Multi-Criteria Decision Making (MCDM) method developed by T.L. Saaty [7], is designed to assist individuals and organizations in making complex decisions by breaking them down into a hierarchical structure and systematically evaluating and comparing the various criteria and alternatives involved. It is widely used in fields such as business, engineering, project management, and environmental planning [6].

AHP method is based on three principles: decomposition, comparative judgments and priority synthesis. It provides a structured approach to decision-making. It allows for a comprehensive evaluation of multiple criteria and alternatives, taking into account both qualitative and quantitative factors. However, it becomes complex, especially when dealing with a large number of criteria and alternatives, making it time-consuming and resource-intensive [8]. Also, The methodology heavily relies on the subjective judgments of decision-makers, which can introduce bias and result in less objective decisions. In summary, AHP method is a valuable decision-making tool known for its systematic approach and ability to handle complex decisions. However, its effectiveness depends on the quality of data and the expertise of decision-makers, and it may not be suitable for all scenarios, particularly those with extremely large datasets or where complete objectivity is essential.

In fact, the application of the AHP method begins with the definition of the problem and the identification of the objective, the determination of the selection criteria and sub-criteria, and the selection alternatives [5]. This first decomposition step can be represented by the family tree, which represents the problem in a logical, organized and hierarchical way. The second step consists on making a pairwise comparison which is a fundamental technique within the AHP methodology. It involves systematically comparing the relative importance or preference of criteria or alternatives in relation to each other. Decision-makers assign numerical values representing the strength of preference between each pair of elements in the hierarchy. Once all pairwise comparisons have been performed by one expert or a group of experts, it is necessary to check the coherence of judgments and consistency which is an important and crucial step in the successful application of the AHP method, leading to reliable decisions.

2.2 Pairwise matrix problem

The AHP uses the pairwise comparison matrix to reveal the relative importance of alternatives and criteria. It is mainly useful to transform judgments into relative weights of importance for both objective and subjective assessments. It makes appropriate for decision problems when one wants to select the best alternative or to calculate the weights of the decision alternatives. The assumption is that decision-makers respond with a numerical answer to the query, "How many times is the ith alternative more important/preferable than the jth alternative?" and then incorporate it into a square matrix called pairwise comparison matrix which has the following form:

$$A = \begin{pmatrix} 1 & a_{12} & \cdots & a_{1n} \\ a_{21} & 1 & \cdots & a_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ a_{n1} & a_{n2} & \cdots & 1 \end{pmatrix}$$

The matrix $A = (a_{ij})$, $i,j = 1,...,n$ has a positive entries everywhere and satisfies the reciprocal property $a_{ji} = 1/a_{ij}$.

The comparisons are made using a scale that indicates the importance of one element over another element with respect to a given attribute. Table 1 shows a scale ranging from 1 for 'least valued than' to 9 for 'definitely most important than'.

Linguistic term	Preference number
Equally important	1
Weakly more important	3
Strongly more important	5
Very strong important	7
Absolutely more important	9
Intermediate values	$2, 4, 6, 8$

Table 1. 1-9 Scale for the pairwise comparison

2.3 Inconsistency of pairwise matrix

The pairwise comparison matrix needs to pass a consistency test to be used. Saaty developed a "consistency ratio" as a consistency test that allows a certain level of acceptable deviations. It's defined as follows:

$$\text{CR} = \frac{CI}{RI}$$

where,

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

$\lambda_{\max}$ is the maximum eigenvalue of the pairwise comparison matrix A, and RI is a random index, whose value depends on n, given in table 2.

n	3	4	5	6	7	8	9	10
RI_n	0.5245	0.8815	1.1086	1.2479	1.3417	1.4056	1.4499	1.4854

Table 2. Random index RI values [1]

CR serves as a measure of inconsistency for the judgments in pairwise comparison matrix. Because it is unavoidable that some degree of inconsistency must be accepted, Saaty (1977) proposed to specify the set of acceptable matrices where CR should be less than 0.1. Otherwise, The pairwise comparison matrix must be revised.

2.4 Incomplete pairwise matrix problem

Definition 2.1. A matrix $\check{A} = (a_{ij})_{n \times n}$ is said to be an incomplete pairwise comparison matrix if it exist $(i, j) \in \{1, ..., n\}$ such that $a_{ij} = *$, where $*$ denotes the missing elements. Alternatively, it can be expressed in the form:

$$\check{A} = \begin{pmatrix} 1 & * & \cdots & a_{1n} \\ * & 1 & \cdots & * \\ \vdots & \vdots & \ddots & \vdots \\ a_{n1} & * & \cdots & 1 \end{pmatrix}$$

Example 2.2. Incomplete pairwise matrix of size 3 and 4

$$\begin{pmatrix} 1 & 2 & * \\ 1/2 & 1 & 1/6 \\ * & 6 & 1 \end{pmatrix}, \begin{pmatrix} 1 & * & 1/3 & 5 \\ * & 1 & 4 & * \\ 3 & 1/4 & 1 & 2 \\ 1/5 & * & 1/2 & 1 \end{pmatrix}$$

In real-world applications, incomplete data could appear due to many reasons, such as the unpredictable or complicated nature of decision-making settings, a shortage of time and/or limited knowledge to make all the $\frac{n(n-1)}{2}$ comparisons [4, 12], or impossibility to compare some of the alternatives [2]. Then, we have to estimate the missing judgments of a given incompete pairwise matrix as first step, and ensure that the obtained matrix is consistent. To this end, we propose an improved genetic algorithm allowing the completion of the elements by suitable values for the missing entries and improving the consistency of the matrix until a satisfactory level is reached.

3 Estimating of missing elements for incomplete pairwise matrix

3.1 Overview of genetic algorithm

Genetic algorithms (GAs), which are primarily developed by Holland, have proven to be effective in solving a variety of optimization problems. They are based on the principles of biological evolution and operate as a searching method. A population of chromosomes is used to represent potential solutions, and genetic operators are applied to progressively improve each chromosome, which becomes the basis for the next generation. This process continues until the desired number of generations has been completed or a predefined fitness value has been reached.

GAs offer a number of advantages over other optimization approaches. First, they search from a population of solutions instead of just one. Second, they can use any fitness function, even if it is not continuous. Third, they use random operators to generate new solutions. Fourth, they do not need to know anything about the problem to find a good solution.

The genetic operators must be adapted according to the nature of the problem to be solved, which can influence its performance. The adapted operators considered in this work are as follows:

- **Initialization:** It consists to randomly generating a set of individuals, where each individual is a potential solution.

  The incomplete pairwise comparison matrix, which is the objectif of the problem, can be identified by $\frac{n(n-1)}{2}$ elements from the set $\{2, 3, ..., 9, 1/2, 1/3, ..., 1/9\}$. Thus, we have to generate randomly k matrices, each of them is encoded by a vector under the form:

  $$\left(a_{1,2}, ., *, ..., a_{1,n}; a_{2,3}, *, ..., a_{2,n}; ....., *, ..., a_{n-1,n}\right)$$

  where $*$ represents the missing elements.
  It should be noted that, in practice, we have to generate a random vectors of m missing data where each element carries its location in the matrix as information, and then, we generate the corresponding complete matrices to continue the AHP process.

  Example: encoding of incomplete pairwise matrix of size 4

  $$\begin{pmatrix} 1 & * & 1/3 & 5 \\ * & 1 & 4 & * \\ 3 & 1/4 & 1 & 2 \\ 1/5 & * & 1/2 & 1 \end{pmatrix} \Rightarrow [*, 1/3, 5, 4, *, 2]$$

- **Crossover operator:** It's the process of combining genetic material from two parents to create a new individuals in the next generation. Different crossover operators can be considered, such as one point crossover, two point crossover. In this study, we consider the Uniform crossover [14] which consist to consider a binary mask where the 1-bits are uniformly distributed in a binary chromosome. Thus, where the mask is 1, copy elements from one parent; and where the mask is 0, choose the remaining elements in the order of the other parent.

Example:

Parent1	3	1/4	7	3	1/6	1/5
Parent2	1/2	7	8	2	4	1/4
mask	0	0	1	0	1	1
Child1	3	1/4	8	3	4	1/4
Child2	1/2	7	7	2	1/6	1/5

- **Mutation operator:** It's involves introducing random changes or mutations in individuals to maintain diversity and explore new regions of the solution space. We consider the insertion mutation, which consists in selecting one or more random genes which will be replaced by new elements. An example of insertion mutation is presented bellow:
  Example:

$$\boxed{2 \mid 1 \mid 1/2 \mid 7 \mid 1/3} \Rightarrow \boxed{2 \mid 1 \mid 1/5 \mid 7 \mid 1/3}$$

The element $1/2$ is choosen randomly and replaced by a random element, in this case for example $1/5$.

- **Elitism:** To generate the new population, we keep 10% of the best chromosomes from the previous population and we replace the remaining 90% with the new individuals.

### 3.2   Approach genetic for incomplete pairwise matrix

The proposed algorithm, as illustrated in figure 1, is based on an improved genetic algorithm to estimate the missing judgments with different sizes of matrices, to help experts to save time and devote more time to debate and choosing the suitable pairwise matrix in the AHP method to take decision for the considered application.

The proposed approach is a combination of an adapted GA and the AHP method. GA method aim to exploit the different choices of missing data through adapted genetic operators; however, the AHP method will make it possible to evaluate the acceptability of the matrices by calculating their consistency ratio CR until a satisfactory level is resched.

The different steps of the Matrix reconstruction process is descriebed bellow.

- **Step 1:** Define the number of criteria n and the number m of missing elements in the incomplete pairwise matrix;

- **Step 2:** Initialization: random generation of initial population $V^{(0)}$ of k vectors $(V_i^{(0)})$, $i = 1, ..., k$; of lenght m from the set $\{2, 3, ..., 9, 1/2, 1/3, ..., 1/9\}$;

- **Step 3:** Encoding: transform each vector of $V^{(0)} = (V_i^{(0)})$ to a population of pairwise matrices $M^{(0)} = (M_i^{(0)})$ with $i = 1, ..., k$;

- **Step 4:** Evaluation: calculate $CR(i)$ for each matrix $M_i^{(0)}$ for $i = 1, ..., k$;

- **Step 5:** Genetic process: generate $V^{(1)} = M_u.C_r.S_e(V^{(0)})$
  with

  - S_e roulette selection;
  - C_r crossover operator with probability p_c;
  - M_u mutation operator with probability p_m;

- **Step 6:** Repeat the step 4 with $M^{(1)}$ replace $M^{(0)}$;

- **Step 7:** The process continue until a stopping test is satisfied.

The stopping test considered is $CR < 0.1$ to ensure the consistency of the pairwise matrix, in addition to the number of iterations to follow the evolution of CR of the pairwise matrices obtained during the genetic process.
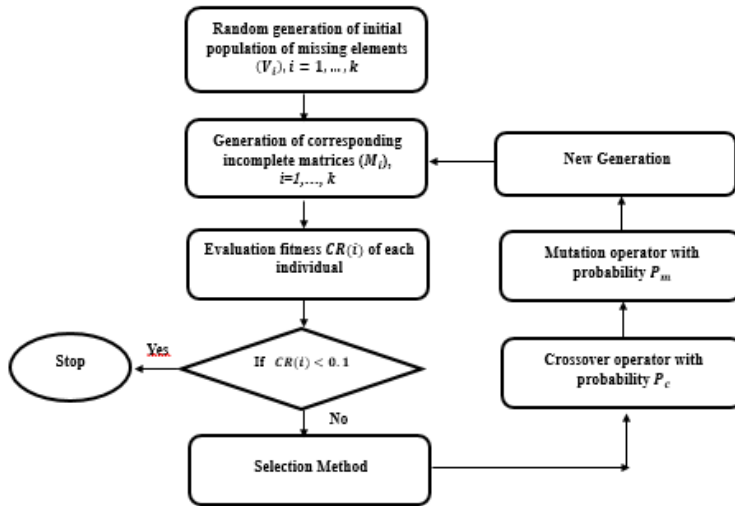
Figure 1. Schema of GA to complete the missing data for incomplete pairwise matrix

4 Numerical results and discussion

Several simulations were performed to highlight the ability and efficiency of GAs to estimate the missing elements for a given incomplete pairwise matrix with different sizes, until a satisfactory level of consistency is reached. The nemerical experiments are developped using an intel (R) Core(TM) i3-6006U CPU @ 2.00 GHz RAM 4.00 GB.

The considered genetic operators and corresponding parameters are described bellow:

- Selection : Roulette selection,

- Crossover : Uniform crossover, with the probability $p_c = 0.9$,

- Mutation : Insertion mutation, with the probability $p_m = 0.05$,

- Insertion : 10% are conserved for the next generation.

Random examples are considered for different sizes which we have generated in the form of vectors as shown in table 3.

Matrix size	Vector
4	[1/2, *, 2, 1/2, *, 9]
5	[7, *, 8, 4, *, 2, 1/2, *, 7, 1/2]
6	[*, 3, 7, 8, 9, *, 5, 9, 5, *, 1/2, 2, 2, *, 1/2]
8	[8, *, 1/3, 4, 5, 4, 8, *, 1/6, 1/2, *, 1/2, 5, 1/6, 1/3, 1/4, 1/2, *, 5, 7, 2, 8, 4, 1/3, 7, *, 2, 6]
10	[1/2, 2, *, 1/2, 1/3, 2, 1/4, 1/2, *, 4, 4, 3, 1/2, 4, 1/4, *, 1/2, 4, 1/3, 1/3, *, 1/7, 1/9, 1/9, 1/5, 1/2, 1/2, 1/6, 1/2, *, 1/2, 4, 1/5, 1/2, 1/2, 2, 1/5, 1/3, 1/4, 1/9, 1/3, 1/7, *, 4, 1/5]
12	[2, *, 5, 1/2, 2, *, 5, 3, 3, 2, 4, 2, 8, *, 2, 5, 5, 6, 4, 2, 3, 4, *, 2, 3, 5, 3, 4, 2, 2, 1/4, *, 4, 2, 1/3, 1/2, 1/3, *, 4, 9, 4, 8, 8, 7, *, 2, 2, 3, 3, 2, 2, *, 1/3, 1/6, 1/5, 1/2, *, 1/4, 1/4, 1/4, 3, 1/4, *, 1/4, 1/2, 2]
15	[2, *, 2, 5, 1/2, 3, 3, 9, *, 5, 2, 7, 1/3, 3, 1/2, *, 2, 2, 1/2, 2, 8, 2, *, 1/3, 4, 1/2, 4, 2, *, 4, 3, 5, 9, 3, 8, 2, *, 1/2, 4, 4, 1/3, *, 3, 6, 5, 4, 1/2, 8, *, 4, 1/3, 1/4, 1/3, *, 3, 2, 1/4, 2, 1/7, *, 1/2, 3, 8, 4, 5, *, 6, 1/3, 7, 5, 8, 2, 8, *, 6, 1/4, 3, 7, 2, 2, 1/3, *, 1/3, 6, 1/3, 1/2, 1/9, 1/4, *, 1/3, 5, 1/4, 4, 1/6, 3, 1/5, *, 1/5, 1/3, 5, 1/3, 5, 1/4, 1/4, 7]

Table 3. Corresponding vectors of random examples of matrices with different sizes

Figure 2 presents the evolution of consistency ratio CR during the iterative process for different number of criteria 4, 5, 6, 8, 10, 12 and 15. It shows that GA is able to construct the incomplete pairwise matrix with different sizes and allows to produce acceptable level of consistency for completed matrix.
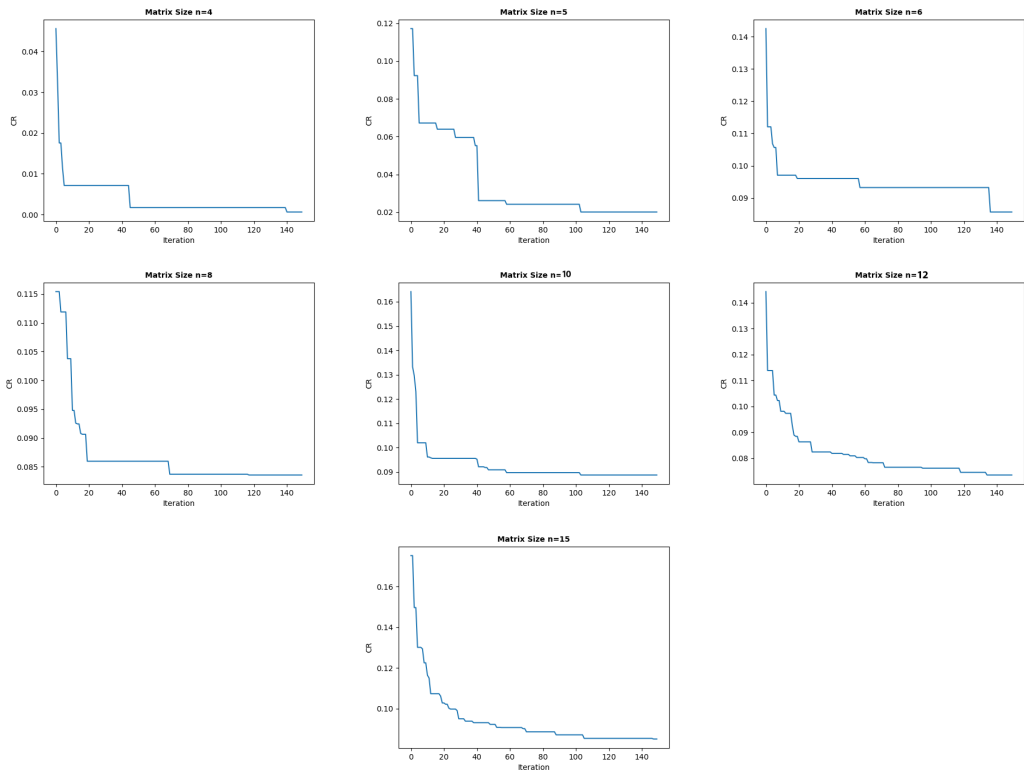
Figure 2. Evolution of CR index during genetic process for incomplete pairwise matrices with different sizes

Matrix size	Population	Initial Min_CR	Initian Max_CR	CR<0.1	Iteration
4	20	0.046	1.413	0.046	1
5	20	0.117	1.528	0.092	3
6	20	0.143	0.936	0.097	8
8	40	0.115	0.731	0.095	11
10	40	0.164	0.545	0.096	11
12	60	0.144	0.590	0.098	10
15	60	0.175	0.560	0.099	29

**Table 4.** Numerical results with matrices of different sizes

In table 4, we present the first obtained value of index $CR < 0.1$ with the corresponding number of iterations from a random generated population. It shows that, we can find the missing elements of the incomplete pairwise matrix in less than 3 iterations for small instances such as 4 or 5. Similarly for higher size of matrices (greater than 6), a 1st accepted level of consistency is obtained in a reduced number of iterations not exceeding 11 iterations for matrices of size $6, 8, 10$ and 12, and 29 iterations are sufficient to get a $CR = 0.099$ as first ratio of consistency for incomplete pairwise matrix of size 15.

It should be noted that during the genetic process the CR index decreases more and more, which allows experts to choose the suitable complete matrix for the considered application as the iterations progress. In addition, the percentage of consistent matrices also increases from one

iteration to another as presented in figure 3, which makes it possible to have a set of complete consistent matrices; thus, the experts have to debate on the right choice among the admissible and acceptable matrices.
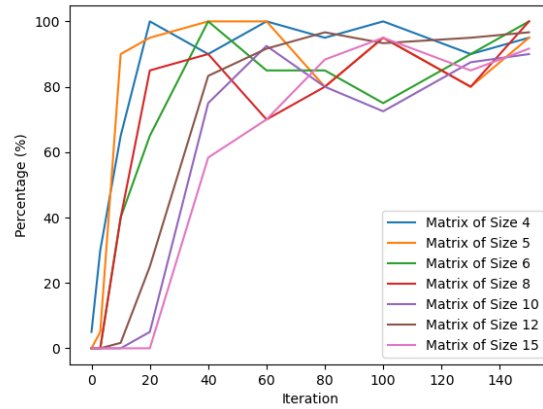
Figure 3. Evolution of the percentage of matrices with $CR < 0.1$ during genetic process for incomplete pairwise matrices
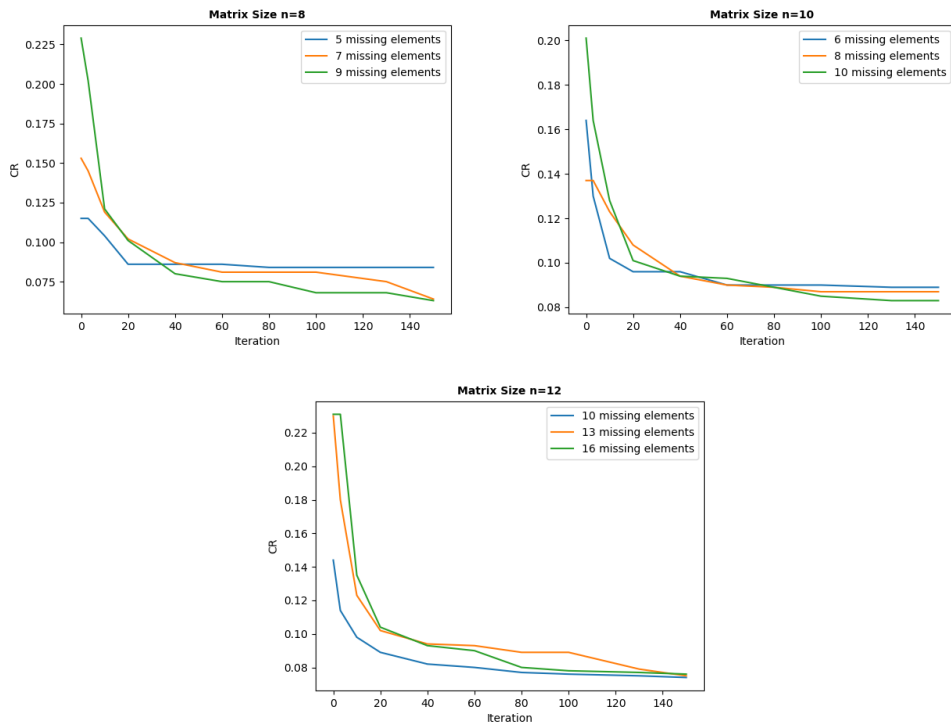
Figure 4. Evolution of CR index during genetic process for incomplete pairwise matrices with different missing elements

To study the effect of number of missing elements in incomplete pairwise matrices, we took different examples of matrices with different number of missing elements. For example, matrix of size 8 with 5, 7 and 9 missing elements (5, 7 and 9 missing elements in the corresponding vectors, which means 10, 14, 18 elements in the pairwise matrix). Figure 4 presents the evolution of CR during the genetic process for some examples of incomplete pairwise matrices of size 8, 10 and 12, with different number of missing elements, showing that the proposed approach make

it possible to recover the missing judgments even for large matrices and even if the number of missing elements is high. In table 5, we present the obtained $1^{st}CR < 0.1$ with the corresponding number of iterations, showing that completion of data does not require a significant increase in the number of iterations even if the number of missing elements increases.

Size	Missing elements	$1^{st}CR < 0.1$	Itération
8	5	0.095	11
	7	0.099	24
	9	0.084	29
10	6	0.096	11
	8	0.099	22
	10	0.099	23
12	10	0.098	10
	13	0.097	24
	16	0.099	26

Table 5. Completing the pairwise matrices corresponding to the number of missing elements

5 Conclusion

Incomplete pairwise comparison matrix is a common problem in many applications when applying the AHP method. In this work, we have exploited genetic algorithms (GAs) as a metaheuristic method for the determination of the missing judgments in incomplete pairwise comparison matrix. In adition, with the process of the proposed improved GA, we are able to define a complete pairwise matrix until a satisfactory level of consistency is reashed. The different results obtained for matrices with different sizes have shown that GA can be considered as a good alternative to suggest the values for empty matrix positions and help the decision maker to make the judgments that he considers relevant.

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