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An integrated multi-objective immune algorithm for optimizing the wire bonding process of integrated circuits

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Abstract Optimization of the wire bonding process of an integrated circuit (IC) is a multi-objective optimization problem (MOOP). In this research, an integrated multi-objective immune algorithm (MOIA) that combines an artificial immune algorithm (IA) with an artificial neural network (ANN) and a generalized Pareto-based scale-independent fitness function (GPSIFF) is developed to find the optimal process parameters for the first bond of an IC wire bonding. The back-propagation ANN is used to establish the nonlinear multivariate relationships between the wire boning parameters and the multi-responses, and is applied to generate the multiple response values for each antibody generated by the IA. The GPSIFF is then used to evaluate the affinity for each antibody and to find the non-dominated solutions. The "Error Ratio" is then applied to measure the convergence of the integrated approach. The "Spread Metric" is used to measure the diversity of the proposed approach. Implementation results show that the integrated MOIA approach does generate the Pareto-optimal solutions for the decision maker, and the Pareto-optimal solutions have good convergence and diversity performance.

Keywords Multi-objective immune algorithm (MOIA) · Multi-objective evolutionary algorithms (MOEA) · Artificial neural networks (ANN) · Wire bonding process

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Introduction

Integrated circuits (IC) chip-package manufacturing processes consist of taping, lapping, de-taping, wafer mounting, wafer sawing, die attaching, epoxy curing, wire bonding, molding, marking, trimming, solder plating, forming, testing and packing (Lo and Tsao 2002). The purpose of wire bonding is to use a fine gold wire to connect the IC bond pad with the substrate inner lead. Since the wire bonding process is the key process in an IC chip-package, it is an urgent problem for the IC chip-packing industry to improve the wire bonding process capability.

The wire bonding process is shown in Fig. 1. It starts from positioning the capillary above the die bond pad with gold ball formed at the end of the gold wire. The capillary then descends and presses the gold ball onto the bond pad to form the first bond. This is also called the ball bond. In a thermosonic wire bonding system, ultrasonic power and vibration force are applied with heat to the pad to facilitate the bonding efficiency. After the ball is bonded to the die, the capillary arises to the loop height position. The gold wire is then led by a capillary to the substrate inner lead. The capillary deforms the wire against the lead, producing a wedge-shaped bond that is called the stitch bond or the second bond. The capillary then arises to a preset height and a new wire ball is formed on the tail of the gold wire. A hydrogen flame or an electric frame may be used to form the ball.

The process parameters that have been proven to have significant effects on the first and second bonds include the vibration force, ultrasonic power, and processing time. The quality criteria for the first bond include the ball shears and ball sizes. It is well known in IC wire bonding practice that the parameters leading to a large ball shear will also produce a large ball bond. However, the ball bond can not be too large. A large ball bond will result in short circuits. Therefore,

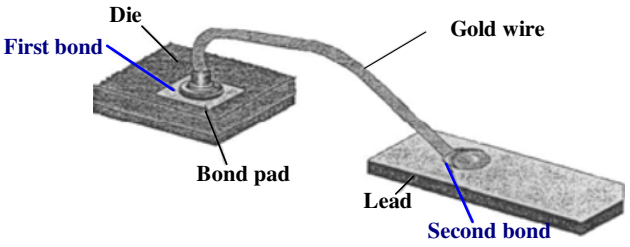

Fig. 1 The wire bonding process

these two quality criteria result in a two-objective optimization problem, i.e., maximizing the ball shear and keeping the ball size at a preset value. However, these two required quality criteria are conflict. It is necessary to capture a set of Pareto-optimal process parameters for setting the IC wire bonding process.

With the rapid development of computational techniques, many multi-objective evolutionary algorithms (MOEAs), multi-objective tabu search (MOTS) and multi-objective simulated annealing (MOSA) have received considerable attention and been used to solve the multi-objective optimization problems (MOOPs) (Schaffer 1985; Goldberg 1989; Fonseca and Fleming 1993; Horn 1994; Srinivas and Deb 1995; Deb et al. 2002; Cochran et al. 2003; Kulturel-Konak et al. 2006; Varadharajan and Rajendran 2005). They all can find the possible Pareto-optimal solutions to decision makers. The most important differences among these algorithms are the strategies used to generate the Pareto-optimal solutions.

Recently, immune algorithm (IA) has been used by some researchers to solve multi-model and combinatorial optimization problems (Khoo and Situmdrang 2003; Chen and You 2005). IA is an adaptive system, inspired by theoretical immunology and observed immune functions, principles and models. It is not only related to the creation of abstraction or metaphorical models of the biological immune system, but also includes theoretical immunology models being applied to tasks such as optimization, control, and autonomous robot navigation. Chun et al. (1999) used IA to optimize the shape of electromagnetic devices. They modified a GA-based search procedure to solve the multi-objective optimal problem (MOOP) in a structural system. Yoo and Hajela (1999) used IA to solve the MOOP by applying a utility function and a weighting mechanism to convert a multi-criteria problem into a single-objective problem. Lin et al. (2003) applied IA to optimize the switching operation for distribution loss minimization and loading balance by merging two objective functions into an overall objective function. Kim and Lee (2004) proposed an intelligent controller for a nonlinear power plant based on IA and the multi-objective fuzzy approach. They used the membership function concept to transform the multiple objective values into a fuzzy set for optimization. In short, these researchers tried to convert the multi-objective functions into a single objective when they applied an IA to optimize the MOOPs. However, the IA is not suitable for solving the multi-objective optimization problems when the objective functions are conflict, such as the IC wire bonding process. Therefore, it is necessary to develop a multi-objective immune algorithm (MOIA) that can find the optimal parameters for the conflict output quality criteria for the IC wire bonding process.

The performance of an MOIA depends on the appropriate design of the fitness evaluation method and the strategies used to generate the Pareto-optimal solutions. The fitness function between the process parameters and quality criteria in the IC wire bonding process is still unknown and needs to be defined. However, the back-propagation neural network (BPN) has been proven to be very useful for modeling a complex manufacturing process. Therefore, in this research the BPN is used to establish the nonlinear multivariate relationships between the wire boning parameters and quality criteria, and used as the fitness function. Regarding to the definition of the Pareto-optimal solutions, Deb (2001) used the domination concept to determine the Pareto-optimal solutions. Ho et al. (2004) proposed a generalized Pareto-based scale-independent fitness function (GPSIFF) that considered the quantitative fitness values in Pareto space for both dominated and non-dominated individuals to determine the Pareto-optimal solutions. The GPSIFF not only maintains the essence of domination concepts proposed by Deb (2001), but also has quantitative evaluation of solutions. Therefore, the GPSIFF is applied in this research to evaluate the candidate solutions and to generate the Pareto-optimal solutions.

In short, the objective of this research is to propose an integrated MOIA that combines IA with BPN and GPSIFF approaches to find out the Pareto-optimal process parameters for the first bond of the IC wire bonding process. The BPN is used to calculate the fitness function values and the GPSIFF is applied to find the Pareto-optimal solutions in optimizing a multi-objective problem. The artificial neural network, Pareto-optimal solution and immune algorithm are briefly described in "Multiple biology-inspired algorithm". The proposed integrated approach is then presented in "The proposed MOIA approach". Implementation results of the proposed approach are then illustrated in "Application to an IC wire bonding process". Finally, concluding remarks are made in "Conclusions".

Multiple biology-inspired algorithm

Biology-inspired algorithms, such as artificial neural networks, evolutionary algorithms, immune algorithm, and ant colony optimization algorithm etc, are computational techniques used to solve scientific and engineering problems by imitating biological principles and behaviors. In the following subsections, artificial neural networks, multi-objective

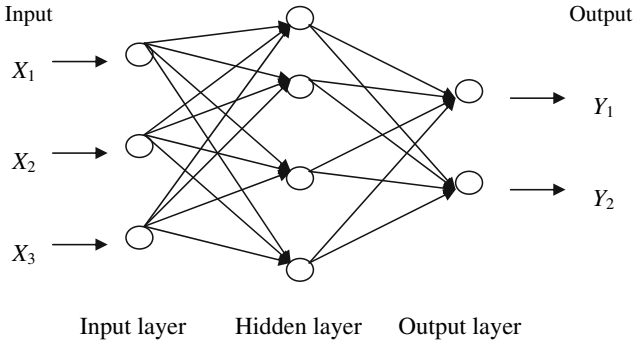

Fig. 2 A three-layer feed-forward neural network structure

evolutionary algorithms, artificial immune system and immune algorithm are introduced.

Artificial neural networks

Artificial neural networks (ANNs) mimic human brains in learning the relationship between certain inputs and outputs from experience. They are information processing systems that have the abilities to learn, recall and generalize from training data. An ANN consists of several layers of a large of highly interconnected computational units called neurons. Figure 2 is the general structure of a three-layer feed-forward ANN. The process of adjusting the connection weights by repeatedly exposing the network to known input–output data is called training. The error back-propagation neural (BPN) learning method is the most popular and successful training technique. For each input–output pair $(\mathbf{x}, \mathbf{y})$, the back-propagation algorithm first calculates the output $\mathbf{y}'$ by propagating $\mathbf{x}$ forward from input layer to output layer. The error signal, $||\mathbf{y} - \mathbf{y}'||$, is back propagated from the output layer to input layer to update the connection weights. A trained ANN can take inputs and produce outputs very quickly, which is an advantage in doing optimization in the proposed approach. Details of the error back-propagation learning method can be found in Hornik et al. (1989).

ANNs have been proved to be universal estimators, hence they are used to model complex manufacturing processes and to identify the optimal process setting. In this research, the ANN with the error back-propagation learning algorithm is used to construct an approximate model for the IC wire bonding process, and used to calculate the fitness function values.

Multi-objective evolutionary algorithms and Pareto-optimal solutions

Many optimization problems in engineering applications inherently involve optimizing multiple conflict objectives. Multi-objective evolutionary algorithms (MOEAs) are especially appropriate to solve these multi-objective nonlinear optimization problems because they can capture a set of Pareto-optimal solutions in a single run of the algorithm. In general, the domination concept is applied to determine the Pareto-optimal solutions in the MOEAs. In the domination concept, a comparison is made to determine whether one solution dominates the other solution or not. A solution X_1 is said to dominate the other solution X_2, if the following conditions are satisfied: (Deb 2001)

Condition 1: The solution X_1 is no worse than X_2 in all objectives.
Condition 2: The solution X_1 is strictly better than X_2 for at least one objective.

If one of the above conditions is not satisfied, the solution X_1 does not dominate the solution X_2. For example, let us consider a two-objective (Max–Min) optimization problem with five different solutions in the objective space, as illustrated in Fig. 3. We assume that objective 1 is to be maximized while objective 2 is to be minimized. Since both objectives are equally important to the decision maker, it is usually difficult to find a solution that is the best with respect to these two objectives. The domination concept can be used to determine the better solution between any two solutions in terms of both objectives. For instance, if solutions A and C are compared, solution C is better than solution A in both objectives 1 and 2. In this way, both of the domination conditions are satisfied. Therefore, solution C dominates solution A. Let us take another example by comparing solution A and solution E. Here, solution E is better than solution A in objective 1 and solution E is no worse (equal) than solution A in objective 2. Therefore, both of the domination conditions are also satisfied, and solution E is said to dominate solution A. By using the domination concept to compare the solutions in multiple

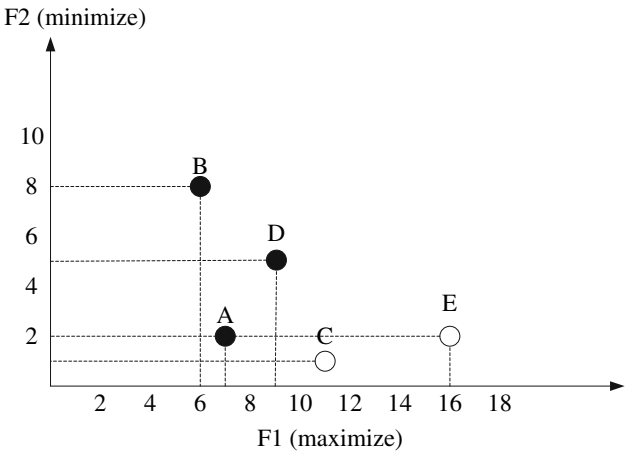

Fig. 3 An example of a two-objective optimization problem with five solutions

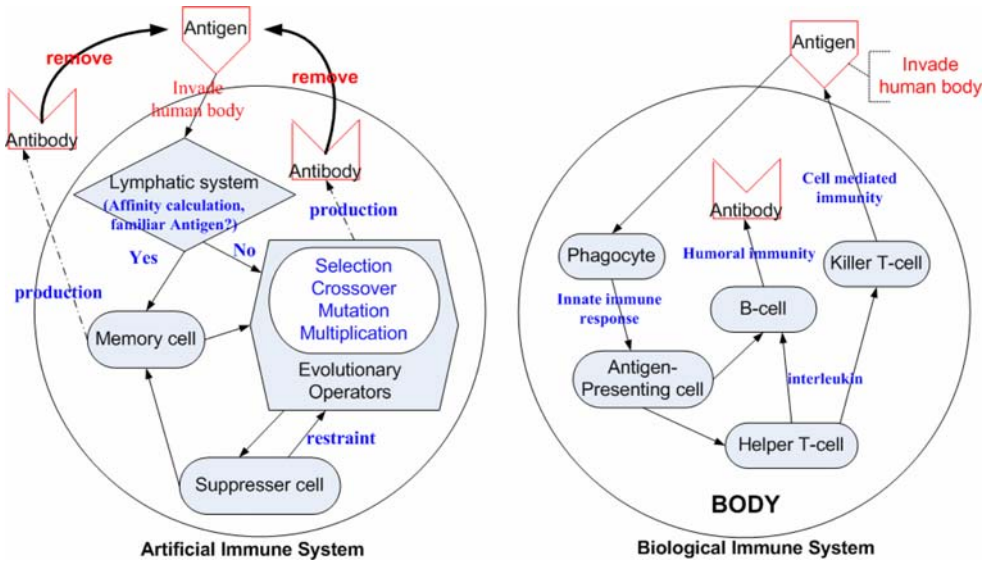

Fig. 4 The mechanisms of the artificial immune system and biological immune system

objectives, most MOEAs can find all of the non-dominated solutions that are also called the Pareto-optimal solution.

Another simple and easy way to determine the Pareto-optimal solution is called the generalized Pareto-based scale-independent fitness function (GPSIFF). The basic idea in GPSIFF is that it evaluates the domination of each solution using a score value. The score value of a solution X is calculated according to the following score function:

$$\text{score}(X) = p - q + c \tag{1}$$

where, p is the number of solutions dominated by X, and q is the number of solutions which dominate X. The scaling constant c is used to get a positive fitness value.

By calculating the score values for all solutions, the Pareto-optimal solutions that have the higher score values can be found. Let us take the five solutions in the Fig. 3 as an example and let's set c to 5. For the solution A, it is found that one solution (B) is dominated by A (i.e., $p = 1$) and two solutions (C and D) dominate A (i.e., $q = 2$). Therefore, the score value of A is $1 - 2 + 5 = 4$. By this way, we can calculate the score value for all solutions and find the Pareto-optimal solutions that have the higher score value. For the case in Fig. 3, score $(B) = 0$, score $(C) = 8$, score $(D) = 4$, and score $(E) = 8$. Therefore, solutions C and E are the two Pareto-optimal solutions illustrated using the white points in Fig. 3 because they have the highest score value. In this study, the GPSIFF concept is applied to determine the Pareto-optimal solutions for the IC wire bonding process.

Artificial immune system (AIS) and immune algorithm (IA)

Artificial Immune System (AIS), emerged in the 1990s as a new branch in computational intelligence by imitating the biological immune system, are used in optimization, pattern recognition, fault detection, and the other applications in the field of science and engineering problems. Immune algorithm is one of AISs used to solve optimization problems. Figure 4 shows the mechanisms of the biological immune system and artificial immune system.

The biological immune system is a complex adaptive system that protects living bodies from the invading of foreign antigens, such as viruses and bacteria. There are three types of immunity in human body, the innate immune response, humoral immunity and the cell-mediated immunity. When an infectious foreign antigen attacks the human body, the innate immune system is activated as the first line of defense. It is called innate immune response (IIR). The most important cell in the IIR is phagocyte. Some phagocytes have the ability to present antigens to other cells, being termed antigen-presenting cell (APC). The APC interprets the antigen appendage and extracts the features, by processing and presenting antigenic peptides on its surface to the T-cells and B-cells. The cells in the adaptive system are able to develop an immune memory so that they can recognize the same antigenic stimulus when it is presented to the organism again. When a B-cell recognizes an antigen, the B-cell will produce antibodies by the bone marrow. The bone marrow then generates a distinct chemical structure which is placed on the outer surface of the lymphocyte to act as a receptor. The antigens will only bind to these receptors with which it makes a good fit. The strength of the binding between an antigen and an antibody is called the affinity or degree of match.

The antibody production in response to a determined infectious antigen is the humoral immunity and the cell-mediated immunity by lymphocytes which are responsible for recognition and elimination of the antigen. The former takes part in

the humoral immunity secretes antibodies by the clonal proliferation while the latter takes part in cell mediated immunity. Moreover, B-cells are also affected by Helper T-cells during the immune responses. The Helper T-cell plays a remarkable key role for deciding the immune system toward the cell mediated immunity or the humoral immunity, and connects the non-specific immune response to make a more efficiency specific immune response. The Killer T-cells destroy the infected cell whenever they recognize the infection and the Helper T-cells trigger clonal expansion and suppress antibody formation.

The AIS is developed by imitating the mechanism of the biological immune system. It consists of antigen, antibody, lymphatic system, memory cells, suppresser cells and evolutionary operators. When AIS is applied to solve an optimization problem, the problem can be treated as the antigen and the solution to the problem as the antibody. The affinity calculation in the lymphatic system is used to judge if the antibody matches the antigen. If it is matched, the memory cells will produce appropriate antibodies to remove the antigen. If it is not matched, the evolutionary operators will be applied to produce matched antibodies to remove the antigen by crossover or mutation operations. Generally, the suppressor cell is used to eliminate the surplus similar candidate solutions while the memory cell is used to keep the candidate solutions. The basic steps of an AIS algorithm in solving a single objective optimization problem can be summarized as follows:

Step 1: Encode the antibodies and generate antibodies (populations) randomly

Represent the problem variable as an antibody with a fixed length similar to a chromosome in genetic algorithms, and randomly generate the initial antibody population. The structure of antibodies is shown in Fig. 5. The size of the antibody population is denoted as N. Each antibody has a length of q digit and each digit is a binary code.

Step 2: Calculate the affinity

Calculate the affinity $ay_{v,w}$ between two antibodies v and w according to Eq. 2:

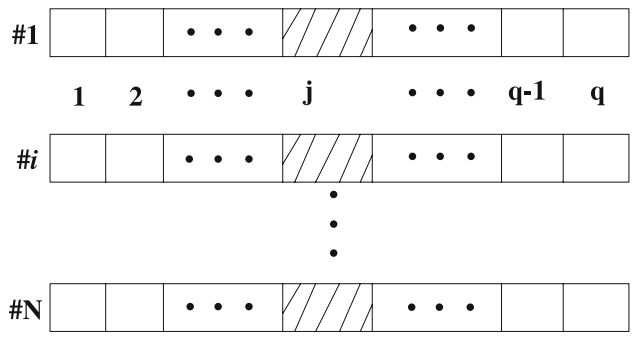

Fig. 5 The structure of the antibody population

$$ay_{v,w} = (1 + E(2))^{-1} \tag{2}$$

$E(2)$ is the diversity evaluation between two antibodies according to Eq. 3 for $N = 2$.

$$E(N) = \frac{1}{q}\sum_{j=1}^{q} E_j(N) \tag{3}$$

$$E_j(N) = \sum_{k=1}^{K} P_{k,j} \log\left(\frac{1}{P_{k,j}}\right) \tag{4}$$

where, $j = 1, 2, \ldots, q$, q is the length of an antibody. $i = 1, 2, \ldots, N$, N is the population of antibodies. $k = 1, 2, \ldots, K$, K is the number of codes. For a binary code, K *equals 2*. $P_{k,j}$ is the probability of j antibody code whose value is k. $E(N)$ is the diversity among all the antibodies.

In addition, the affinity ax_v between an antibody v and an antigen is calculated according to the Eq. 5.

$$ax_v = opt_v \tag{5}$$

where, opt_v corresponds to the evaluated value of the function being optimized. It is the affinity between an antigen and the antibody v.

Step 3: Create the memory cell and the suppresser cell

Determine the concentration C_v of each antibody according to the following equations:

$$c_v = \frac{1}{N}\sum_{w=1}^{N} ac_{v,w} \tag{6}$$

$$ac_{v,w} = \begin{cases} 1 & ay_{v,w} \geq \delta_1 \\ 0 & \text{otherwise} \end{cases} \tag{7}$$

where δ_1 is the pre-specified threshold and $ay_{v,w}$ is the affinity between antibodies v and w.

If C_v is greater than a given threshold δ, it means that the antibody v is very similar to other antibodies in the candidate pool and therefore must be put into a suppressor cell. Otherwise, it is put into a memory cell. The suppressor cell is used to eliminate the surplus similar candidate solutions while the memory cell is used to keep the candidate solutions

Step 4: Proliferation and selection

The antibodies that are put into the suppressor cell or are the same with the antibodies in the suppressor cell are deleted from the candidate pool and replaced with the antibodies in the memory cell. The expected proliferation rate e_v of the antibody v in the memory cell is calculated according to the Eq. 8. Antibodies presenting higher affinities with an antigen ax_v have higher probability of being selected for

proliferation, while antibodies having higher affinity with antibodies in the suppressor cell are suppressed for proliferation.

$$e_v = ax_v \prod_{l=1}^{s} (1 - ay_{v,l}) \tag{8}$$

where, s is the number of suppressor cell.

Step 5: Generation of new antibodies using GA operations, e.g., crossover and mutation

To allow for a response to unknown antigens, generate new antibodies by using genetic operators such as crossover and mutation procedures corresponding to its probability.

Step 6: Termination criterion

Repeat steps 2–5 until the predefined terminal condition is reached.

The proposed MOIA approach

In this study, an integrated MOIA approach that can be used to find the Pareto-optimal solutions for the multi-objective optimization problem with conflict objectives is proposed. The advantages of the proposed MOIA are that this approach not only can be applied to solve multi-objective optimization problem when the objectives are conflict but also can quickly and effectively find the Pareto-optimal solutions because of the characteristics of adaptive immune system and recognition memory. The MOIA approach integrates artificial immune algorithm with BPN and GPSIFF. The integration of BPN and GPSIFF allows the MOIA approach to quantitatively evaluate the solutions and find the Pareto-optimal solution. The MOIA approach, being based on the artificial immune algorithm, takes advantages of the memory cell and suppressor cell mechanisms, and can efficiently and effectively find the Pareto-optimal solutions because the suppressor cell has the effect of eliminating the search of the similar candidate solutions and the memory cell has the effect of keeping the good candidate solutions. The flow diagram of the proposed approach is shown in Fig. 6. The first step of the proposed approach is to initialize the problem and generate some candidate solutions. The second step is to calculate the affinity between the candidate solutions and calculates evaluation value for each solution. The third step is to create the memory cell and the suppressor cell and assign antibodies to the memory cell or the suppressor cell. The fourth step is to delete the dominated solution from the candidate solution pool and replace the solution from the memory cell. The fifth step is to generate new candidate solutions using GA operators. The details of the proposed approach are shown as follows:

Step 1: Antibody representation and generation

Represent the problem variable as an antibody with a fixed length which is similar to a chromosome in GA, and randomly generate initial antibody population that is also called the candidate pool. The structure of an antibody population is shown in Fig. 5. The size of the antibody population is N. Each antibody has a length of q digit (e.g., $q = 30$) and each digit is a binary code. The process parameters of an IC wire bonding are used to create the antibody for the MOIA. The search ranges for these three parameters are 5–15 for force, 40–60 for power and 15–25 for time. The binary string representation for coding antibody (chromosome) is adopted for this MOIA and each process parameter that is normalized in the interval of 0–1 is encoded into 10 binary digits. For example, if $X_1 = 0.129$, $X_2 = 0.256$, and $X_3 = 0.065$, then the antibody will be shown as follows:

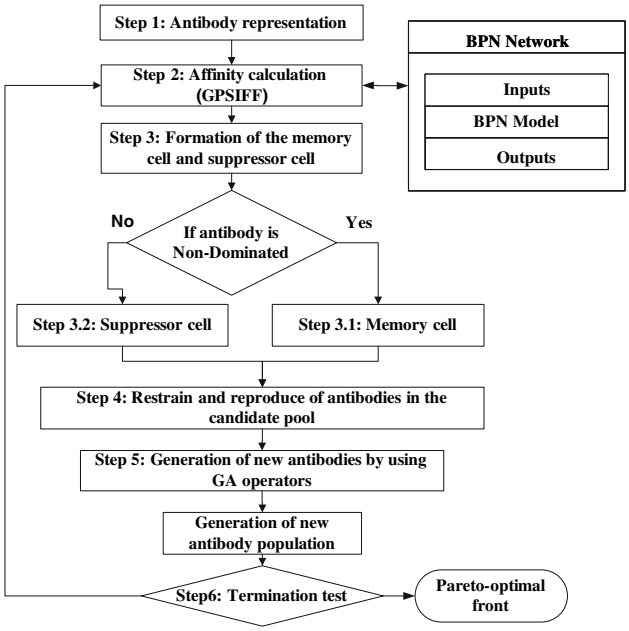

Fig. 6 Flow diagram of the proposed MOIA and BPN approach

0010000001	0100000000	0001000001

Step 2: Affinity calculation

This step calculates the affinity between any two antibodies in the candidate pool using Eqs. 2–4 and generates the affinity between an antibody and the antigen using Eq. 5. In this research, the BPN is used to generate the multiple response values for each antibody. The affinity score(v) for an antibody v is then calculated using the GPSIFF as shown in Eq. 1 to represent the affinity between the antibody v and the antigen, and to find the Pareto-optimal solutions.

Step 3: Formation of the memory cell and the suppressor cell

According to Eq. 1, if an antibody v has $q = 0$, then it is a non-dominated (Pareto) solution. If an antibody v has $q > 0$, then it is a dominated solution. Therefore, an antibody is put into the memory cell if its q value is zero ($q = 0$); Otherwise, it is put into the suppressor cell. The mechanisms

of the memory cell and the suppressor cell are shown in the following:

Step 3.1: The memory cell (when q = 0)

Assume the number of memory cells is $w(w = 1, 2, \ldots, m)$ in the MOIA system. In this research, the memory cell is used to store the non-dominated (Pareto) solutions according to the value of score(v) and $ay_{v,w}$.

1. When the memory cell is not full, the new non-dominated solution v is put into the memory cell.
2. If the memory cell is full, the new non-dominated solution v is stored in a virtual memory cell and an affinity calculation $ay_{v,w}$ between the new non-dominated solution v and those old non-dominated solution w $(w = 1, 2, \ldots, m)$ in the memory cell is required for this assignment. The calculation and assignment processes are as follows:

   (1) Calculate the affinity $ay_{v,w}$ between the antibody v in the virtual memory cell and the antibody w(for $w = 1, 2, \ldots, m$) in the memory cell according to Eqs. 2–4.
   (2) If the score (v) of the new non-dominated solution v is larger than that of the old non-dominated solution $w(w = 1, 2, \ldots, m)$ in the memory cell and all the affinity $ay_{v,w}$ are smaller than the threshold δ_1, which means that the new non-dominated solution v and the old non-dominated solution w are not similar, the new non-dominated solution v is put into the memory cell to substitute for the old non-dominated solution that has the minimum score value.
   (3) If the score (v) of the new non-dominated solution v is larger than that of the old non-dominated solution $w(w = 1, 2, \ldots, m)$ in the memory cell and one of the affinity value $ay_{v,w}$ is greater than the threshold δ_1, which means that the new non-dominated solution v and the old non-dominated solution w are similar. The new non-dominated solution v is not put into the memory cell.

The δ_1 is the pre-specified threshold to check if the new antibody v and antibody w are similar.

Step 3.2: The suppressor cell (when $q > 0$)

Assume the number of suppressor cells is t $(t = 1, 2, \ldots, s)$ in the MOIA system. In this research, the suppressor cell is used to store the dominated (Non-Pareto) solutions according to the value of score(v) and $ay_{v,t}$.

1. When the suppressor cell is not full, then the new dominated solution v is put into the suppressor cell.
2. If the suppressor cell is full, the new dominated solution v is stored in a virtual suppressor cell and an affinity calculation $ay_{v,t}$ between the new dominated solution v and the old dominated solutions $t(t = 1, 2, \ldots, s)$ in the suppressor cell is required for this assignment. The calculation and assignment processes are as follows:

   (1) Calculate the affinity $ay_{v,t}$ between the antibody v in the virtual suppressor cell and the antibody t (for $t = 1, 2, \ldots, s$) in the suppressor cell according to Eqs. 2–4.
   (2) If the score (v) of the new non-dominated solution v is larger than that of the old non-dominated solution $t(t = 1, 2, \ldots, s)$ in the suppressor cell and all the antibody $ay_{v,t}$ are smaller than the threshold δ_1 which means the new non-dominated solution v and the old non-dominated solution t are not similar, the new dominated solution v is put into the suppressor cell to substitute for the old non-dominated solution that has the minimum score value.
   (3) If the score (v) of the new non-dominated solution v is larger than that of the old non-dominated solution $t(t = 1, 2, \ldots, s)$ in the suppressor system and one of the affinity value $ay_{v,t}$ is greater than the threshold δ_1 which means that the new non-dominated solution v and the old non-dominated solution t are similar. The new non-dominated solution v is not put into the suppressor cell.

A brief illustration of the Step 3 is shown in Fig. 7. In this example, the number of population N is 6, the number of memory cell m is 3, the number of suppressor cell s is 3, the constant c of score(v) is 5, a pre-specified threshold δ_1 is 0.75 and both the objectives Y_1 and Y_2 are to be maximized. According to the score (v) value and the q value, the first and the fourth antibodies are put into the suppressor cell, and the second, the third, and the fifth antibodies are put into the memory cell, which results in the memory cell being full. The sixth antibody is put into the virtual memory cell and finally replaces the third antibody in the memory cell.

Step 4: Restrain and reproduce of antibodies in the candidate pool

In this step, the restrain procedure is used to avoid another searching for the dominated solutions stored in suppressor cell again. The reproduce procedure is used to keep the non-dominated solutions in the candidate pool in the next generation. In the restrain procedure, an affinity calculation between the antibody v in the candidate pool ($v = 1, 2, 3 \ldots, i$, i is the number of populations in the candidate pool) and the dominated solution t ($t = 1, 2, 3, \ldots, s$, s is the number of suppressor cell) in the suppressor cell is conducted. If the antibody v is similar to the dominated solution t, the antibody v is then deleted from the candidate pool. Otherwise, the antibody is kept in the candidate pool. The deleted antibodies will be replaced by the non-dominated solutions stored in the memory cell. In the reproduce procedure, the non-dominated

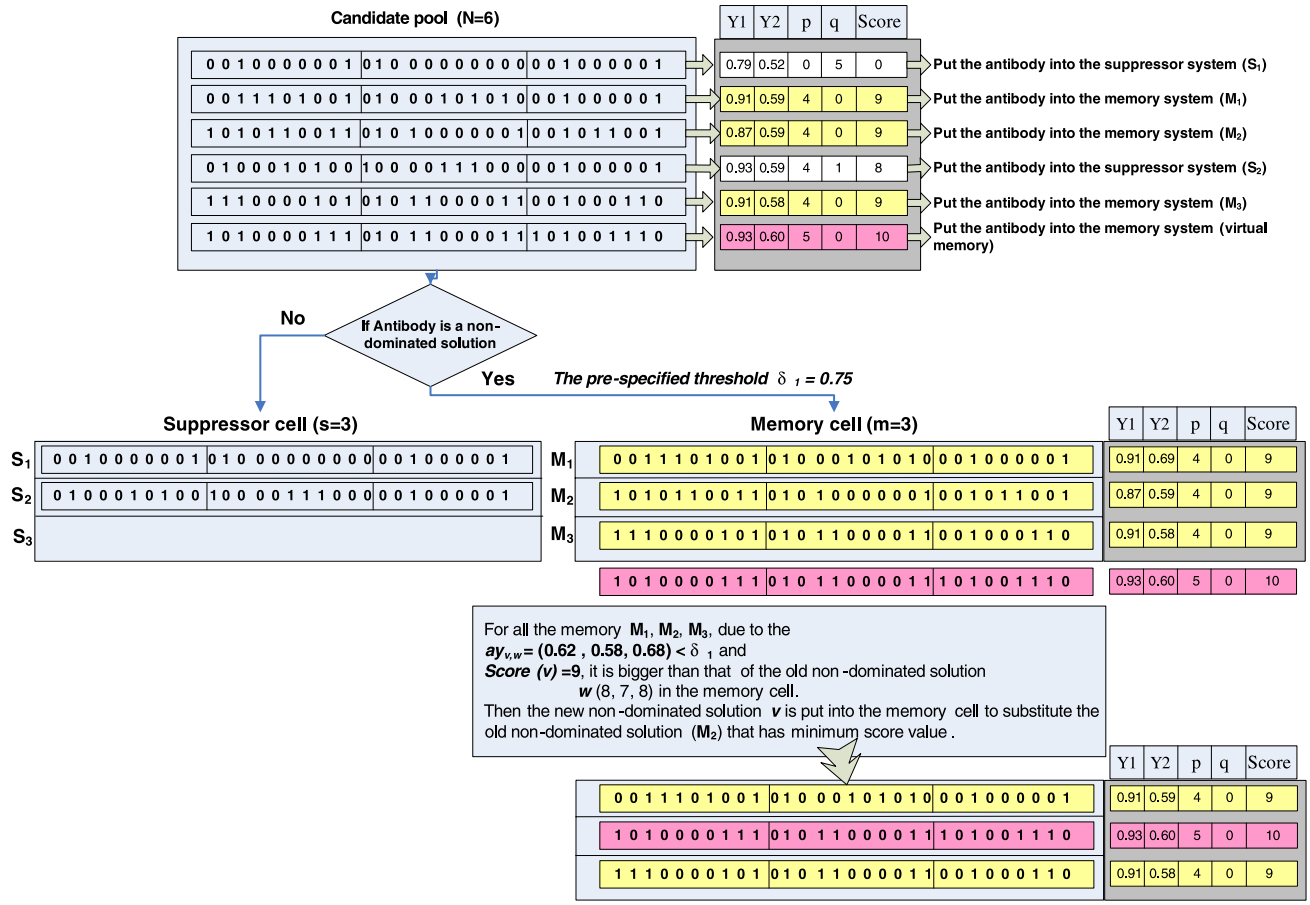

Fig. 7 A brief illustration of Step 3 of the proposed MOIA

solution with the highest expected value e_v in the memory cell will be selected and reproduced first. The reproduce procedure proceeds in this way until all the deleted antibodies in the candidate pool have been substituted. The expected value e_v of the proliferation of the antibody v is calculated using the following equation:

$$e_v = \frac{\text{score}(v)}{\sum_{1}^{m} \text{score}(v)} \tag{9}$$

where m is the number of the memory cell.

Step 5: Generation of new antibody population by using GA operators

Create a couple of new antibodies by applying genetic operators in this step, such as the crossover and mutation. A two-cut-point crossover operation is applied to generate the new antibodies with the crossover probability P_c and the one-gene mutation operation with a pre-specified mutation probability P_m is applied to generate the new antibodies.

Step 6: Termination criterion

Stop the evolution of the MOIA when a pre-defined maximum evolution (e.g., generation number = 5000) is reached. The **Step 2** to **Step 5** are repeated until the maximum evolution is reached.

Application to an IC wire bonding process

Experimental results and BPN results

The three process parameters, each with three levels, and some interactions between process parameters are investigated in this research. The process parameters and their factor levels are summarized in Table 1. The required quality responses of the IC wire bonding process are to maximize the ball shear and to keep the ball size at a preset value.

Table 1 Factors and levels

Factors		Levels		
		Level 1	Level 2	Level 3
A	Force	5	10	15
B	Power	40	50	60
C	Time	15	20	25

In order to save on experimental costs and time, the orthogonal array (OA) experiment rather than a full factorial experiment design is applied to obtain the quality response measurements of the IC wire bonding process. The selection of use of an OA depends on the degree of freedom of the factors and interactions. In this research, three process parameters, each with three levels, and the interactions between force (A) and power (B), force (A) and time (C) are investigated. The calculations of the degrees of freedom are shown as follows:

The degrees of freedom of the main factors = $(3-1) * 3 = 6$;
The degrees of freedom of the interactions $=(3-1) * (3-1) * 2 = 8$;

The summation of the degrees of freedom from the main factors and interactions is 14. This means we have to choose an L_{14} OA at least. However, all of the parameters have three levels, the OA must be a cube of 3 (e.g., L_9, L_{27}, L_{81}). Therefore an $L_{27}(3^{13})$ OA is used to conduct the experiment in this research. The $L_{27}(3^{13})$ can lay out 27 trials, up to 13 factors in columns, and 3 factor levels. The layout of the $L_{27}(3^{13})$ OA is shown in Table 2. It also shows the two output responses for each experimental trial. For each trial in the Table 2, 20 replications are conducted and the output responses (ball shear and ball size) are average values.

The ball shear and ball size for training are the output response based on the process parameters shown in Table 1 and used to train the BPN. The ball shear and ball size for testing are the output response based on the process parameters that are slightly different from those on Table 1, and used to test the BPN. A BPN with three input nodes, one hidden layer with four nodes, two output nodes (as shown in Fig. 2) is applied to learn the nonlinear relationships between the process parameters and the ball shear and ball size for training. The learning rate is set at 0.7 and momentum rate is set at 0.3. After 5,000 epochs the BPN converges to reasonable outputs. The trained BPN is then tested using the test ball shear

Table 2 The L_{27} (3^{13}) orthogonal array and output responses

	Input parameters													Output responses	
	A	B	A × B	A × B	C	A × C	A × C	e	e	e	e	e	e	Ball shear	Ball size
1	1	1	1	1	1	1	1	1	1	1	1	1	1	10.0	35.0
2	1	1	1	1	2	2	2	2	2	2	2	2	2	11.0	36.0
3	1	1	1	1	3	3	3	3	3	3	3	3	3	13.0	38.0
4	1	2	2	2	1	1	1	2	2	2	3	3	3	12.5	40.0
5	1	2	2	2	2	2	2	3	3	3	1	1	1	14.0	38.5
6	1	2	2	2	3	3	3	1	1	1	2	2	2	14.5	39.5
7	1	3	3	3	1	1	1	3	3	3	2	2	2	13.0	38.0
8	1	3	3	3	2	2	2	1	1	1	3	3	3	14.0	39.0
9	1	3	3	3	3	3	3	2	2	2	1	1	1	15.5	40.0
10	2	1	2	3	1	2	3	1	2	3	1	2	3	11.5	36.5
11	2	1	2	3	2	3	1	2	3	1	2	3	1	13.0	38.0
12	2	1	2	3	3	1	2	3	1	2	3	1	2	15.0	40.0
13	2	2	3	1	1	2	3	2	3	1	3	1	2	15.5	40.5
14	2	2	3	1	2	3	1	3	1	2	1	2	3	16.5	41.5
15	2	2	3	1	3	1	2	1	2	3	2	3	1	17.5	42.0
16	2	3	1	2	1	2	3	3	1	2	2	3	1	15.5	40.5
17	2	3	1	2	2	3	1	1	2	3	3	1	2	17.0	41.5
18	2	3	1	2	3	1	2	2	3	1	1	2	3	16.5	41.5
19	3	1	3	2	1	3	2	1	3	2	1	3	2	9.0	35.0
20	3	1	3	2	2	1	3	2	1	3	2	1	3	12.5	37.5
21	3	1	3	2	3	2	1	3	2	1	3	2	1	13.0	40.0
22	3	2	1	3	1	3	2	2	1	3	3	2	1	16.0	41.0
23	3	2	1	3	2	1	3	3	2	1	1	3	2	14.5	39.5
24	3	2	1	3	3	2	1	1	3	2	2	1	3	17.0	42.5
25	3	3	2	1	1	3	2	3	2	1	2	1	3	16.0	41.0
26	3	3	2	1	2	1	3	1	3	2	3	2	1	17.0	42.0
27	3	3	2	1	3	2	1	2	1	3	1	3	2	18.5	42.0

Table 3 BPN test results for the first bond

NO.	Ball shear	Ball size	Ball shear test	Ball size test	Ball shear error	Ball size error
1	14	38	13.3752	38.8292	0.6248	0.8292
2	13.5	37.5	13.7111	39.1360	0.2111	1.6360
3	13	38	14.3632	39.6869	1.3632	1.6869
4	13.5	40	13.6539	39.0883	0.1539	0.9117
5	13	38.5	13.9948	39.3856	0.9948	0.8856
6	13.5	39.5	14.7618	40.0147	1.2618	0.5147
7	13	38	13.9410	39.3259	0.9410	1.3259
8	14	39	14.3182	39.6514	0.3182	0.6514
9	14.5	40	15.1890	40.3513	0.6890	0.3513
10	14	38.5	13.4978	38.9285	0.5022	0.4285
11	13	38	13.8837	39.2785	0.8837	1.2785
12	14	40	14.6609	39.9270	0.6609	0.0730
13	13.5	39.5	13.8730	39.2592	0.3730	0.2408
14	13.5	39.5	14.2472	39.5883	0.7472	0.0883
15	14	40	15.1084	40.2862	1.1084	0.2862
16	14	40.5	14.3262	39.6187	0.3262	0.8813
17	13.5	41.5	14.6888	39.9399	1.1888	1.5601
18	14.5	39.5	15.5697	40.6395	1.0697	1.1395
19	13	39.5	13.7206	39.1045	0.7206	0.3955
20	13.5	38.5	14.1322	39.4798	0.6322	0.9798
21	14	40	15.0060	40.1997	1.0060	0.1997
22	13.5	40.5	14.2587	39.5536	0.7587	0.9464
23	14.5	39.5	14.6132	39.8741	0.1132	0.3741
24	14	39	15.4918	40.5782	1.4918	1.5782
25	13.5	40.5	14.8988	40.0456	1.3988	0.4545
26	13	41	15.2077	40.3301	2.2077	0.6699
27	14.5	37	15.9797	40.9381	1.4797	3.9381

Ball shear (Mean error = 0.8603); Ball size (Mean error = 0.9002)

and ball size and its corresponding process parameters. The result on Table 3 shows that the BPN has very small square root error (SRE) and is an useful tool to model the relationships between the process parameters and output responses.

MOIA results

It is very common in the wire bonding practice that the parameters leading to a large ball shear will also produce a large ball bond. However, the ball bond can not be too large. A large ball bond will result in short circuits. The reason of the ball size should be smaller than 40μm is a production engineering consideration. In the wire bonding process, the ball size is about 1.5–2 times of the diameter of the gold wire (20μm) and the ball size cannot be larger than the open window of the bond pad (43μm). Hence, in this research the ball size is set to be smaller than 40μm. Therefore, the "ball sizes" response is nominal the best. In general, the max-nominal case is less frequently discussed due to the Pareto-optimal solutions display. To easily display the solution space and the Pareto-optimal front, the Max-Nominal problem is transformed into a Max–Max multi-objective optimization problem using the following equation.

$$\text{index} = -[\log(|\text{ball size} - 40|)], \ \text{index} > 0 \tag{10}$$

In order to show the solution space of the multi-objective problem, 10,000 antibodies are randomly generated and the BPN is applied to calculate the multiple response values for each antibody. Figure 8a shows the original solution space and the Pareto-optimal front of the Max-Nominal two-response problem. Figure 8b shows the transformed solution space and the Pareto-optimal front of the Max–Max two-response problem. In the Fig. 8a, b, the set of the black points is the solution space of the multi-objective wire bonding problem and the gray curve represents the possible Pareto-optimal front.

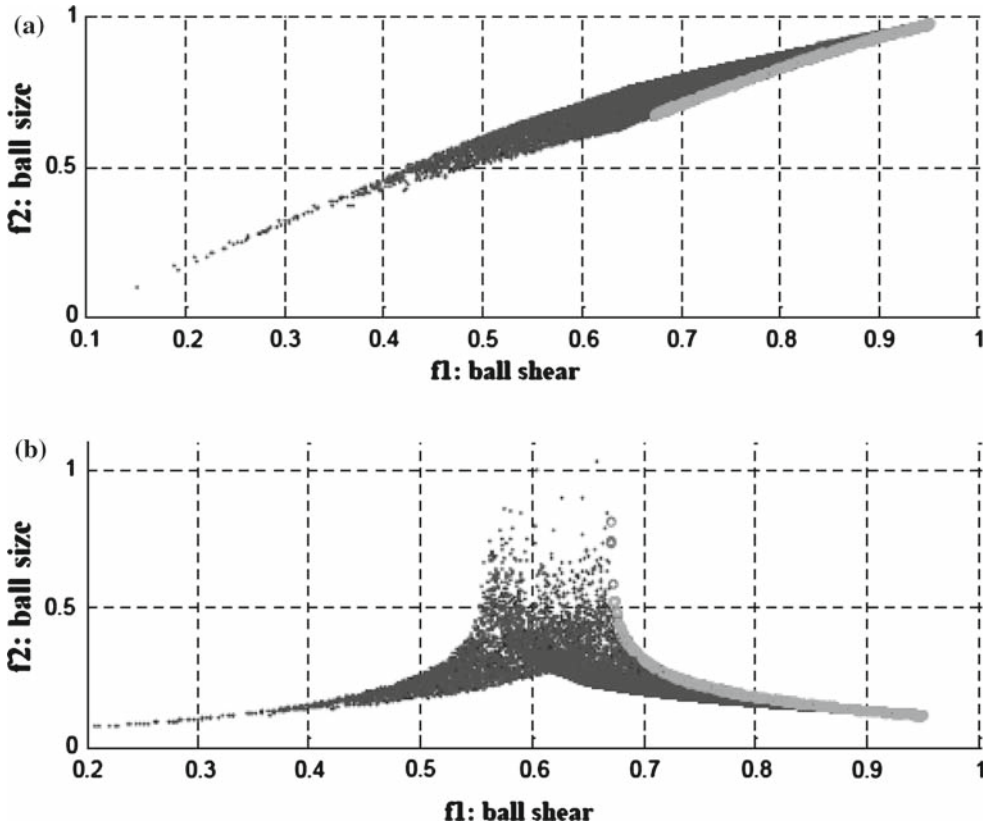

Fig. 8 (**a**) The original solution space of the two-response problem (Max-Nominal); (**b**) The transformed solution space of the two-response problem (Max–Max)

Table 4 The MOIA parameters

The parameters of MOIA	Value
A. Antibody population size	20
B. Iteration number	2,000
C. Affinity threshold δ_1	0.95
D. Memory cell size	20
E. Suppressor cell size	40
F. Crossover rate	0.8
G. Mutation rate	0.02

The parameters that may affect the MOIA search quality include antibody population size, iteration number, affinity threshold δ_1, memory cell size, suppressor cell size, crossover rate and mutation rate. By performing an orthogonal array experiment for these factors, the optimal parameters of the MOIA in this study are shown in Table 4. These parameters of the MOIA are used to find the optimal process parameters for the IC wire bonding process. After running the proposed MOIA, as described in "The proposed MOIA approach" with the parameters for the two-response (Max–Max) problem in this study, 20 Pareto-optimal solutions were found and

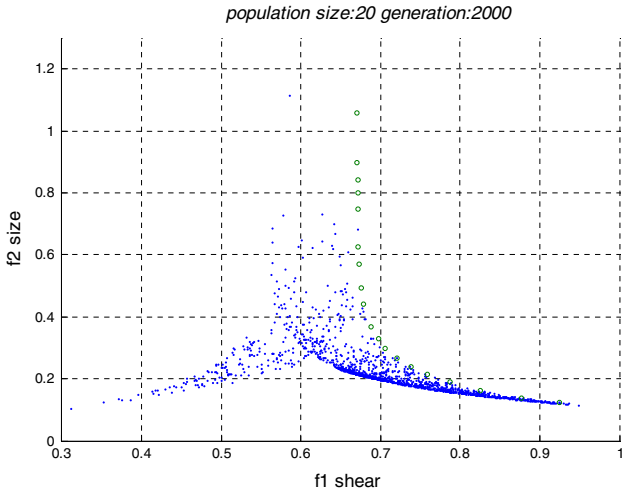

Fig. 9 The solution space and the Pareto-optimal front of the Max–Max optimal problem in an IC wire bonding process

shown as the small circle points in Fig. 9. The normalized process parameter values and their corresponding response values are summarized in the Table 5. Because these process parameter values and the corresponding response values had

Table 5 The summary table of the normalized parameter values and corresponding response values of the 20 Pareto-optimal solutions

	Force	Power	Time	Ball shear	Ball size
1	0.4800	0.9663	0.9995	0.8246	0.1636
2	0.5518	0.9751	0.9966	0.8609	0.1454
3	0.8096	0.9990	0.9995	0.9305	0.1177
4	0.1929	0.9995	0.9981	0.6784	0.4493
5	0.1694	0.9995	0.9976	0.6710	1.2237
6	0.2105	0.9995	0.9966	0.6846	0.3910
7	0.3506	0.9487	0.9961	0.7559	0.2166
8	0.2964	0.9976	0.9966	0.7206	0.2679
9	0.4194	0.9966	0.9985	0.7851	0.1905
10	0.2651	0.9858	0.9990	0.7077	0.2958
11	0.1699	0.9985	0.9966	0.6712	0.7987
12	0.1851	0.9995	0.9976	0.6759	0.4896
13	0.1714	0.9888	0.9981	0.6723	0.5860
14	0.1714	0.9995	0.9985	0.6715	0.7259
15	0.1694	0.9981	0.9990	0.6710	0.9416
16	0.3272	0.9888	0.9990	0.7367	0.2413
17	0.2334	0.9946	0.9966	0.6937	0.3417
18	0.1714	0.9956	0.9995	0.6718	0.6252
19	0.1694	0.9990	0.9981	0.6710	1.0593
20	0.1699	0.9985	0.9995	0.6711	0.8414

Table 6 The actual parameter values and corresponding response values of the 20 Pareto-optimal solutions

	Force	Power	Time	Ball shear	Ball size
1	9.800	59.326	24.995	16.833	36.227
2	10.518	59.502	24.966	17.179	36.090
3	13.096	59.980	24.995	17.840	35.883
4	6.929	59.990	24.981	15.445	38.370
5	6.694	59.990	24.976	15.374	44.178
6	7.105	59.990	24.966	15.504	37.933
7	8.506	58.975	24.961	16.181	36.624
8	7.964	59.951	24.966	15.845	37.009
9	9.194	59.932	24.985	16.458	36.429
10	7.651	59.717	24.990	15.724	37.219
11	6.699	59.971	24.966	15.376	40.990
12	6.851	59.990	24.976	15.421	38.672
13	6.714	59.775	24.981	15.387	39.395
14	6.714	59.990	24.985	15.379	40.444
15	6.694	59.961	24.990	15.375	42.062
16	8.272	59.775	24.990	15.998	36.810
17	7.334	59.893	24.966	15.590	37.563
18	6.714	59.912	24.995	15.382	39.689
19	6.694	59.980	24.981	15.374	42.945
20	6.699	59.971	24.995	15.376	41.310

been normalized for the BPN operation, we have to make a transformation for the data in order to restore them. The final actual process parameters and their corresponding responses are shown in Table 6. These 20 process parameters are the optimal process parameters that should be shown to the decision maker in the IC wire bonding process.

Performance of the proposed MOIA approach

In general, convergence and diversity are two key indexes used to measure the search performance for the non-dominated solutions. Convergence is the measure of the non-dominated solutions that are close to the Pareto-optimal-front. Diversity is the measure of non-dominated solutions that are spread at the Pareto-optimal-front as far as possible. A good MOEA technique should meet with these two key performances. In this study, the "Error Ratio" proposed by Veldhuzin and Lamont (2000) is applied to measure the convergence of the MOIA, and the "Spread metric" proposed by Deb (2001) is applied to measure the diversity of the MOIA. The formula used to calculate the convergence (Error Ratio, ER) is shown in the following:

$$ER = \frac{\sum_{i=1}^{|Q|} e_i}{|Q|}, \text{ where } e_i = 1 \quad \text{if } \notin P^*;\ e_i = 0, \quad \text{otherwise.} \tag{11}$$

where, Q is the number of non-dominated solutions; P^* is the Pareto-optimal front solution.

The ER simply counts the number of the solutions of Q which are not members of the Pareto-optimal front P^*. The Eq. 11 reveals that the ER takes a value between zero to one and a smaller ER value means a better convergence to Pareto-optimal front. When the ER = 0, it means that all solutions are members of the Pareto-optimal front P^*. This is the best situation in applying the MOEA. In general, the smaller "ER" value represents the better performance of the MOIA. For example, let us consider a Max–Min optimization problem as illustrated in Fig. 10. We assume that the set P^* (dot 1–5) is the Pareto-optimal front solutions and the set Q (point A, B, C and point D) is the non-dominated solutions. Once one element of set Q lies on the Pareto-optimal front solutions (P^*), then the value of $e_i = 0$. Otherwise, $e_i = 1$. In the case shown on the Fig. 10, we can find out that all the elements of set Q don't lie on P^*. So all the value of e_i for all four points A to D are equal one ($e_i = 1$). Therefore, the ER value is calculated and shown as follows:

$$ER = \frac{\sum_{i=1}^{|Q|} e_i}{|Q|} = \frac{1+1+1+1}{4} = 1$$

In the best situation, all the elements of the non-dominated solution set Q obtained by the MOIA lie on the Pareto-optimal front (P^*). In this way, the ER value will be equal zero.

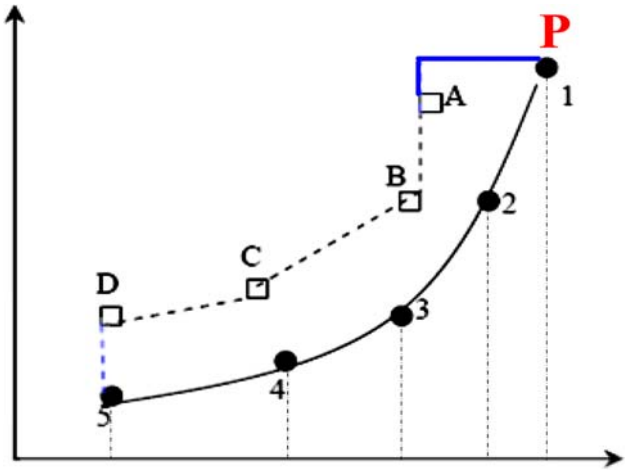

Fig. 10 The illustrated example of Max–Min optimization problem to calculate the convergence and diversity of MOIA

The formula used to calculate the diversity (Spread metric, $\triangle$) is shown as follows:

$$\Delta = \frac{\sum_{m=1}^{M} d_m^e + \sum_{t=1}^{|Q|} |d_i - \bar{d}|}{\sum_{m=1}^{M} d_m^e + |Q|\,\bar{d}}, \quad 0 \le \Delta \le 1 \qquad (12)$$

where, d_i is the crowding distance for the neighbor point solution, d_m^e is the distance between Q and P^*, M is the number of objectives (i.e., in two-objective problem, $M = 2$), $\bar{d}$ is the mean of summation d_i.

When $\triangle = 0$, it is an ideal outcome and it means that the distribution of the obtained non-dominated solutions is uniform. In general, a smaller "diversity" value means better MOIA performance. Using the same case in Fig. 10, we show the detailed coordinates for the Pareto optimal set (P^*) and non-dominated solution set (Q) in Table 7. We then used this example to calculate the diversity value in the following:

$$d_1 = |0.76 - 0.75| + |0.9 - 0.7| = 0.21;$$

$$d_2 = |0.75 - 0.3| + |0.7 - 0.4| = 0.75;$$

$$d_3 = |0.3 - 0.25| + |0.4 - 0.3| = 0.15;$$

$$d_1^e = |0.9 - 0.76| + |0.9 - 0.9| = 0.14;$$

$$d_2^e = |0.95 - 0.9| + |0.2 - 0.3| = 0.14;$$

$$\bar{d} = \frac{(0.21 + 0.75 + 0.15)}{3} = 0.37;$$

$$\text{diversity} = \frac{(0.14+0.15)+|0.21-0.37|+|0.75-0.37|+|0.15-0.37|}{(0.14+0.15)+0.37*3} = 0.75$$

Using the MOIA parameters shown in Table 3 and 5 replications are conducted to test the performance of the proposed MOIA. The summary "Error Ratio" and "Spread metric" of the MOIA technique is shown in Table 8. It is clearly shown that the mean of "Error Ratio" = 0.259. This means that 74.1% of the whole non-dominated solutions found by the MOIA are the Pareto-optimal front. In other words, they are close to the Pareto-optimal front. The mean of "Spread metric" = 0.35. This means that diversity of the non-dominated solution found using the MOIA is not an ideal uniform, but is satisfactory. In short, the proposed integrated MOIA approach can find the Pareto-optimal solutions for the decision maker, and the Pareto-optimal solutions have good performance in convergence and diversity.

Table 7 The detail coordinates for the Pareto optimal set (P^*) and non-dominated solution set (Q) in calculating "diversity" value

P^*	f1	f2	Q	f1	f2
1	0.9	0.95	A	0.76	0.9
2	0.8	0.7	B	0.75	0.7
3	0.7	0.45	C	0.3	0.4
4	0.5	0.35	D	0.25	0.3
5	0.25	0.2			

Table 8 The summary table of "Error Ratio" and "Spread metric" of MOIA technique

Trial no.	Performance		CPU time (min)
	ER	Spread	
1	0.217	0.254	77.79
2	0.167	0.413	80.71
3	0.227	0.339	78.53
4	0.350	0.303	76.98
5	0.333	0.441	74.92
Mean	0.259	0.350	77.79

Conclusions

The wire bonding process is the key process in an IC chip-package. It is an urgent problem for IC chip-package industry to improve the wire bonding process capability. The first bond of the wire bonding process is a multi-objective optimization problem. Multi-objective evolutionary algorithms (MOEAs) have been used to solve multi-objective optimization problems. They can provide all the possible Pareto- optimal solutions for the decision maker. Artificial immune systems (AISs), inspired by theoretical immunology and observed immune functions, principles and models, are adaptive systems which have been applied to problem solving tasks such as optimization, control, and autonomous robot navigation. When compared to other well established MOEA techniques such as vector evaluated genetic algorithm (VEGA),

non-dominated sorting genetic algorithm(NSGA), multiple objective genetic algorithm (MOGA), elitist non-dominated sorting GA(NSGA), Niched-Pareto genetic algorithm (NPGA), multi-population genetic algorithm (MPGA), NSGA-II… etc., the field of the multi-objective immune algorithm (MOIA) is still in its infancy. Not many industrial MOIA applications have been reported in the literature.

In this research, an integrated MOIA that combines immune algorithms with ANNs and GPSIFF approach is proposed to find the optimal process parameters for an IC wire bonding. The BPN neural network is used to establish the nonlinear multivariate relationships between the wire boning parameters and the multi-responses, and is applied to generate the multiple response values for each antibody. The GPSIFF is used to measure the affinity for each antibody and to find the Pareto-optimal solution. The algorithm of MOIA with memory cell and suppressor cell mechanisms is developed. The antibody is put into memory cells or suppressor cells depending on its affinity score value. The candidate antibody that is similar to the antibodies in the suppressor cell is deleted from the candidate pool and then is replaced by the antibody in the memory cell. Because of this mechanism, the MOIA can find the optimal solution in an efficient and effective way. The proposed MOIA that integrated BPN, GPSIFF, and IA is then applied to find the Pareto-optimal parameters for the first bond of the IC wire bonding process. Finally, we applied the "Error Ratio" to measure the convergence of the MOIA, and applied the "Spread metric" to measure the diversity of the MOIA. Implementation results show that the proposed MOIA approach does provide Pareto-optimal solutions for the decision maker. The Pareto-optimal solutions have good convergence and diversity performance.

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