Chapter 4

Evolutionary Algorithms for Hard Combinatorial Optimization Problems

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Since the complexity of the deductive games grows at an exponential rate, it is very difficult to obtain optimal strategy for them when they have higher dimensions, as well as for hard-combinatorial problems with lager sizes. Therefore, evolutionary algorithms [Ben99, Kal03] were employed to solve deductive games. Very often these algorithms are able to find approximately optimal solutions for these complicated problems within a reasonable time. In this chapter, we will investigate *evolutionary algorithms* for solving hard-combinatorial problems. First, we introduce the fundamental concepts of evolutionary algorithms in Section 4.1. Then, in Section 4.2, we apply evolutionary algorithms to solve deductive games. Section 4.3 introduces a state-of-the-art CO problem: minimization of Binary Decision Diagrams (BDDs). Section 4.4 presents the new model, elitism-based evolutionary algorithms (*EBEA),* to solve BDD minimization problems. The distributed implementation of EBEA, DEBEA, is developed in Section 4.5. Section 4.6 reports some experimental results performed by EBEA and DEBEA. Section 4.7 contains our conclusions.

4.1 Evolutionary Algorithms (EAs)

Evolution-based computational approaches have been explored since the early day of computer science [Box57]. The approaches are derivative-free, general-purpose optimization methods based on the concepts of generation-to-generation evolutionary process. Genetic algorithm (GA) [Hol75], based purely on natural selection, is the most popular branch of EA. The characteristic of GA is the notion of emphasizing *crossover* as the key operation in such system. An important property for these evolution-based search methods is that they maintain a population of potential solutions while other methods process a single point of the search space. Therefore, for a large class of hard combinatorial problems, EAs are robust and able to efficiently find solutions that are approximately optimal. Fig. 4.1 shows the structure of EA.

In Fig. 4.1, $P(t) = \{ind_1, ind_2, ind_3, \ldots, ind_n\}$ denotes a population of *n* individuals of generation t, where *n* is the size of a population. Each individual represents a potential solution to

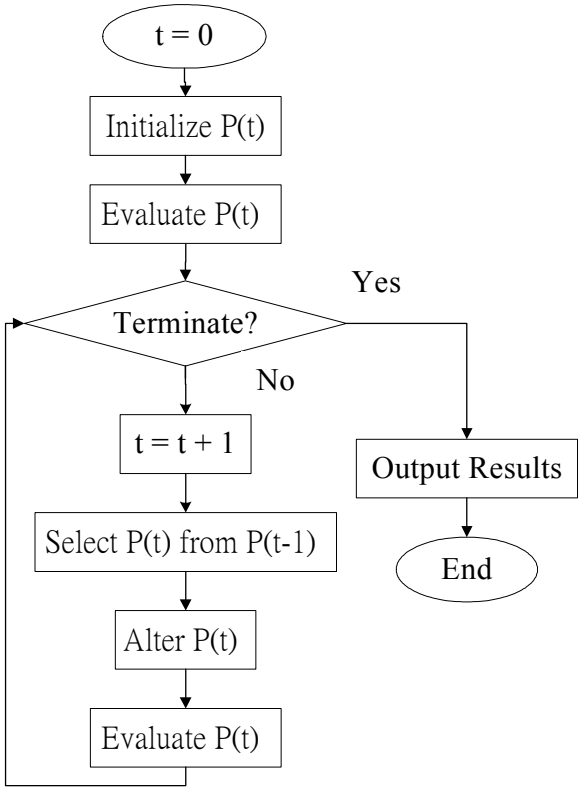


Fig. 4.1. The structure of an evolutionary algorithm.

the problem at hand. At each generation, each individual will be evaluated to give some "fitness". At *select step*, a new population P(t+1) is formed by selecting the more fit individuals. *Alter step* performs some *genetic* operators, e.g., crossover or mutation operators, to form (possibly more promising) new solutions. This process will be repeated until the termination condition is satisfied.

EAs have been quite successfully applied to optimization problems [Mic99] like *wire routing*, *scheduling*, *adaptive control*, *game playing*, *cognitive modeling, transportation problems, traveling salesman problems, optimal control problems, database query optimization*, etc. More recently, EAs have become important for the applications such as *machine learning* [Mit97] and *data mining* [Blu03]. Furthermore, EAs also play an important role in *parallel computing* [Wil99] and *Artificial Intelligence* [Fer99] [Rus03] communities.

In general, characteristics of EAs include:

- EAs can efficiently explore the search space in order to find (near-)optimal solutions.
- EAs are easily *parallelized* and implemented on parallel processing machines.
- EAs are a general, not problem-specific, model for various optimization problems.
- EAs are less likely to get trapped in local optimal.

In the following sections, we will take advantage of the characteristics and apply EAs to solve deductive games and hard-combinatorial problems with lager sizes.

4.2 Solving Deductive Games Using EAs

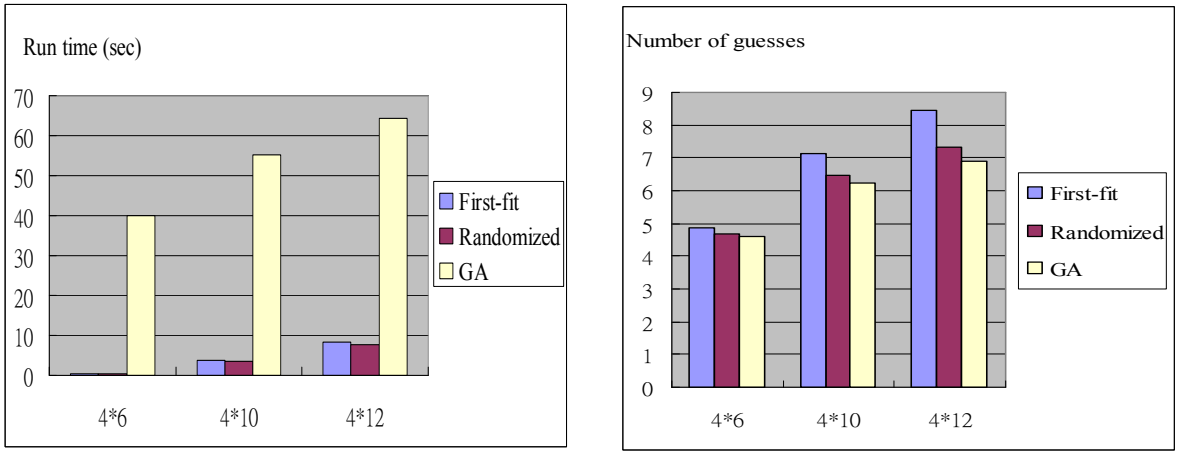
With excellent ability to solve hard CO problems, EAs have been applied to solve deductive games in many published results [Ben99, Ber96, Kal03, Mer99]. In this study, we have also implemented a *simple* EA to solve deductive games. A simple heuristic function was given to measure "fitness" of individuals, as the following formula:

$$\text{Score} = (2*A+B)$$

where A = number of "direct hits" and B = number of "indirect hits".

Each individual, encoded as an integer string, represents a potential guess in the game. To calculated fitness for an individual, it is evaluated against all previous guesses as if the previous guess is a secret code and the individual is a guess to that code. The individuals with higher scores will survive to the next generation. One-point crossover [Hol75], and no mutation, operators are used in the EA. To compare performances of variant algorithms, we have further implemented two algorithms, namely, *first-fit* and *randomized* algorithms, in addition to the genetic algorithm. The *first-fit algorithm* keeps a set of remaining candidates, which are compatible with the responses given so far, and chooses the first remaining candidates to be the next guess. The *randomized algorithm* is almost the same as the first-fit algorithm except that it *randomly* chooses a remaining candidate as the next guess.

This series of experiments are performed for Mastermind games with different dimensions, named 4×6, 4×10, and 4×12. The three algorithms for the three games mentioned above are considered. For each of 9 (3*3) combinations, 1000 independent runs have been realized. For each independent run, GA performs 5 generations and 300 individuals in a population. The *average runtime* and *number of guesses* required for each combination are given in Figs. 4.2(a) and 4.2(b), respectively. In general, the empirical results can be summarized as follows:



(a) (b)

Fig. 4.2. (a) The run time for Mastermind games with different dimensions. (b) The numbers of guesses required for Mastermind games with different dimensions.

- The randomized algorithm achieves better results than the first-fit algorithm.
- The genetic algorithm achieves best results although the run time is longer (but still much shorter than that for the deterministic algorithms employed in Chapter 3).
- The genetic algorithm can not only *effortlessly* solve games with different sizes but also *efficiently* obtain "pretty good" results. For the example of 4×6 Mastermind game, the average numbers of guesses required for the genetic algorithm is 4.61, which is not too far to 4.34 for the optimal strategy [Koy93].

4.3 Binary Decision Diagrams (BDD)

In this section, we will introduce a popular CO problem: minimization of BDD, which is NP-complete. Some fundamental concepts will be presented, including *BDD representation* for Boolean functions, *properties* of BDD, *reduction rules* for BDD, *BDD minimization problems*, and *heuristic algorithms* for BDD minimization.

4.3.1 BDD representation

A Binary Decision Diagram represents a Boolean function as a rooted, directed acyclic graph. Fig. 4.3 illustrates both truth table and BDD representation of a Boolean function $f(w, x, y, z) = wx + yz$. Initially, the graph is a binary tree.

Input				Output
w	*x*	*y*	*z*	*f*
0	0	0	0	0
0	0	0	1	0
0	0	1	0	0
0	0	1	1	1
0	1	0	0	0
0	1	0	1	0
0	1	1	0	0
0	1	1	1	1
1	0	0	0	0
1	0	0	1	0
1	0	1	0	0
1	0	1	1	1
1	1	0	0	1
1	1	0	1	1
1	1	1	0	1
1	1	1	1	1

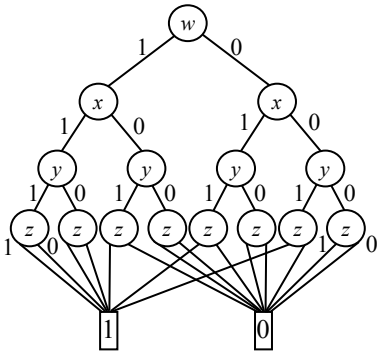


Fig. 4.3. Truth table and BDD representation of the Boolean function $f(w, x, y, z) = wx + yz$.

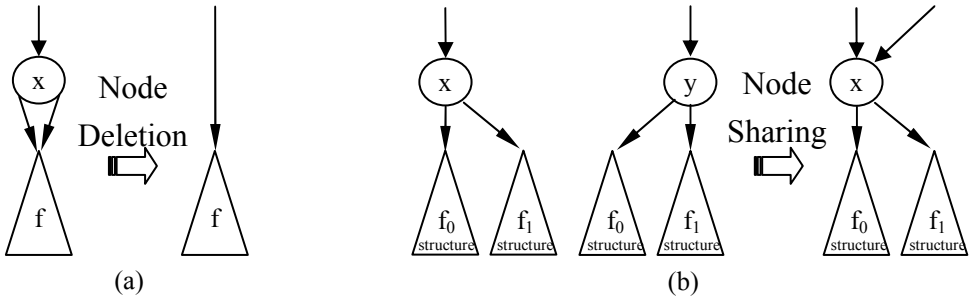


Fig. 4.4. The reduction rules for BDDs. (a) Node deletion. (b) Node sharing.

The BDD discussed in this study means ordered BDD, which imposes a total ordering '<' over the set of variables and requires that, for any two nodes *u* and *v* in any path, their respective variables must be in the same order. Fig. 4.3 shows an example of variables ordered with $w < x < y < z$.

4.3.2. Reduction Rules

Since the efficiency of BDD depends on the number of nodes, a BDD should first be reduced before it is manipulated. The following two reduction rules give a canonical form of BDD to a Boolean function under a fixed variable ordering [Bry86].

(a) *Node deletion rule*: We can delete a node *x* if its two-child links point to the same node, as shown in Fig. 4.4(a).

(b) *Node sharing rule*: We can merge two (or more) nodes *x* and *y* if each of their two child links point to a subtree with the same structure, as shown in Fig. 4.4(b).

We now apply the two reduction rules to the BDD shown in Fig. 4.3. Fig. 4.5 illustrates the reduction process step by step.

The variable order can be arranged arbitrarily and is very critical for the efficiency of the follow-up manipulation. Fig. 4.6 shows the effect of different variable orderings. Both Figs. 4.6(a) and 4.6(b) represent the function $f = x_1x_2 + x_3x_4 + x_5x_6$. In Fig. 4.6(a) the variable ordering with $x_1 < x_2 < x_3 < x_4 < x_5 < x_6$ yields a BDD with a size (the number of nodes) of O(n). (The number of variables is denoted as n.) On the other hand, in Fig. 4.6(b), the variable ordering with $x_1 < x_3 < x_5 < x_2 < x_4 < x_6$ yields a BDD with a size of O(2^n).

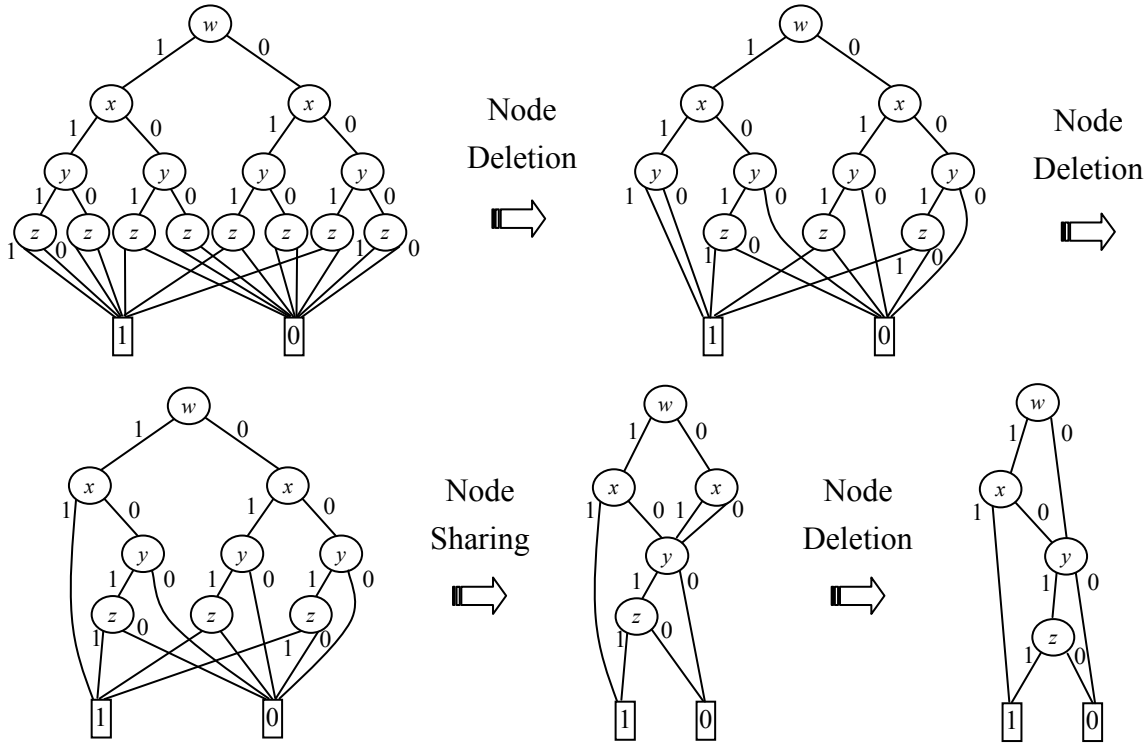


Fig. 4.5. The BDD reduction of the Boolean function $f(w, x, y, z) = wx + yz$.

4.3.3 Minimization of BDD

Binary Decision Diagrams (BDDs) [Bra84, Bry86, Gun99, Keb92] are the most popular data structures used for handling Boolean functions because of their efficiency. By using BDDs, Boolean functions can be manipulated in polynomial time/space (in term of the number of nodes of the graph) [Bry92].

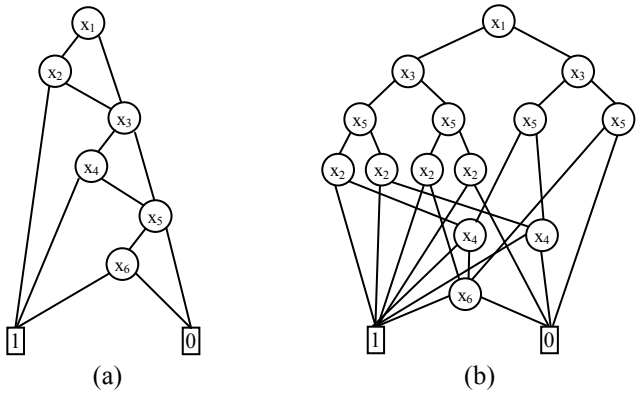


Fig. 4.6. Different BDD representations for the function $f = x_1x_2 + x_3x_4 + x_5x_6$.

Though BDDs are excellent representations for Boolean functions, their sizes are sensitive to the order of the input variables and they may vary from linear to exponential. Finding the optimal variable ordering which results in minimizing the size of a BDD is known to be NP-complete [Bol96a], so that most minimization algorithms are only applicable to small-sized functions [Dre00, Dre01, Ish91, Jeo93]. Also, both the number of variables and their order affect the performance of a minimization algorithm, i.e., changing the initial variable ordering of the same function may prevent an algorithm from finding the exact minimum. This nature of BDDs makes the feature of a minimization algorithm unable to be properly measured. To reduce run time and space requirement, Drechsler et al. [Dre01b] proposed a statistical approach for constructing BDDs.

For BDD-based technology, quality is a very important issue, since a small improvement in the number of nodes often simplifies the follow-up problem tremendously. Various techniques for BDD minimization have been developed in the past decade [Bol96b, Dre01, Ish91, Jeo93, Mol94, Rud93, Sch99, Pan95]. These enable their minimization algorithms to determine the best variable ordering of functions with 7 variables [Fri90], and with 64 variables (for those with partially symmetric functions) [Dre00]. A randomized algorithm has been applied to the problem [Lin01] and has obtained the best size for some benchmark circuits with less than 500 variables. Recently, scatter search is used to minimize the BDD size [Hun02], which shows robust results compared with the Exact algorithm [Dre00] and other heuristics [Dre01]. However, among 30 benchmark circuits that are manageable by the Exact algorithm, it still could not find the optimal variable orders for five of them.

The BDD minimization problem is to choose a variable ordering leading to minimal BDD size. The *Exact minimization problem* [Dre00] is to find the optimal variable ordering leading to the smallest BDD. Since it is NP-hard to find the exact minimum, no heuristic algorithms [Dre01] can find the best variable ordering when n is large. The most promising methods for BDD minimization are based on dynamic variable ordering (DVO) [Rud93], i.e., the BDD size is

improved using exchanges of neighboring variables. One application of DVO, Sifting [Rud93], is the most popular heuristics for BDD minimization.

4.3.4 Heuristic Algorithms for BDD Minimization

In this study, we will make use of the problem-specific heuristics, *Sifting*, and the basic operation of DVO, *exchange of adjacent variables (EAV)*. We now briefly describe these algorithms and analyze the computational complexities.

A. Exchange of adjacent variables (EAV). The exchange is performed very quickly since only partial edges should be redirected within these levels. Hence, the BDD doesn't need to be completely reconstructed. The resultant BDD would be efficiently minimized if the BDD size becomes smaller after performing EAV. To simplify the analysis, we extend EAV to include the operation of computing BDD size after EAV. In this study, we consider EAV as an elementary operation; in addition, we denote the time complexity of the elementary operation as T_{EAV}.

B. Sifting. The sifting algorithm successively considers each variable of a given BDD. At each step, it chooses a variable v_{max} and finds the best position of the variable, assuming that the relative order of all other variables remains the same. The variable with the maximum level size is chosen to be variable v_{max}. For example, in Fig. 4.6(b), variables x_5 and x_2 both have size 4 in their respective levels. Either x_5 or x_2 could be chosen as v_{max}. To find the best position, at least O(n) EAVs should be performed. Since there are n variables for an individual, the time complexity of sifting operation is $T_{sifting}= O(n^2)*T_{EAV}$.

4.4 Elitism-Based Evolutionary Algorithm (EBEA)

The fundamental idea of the elitism-based evolutionary algorithm (EBEA) is that individuals in a population always have aggressive tendencies towards becoming elites and that only the fittest individuals in a population are chosen for reproduction. Similar idea has been employed in previous studies – the *CHC model* [Esh91] and *family competition models* [Cul93, Thi94, Yan00]. All of these models use *enlarged sample space* and *deterministic sampling mechanism*, i.e., selecting the best individuals from parents and offspring to form the next generation.

EBEA differs from all previous models in the following two important features. One is the termination criterion, called *stable function*, which provides information to judge the degree of convergence for a population. The other is the effective ad hoc operators, called SteepestEAV and Sifting operators in the *genetic engineering phase*. Besides, EBEA employs a *global competition mechanism*, *in which* the best individuals out of the union of parents and offspring form the next generation. The mechanism is similar to CHC algorithm but not *family competition models,* which use *local competition,* i.e., each competition takes place within a family. The family members may consist of two parents and two children [Cul93, Thi94] or consist of one parent and L children [Yan00]. Furthermore, EBEA does not perform any mutation in the main evolutionary loop, which also distinguishes it from *family competition models* but not CHC.

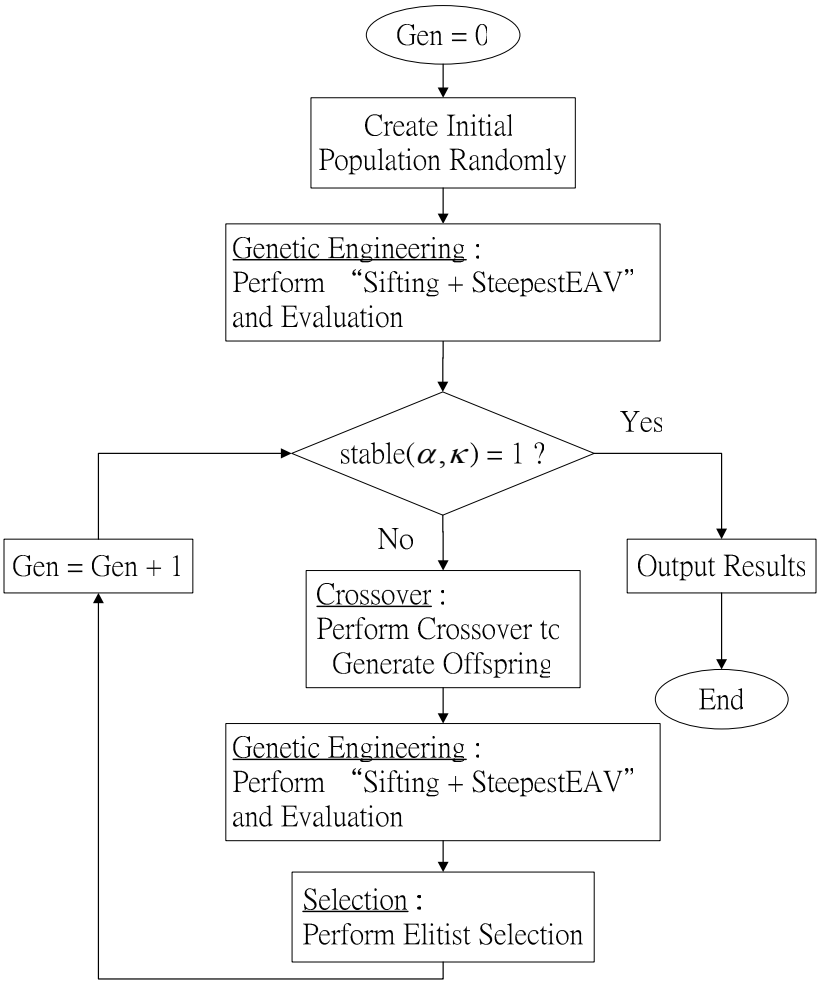


Fig. 4.7. The flowchart of EBEA.

In this section, we propose a *stable function* approach for the EBEA, which provides information to judge the degree of convergence for a population. This not only helps to choose a termination criterion for achieving the speed and quality requirements of a system, but also reduces the run time of redundant generations if the system almost has no chance obtaining superior results. Fig. 4.7 illustrates the flowchart of EBEA, whose details are described in the following subsections.

4.4.1 Representation, Initialization and Evaluation

Each individual in EBEA is represented by an integer string of length n, which stands for a variable ordering for a benchmark circuit with n input variables. All $n!$ permutations of the variable orders are feasible solutions. The representation and related operators has been well studied for solving the *Traveling Salesman Problem* [Fog88, Fog90, Fog93, Gol85, Oli87, Whi89] as well as for some combinatorial optimization problems.

The initial population is chosen at random. The size of the initial population is denoted by *popsize* and is fixed during all generations. Since the goal of this research is BDD size minimization, we evaluate individuals by their resultant BDD size.

4.4.2 Operators

Unlike other evolutional algorithms (EAs), as the name "*elitism-based* evolutional algorithms" shows, the operators of our EBEA have an *aggressive* property to let the individuals become elites. We describe the operators in detail as follows:

A. Selection. *Enlarged sampling space* and *deterministic sampling strategy* are used; that is, EBEA selects the best *popsize* individuals from a pool, including not only the offspring but also the old individuals, to produce the next generation.

B. Crossover. The two-point crossover, order crossover *OX* [Dav85], is used, whose positions are selected randomly. In EBEA, the crossover operator reserves at least an n/5 proportion of the chromosome to guarantee "excellent heredity factors" passed on to the next generation. To keep

the proportion intact, no mutation is used in the main evolutionary loop in EBEA.

We have also tried to use other kinds of crossover operators ER [Whi89], CX [Oli87], and PMX [Gol85] and added mutation operators IVM [Fog88] and ISM [Fog90, Fog93] to EBEA. However, they often did not improve the results obtained. In contrast, the quality of solutions sometimes decreased. Hence we only apply OX operator in our system.

C. Operators in the genetic engineering phase. In this phase, EBEA changes the genetic structure of individuals in order to make them stronger or more suitable for achieving the goal, i.e., BDD minimization. This is the crux of EBEA and its most time-consuming phase. We take advantage of state-of-the-art heuristics specifically tailored to BDD minimization, namely *Sifting*. Furthermore, we design an efficient operator, *SteepestEAV*, cooperating with *Sifting* in order to find advanced results more efficiently. In the genetic engineering phase of EBEA, we perform SteepestEAV after Sifting to achieve more superior results. The Sifting algorithm was described in Section 4.2 and has a time complexity of $O(n^2)*T_{EAV}$. We now describe *SteepestEAV* and analyze its time complexity.

SteepestEAV. A sketch of SteepestEAV algorithm is given in Fig. 4.8. In the first step, we perform EAV n-1 times and keep a *gain*, i.e., the differences in size before and after EAV, for each adjacent levels (i and i+1) in the array Gain[0~n-1]. If any element of the array contains positive values, then the BDD size can be improved (i.e., become smaller) after doing the corresponding EAV. In the second step, we repeatedly perform the EAV *with the largest gain* to improve the BDD. After performing each of the EAVs, we have to modify two elements of the Gain array to reflect the variable ordering change due to the EAV operation. Thus, three additional EAVs have to be done for each improvement. Therefore, the complexity of SteepestEAV is $T_{SteepestEAV}= O(n+3i)*T_{EAV}$, where i is the number of improvements in the SteepestEAV operation.

```
SteepestEAV(CurrentBDD)
 {  Integer Gain[n] ;                                  // the gain for each EAV
    Integer OriginalSize = size_of (CurrentBDD);
    Integer NewSize;
    for ( i = 0 ; i < n - 1 ; i++ )
     { NewBDD = EAV(CurrentBDD, i, i + 1) ;           // perform variable exchange between levels
                                                         i and i+1
       NewSize = size_of (NewBDD) ;                   // compute BDD size for NewBDD
       Gain[i] = OriginalSize - NewSize ;             // compute the gain due to the variable exchange
     }                                                   between levels i and i+1 and save it in Gain[i]
    while (∃x ϶ Gain[x]>0))                           // do the EAV until no gain for all adjacent
                                                         variables exchange
     {  k = max{ x |Gain[x] > 0} ;                    // the EAV with largest gain first
        CurrentBDD = EAV(CurrentBDD, k, k + 1) ;      // perform variable exchange between levels k
                                                         and k+1
        Gain[k] = 0 ;                                 // reset Gain[k] to 0
        Update Gain[k - 1] ;                          // perform variable exchange between levels k-1
                                                         and k and update Gain[k-1]
        Update Gain[k + 1] ;                          // perform variable exchange between levels k+1
     }                                                   and k+2 and update the Gain[k+1]
 }
```

Fig. 4.8. A sketch of the SteepestEAV algorithm.

According to the above analysis, the complexity for Sifting and SteepestEAV is $(O(n^2) + O(n+3i))*T_{EAV}$. Although the run time for the combination is slightly longer than $O(n^2)*T_{EAV}$ for Sifting, the experimental results show that it has an excellent ability to discover advanced results.

Example 4.1. We have tested 103 benchmark circuits in the LGSynth91. Experimental results show that 31 circuits can obtain more superior results by using the proposed operator compared to Sifting. Notice that, the superior results cannot be easily discovered by another independent run with the Sifting method. Moreover, our approach finds the exact minimization solution for circuit *cm163a*, the results of which cannot be found even for *convergent sifting* [Som01], a heuristic algorithm that iteratively does *Sifting* until no further improvement is obtained.

4.4.3 Termination Criteria

Conventional EAs [Dre97] for BDD minimization usually do not stop until the current best result does not change after hundreds or thousands of additional generations. Such a long time for the redundant generations is not acceptable by our EBEA since the strong operators for the genetic engineering phase are more time-consuming than conventional EAs. In contrast, we propose an

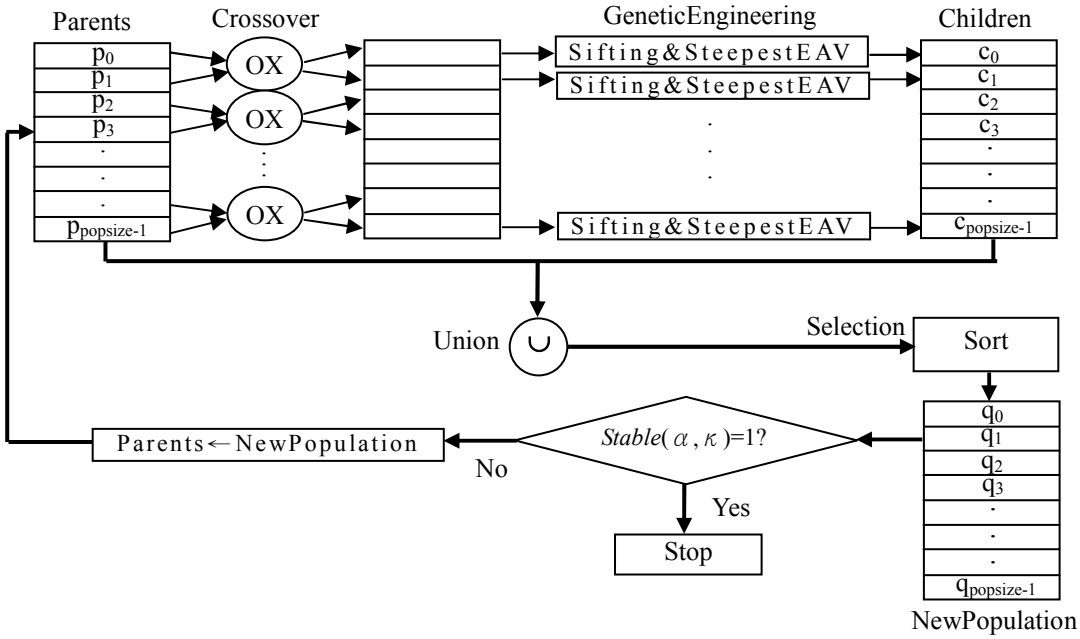


Fig. 4.9. The general structure of EBEA showing the relation of three populations, parents, children, and new population. The items, p_i, c_i, and q_i, $0 \le i \le popsize-1$, inside the rectangles refer to the BDD sizes for individuals, i.e., the elements in sets P, C, and Q, respectively.

effective termination criterion for EBEA, which supervises the states of all individuals of a generation instead of just measuring the current best result. To be more precise, we develop our termination criteria as follows.

Let $P=\{p_0, p_1, p_2, \ldots, p_{popsize-1}\}$, $C=\{c_0, c_1, c_2, \ldots, c_{popsize-1}\}$, and $Q=\{q_0, q_1, q_2, \ldots, q_{popsize-1}\}$ be the sets of sizes for individuals of the *parent*, the *children*, and the *new population*, respectively. Fig. 4.9 shows the general structure of EBEA and illustrates the relation of these sets in EBEA. Here we assume that $p_0 \le p_1 \le p_2 \le \ldots \le p_{popsize-1}$ and $q_0 \le q_1 \le q_2 \le \ldots \le q_{popsize-1}$. The set of differences is defined as $D = \{d_i \mid d_i = p_i - q_i,\ 0 \le i \le popsize-1\}$. In EBEA the selection strategy, which includes the techniques of *enlarged sampling space* and *deterministic sampling,* makes all the elements in D be nonnegative integers, as proven in Property 4.1. This property is important for developing the termination criteria for EBEA.

Property 4.1. $\forall d_i \in D,\ d_i \in N,$ i.e., all the elements in the set belong to {0,1,2,3,…}.

Proof. Let sequence S, $s_0 \le s_1 \le s_2 \le \ldots \le s_{2*popsize-1}$, be the result of sorting all the elements in sets P and C. We have $s_i = q_i$ for $0 \le i \le popsize-1$, since the selection rule, *enlarged sampling space,* is

used in EBEA. Accordingly, $s_i \le p_i$ and hence $q_i \le p_i$ for all $0 \le i \le$ popsize-1. By definition, $d_i = p_i - q_i \ge 0$. The result of this property follows. ■

From Property 4.1, we have the following observations.

Observation 4.1. If $d_0 = 0$, then the best size of the population has no change in this generation. In addition, the more elements in set D that equal zero, the more *stable* the population, i.e., with a lower probability of obtaining better results. In the extreme case, if all elements in set D are equal to zero, then we call the population *stagnant,* i.e., no individual obtains a better result in this generation.

Observation 4.2. *The effect of d_i on the final result of a population decreases as i increases.* For example, if $d_0 > 0$, then the current best results have improved during this *evolution,* and the current *best* individual, denoted by ind_0, is still not stable; in addition, any improvement of ind_0 in the next evolution will obtain more superior results. On the other hand, an improvement of d_k from an unstable individual ind_k should be large enough so as to improve the best results since its resultant BDD has to be smaller than those of ind_0, ind_1, …, ind_{k-1}, whose results are all smaller than that of ind_k in the preceding generation.

Accordingly, the termination criterion of EBEA is determined by the following formula:

Stable function:

$$stable(\alpha, \kappa) = \begin{cases} 1, & \sum_{i=0}^{popsize-1} \alpha^{-\lfloor \log_2(i+1) \rfloor} d_i < \kappa, \text{ where } \alpha \in Z^+, \kappa \in R^+, \\ 0, & otherwise. \end{cases}$$

That is, EBEA will stop if the value of the *stable* function is equal to 1. Notice that we give different weights to d_i according to the effect on the final result. In addition, a problem specific parameter α is used, which depends on the *range* of the problem in hand; for example, we choose α=5 in the BDD minimization problem. Now, we derive the properties of the stable function and give two examples to show how it works in Property 4.2 and Examples 4.2 and 4.3.

Property 4.2. If $\kappa = \alpha^{-k}$ and $stable(\alpha,\alpha^{-k}) = 1$, $k \in \boldsymbol{N}$, then the set of differences D satisfies all the following constraints.

(i) $d_i = 0$, for $0 \le i \le 2^{k+1}-2$, and

(ii) $\sum_{i=2^{k+m}-1}^{2^{k+m+1}-2} d_i < \alpha^m$, for $1 \le m \le \alpha^{\lfloor \log_2 popsize \rfloor - k}$, $m \in \boldsymbol{Z}$.

Proof: By definition, we have $\sum_{i=0}^{popsize-1} \frac{1}{\alpha^{\lfloor \log_2 (i+1) \rfloor}} d_i < \alpha^{-k}$, which implies that

$$d_0 + \frac{d_1 + d_2}{\alpha} + \frac{d_3 + d_4 + d_5 + d_6}{\alpha^2} + \ldots + \frac{\sum_{i=2^k-1}^{2^{k+1}-2} d_i}{\alpha^k} + \ldots + \frac{\sum_{i=2^{\lfloor \log_2 popsize \rfloor}}^{popsize-1} d_i}{\alpha^{\lfloor \log_2 popsize \rfloor}} < \alpha^{-k}.$$ That is,

$$d_0\alpha^k + (d_1+d_2)\,\alpha^{k-1} + \ldots + \sum_{i=2^k-1}^{2^{k+1}-2} d_i + \Big(\sum_{i=2^{k+1}-1}^{2^{k+2}-2} d_i\Big)\,\alpha^{-1} + \ldots + \Big(\sum_{i=2^{\lfloor \log_2 popsize \rfloor}}^{popsize-1} d_i\Big)\,\alpha^{-(\lfloor \log_2 popsize \rfloor - k)} < 1.$$

Since d_i is nonnegative integer and $\alpha \in \boldsymbol{Z}^+$, we have

$$d_0\alpha^k + (d_1+d_2)\,\alpha^{k-1} + \ldots + \sum_{i=2^k-1}^{2^{k+1}-2} d_i = 0, \tag{1}$$

$$\Big(\sum_{i=2^{k+1}-1}^{2^{k+2}-2} d_i\Big) < \alpha, \ldots, \text{and } \Big(\sum_{i=2^{\lfloor \log_2 popsize \rfloor}}^{popsize-1} d_i\Big) < \alpha^{(\lfloor \log_2 popsize \rfloor - k)}. \tag{2}$$

From (1) and (2), we can obtain conditions (i) and (ii). This completes the proof. ■

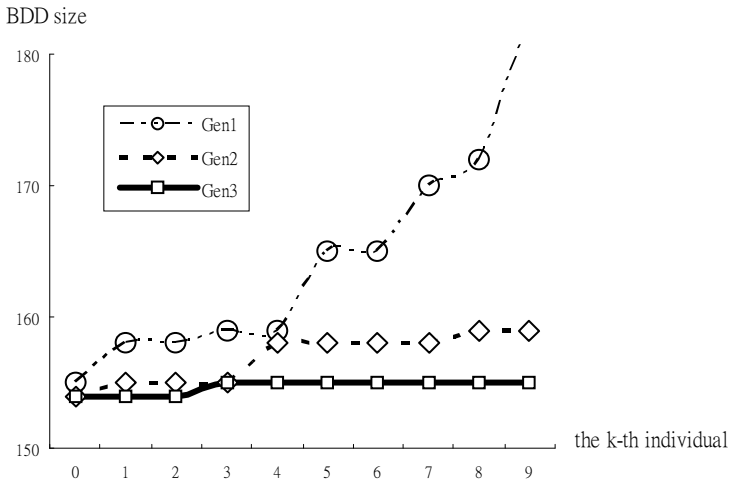


Fig. 4.10. The resultant BDD sizes for individuals in three successive generations for the benchmark circuit *alu2*. The sets of differences for generations 2 and 3 are D_2= {1,3,3,4,1,7,7,12,13,24} and D_3={0,1,1,0,3,3,3,3,4,4}, respectively.

Example 4.2. From Property 4.2, if *stable(α,1)* is chosen, then the termination criterion for EBEA will be (i) $d_0=0$, and (ii) $d_1+d_2<\alpha$, $d_3+d_4+d_5+d_6<\alpha^2$, …, $\sum_{i=2^k-1}^{2^{k+1}-2} d_i < \alpha^k$, …, and $\sum_{i=2^{\lfloor \log_2 popsize \rfloor}}^{popsize-1} d_i <\alpha^{\lfloor \log_2 \text{popsize} \rfloor}$. For example, Fig. 4.10 illustrates the resultant BDD sizes for individuals in three successive generations for the benchmark circuit *alu2*. Observe that the sets of differences for generations 2 and 3 are D_2={1, 3, 3, 4, 1, 7, 7, 12, 13, 24} and D_3={0, 1, 1, 0, 3, 3, 3, 3, 4, 4}, respectively. If stable(5,1)=1 is chosen, then EBEA stops at generation 3 and outputs the best size 154 since D_3 satisfies the termination criterion. ■

Example 4.3. If *stable(α,1/α)* is chosen for an EBEA, then the termination criterion would be more strict, that is, $\sum_{i=0}^{\text{popsize}-1} \frac{1}{\alpha^{\lfloor \log_2 (i+1) \rfloor}} d_i <1/\alpha$, which implies that it should also satisfy all the following conditions: (i) $d_0=d_1=d_2=0$, (ii) $d_3+d_4+d_5+d_6<\alpha$, …, $\sum_{i=2^k-1}^{2^{k+1}-2} d_i < \alpha^{k-1}$, …, and $\sum_{i=2^{\lfloor \log_2 \text{popsize} \rfloor}}^{\text{popsize}-1} d_i < \alpha^{\lfloor \log_2 \text{popsize} \rfloor -1}$. ■

We now summarize the important features of the proposed termination strategy.

- It can supervise not only the overall status of a population, but also the most important factor, i.e., whether d_i is equal to zero or not, for smaller i.
- It is very easy to implement since the stable function deals only with differences of the evaluated values, e.g., the BDD sizes, in each generation.
- It can be applied to any optimization problem if the selection strategy, which includes the techniques of *enlarged sampling space* and *deterministic sampling,* is used in the EA.
- Both computation and space requirements are only O(*popsize*). In implementation, we keep just an extra array with *popsize* elements to memorize the evaluated values for individuals of the preceding generation, and only additional O(*popsize*) operations are required to evaluate the function.

In Section 4.5, experimental results show that EBEA is feasible and effective for the BDD minimization problem, although it places more emphasis on *local exploitation* rather than *global exploration*. The following key features make EBEA robust for BDD minimization.

- The problem-specific heuristic, *Sifting*, is effective for finding locally optimal solutions (variable orderings).
- With the help of the additional SteepestEAV, EBEA can efficiently find further minimized solutions if any of them can be produced by an additional EAV. Notice that the results cannot be easily discovered by another independent run with the Sifting method.
- EBEA reduces the run time for redundant generations, since the *termination strategy* is able to supervise the degree of convergence.
- EBEA not only enforces "heredity factors of elites" passing on to the generations of offspring, but also efficiently explores the most promising area to obtain minimized results.

4.5 Distributed Model of EBEA (DEBEA)

In this section, we present the distributed model of EBEA, DEBEA, which is developed by an elaborate cooperation of components' EBEA. We have implemented DEBEA on a dedicated PC cluster which is located at the Graduate Institute of Computer Science and Information Engineering, National Taiwan Normal University. The hardware includes 8 *CPUs* (AMD Athlon MP 2200+), 8 *RAM boards* (each with 2G bytes), and a *switch hub* (1G bytes/sec communication rate). In addition, CUDD [Som01], Linux RedHat 7.3, gcc compiler, and MPICH are installed on the PC cluster. MPICH is a portable implementation of MPI, a standard for message-passing libraries for parallel processing. The sketch of DEBEA is shown in Fig. 4.11. We first introduce the migrations employed in DEBEA. Then, the termination criteria of DEBEA are developed.

```
void main( )
{ Initialization(deme);                          // randomly generate popsize individuals
  GeneticEngineering (deme);
  while ( StopFlag != true)                      // terminate if StopFlag=true
       {   stepping_stone_ migration( );         // perform stepping stone migration
           global_migration( );                  // perform global migration
           termination_judgment( );              // communication for termination criterion
           deme' = CrossOver(deme);              // perform crossover on the local deme
           GeneticEngineering(deme');            // perform Sifting and SteepestEAV
           deme = Selection(deme, deme');        // select the best popsize individuals from deme and
           UpdateCurrentOpt( );                    deme'
       }
}
void stepping_ stone migration( )
{   send (migrants, (MyRank+1)% p);              // send popsize/10 migrants to the neighboring node
    Immigrants =                                 // receive immigrants from the neighboring node;
    Receive (migrants, (MyRank-1) % p);            p: the number of demes in DEBEA
    Join(deme, Immigrants);                      // the new immigrants join with the local deme
}
void global_migration ( )
{   If ( MyRank != leaf_node )                   // if my node is a leaf of the tournament tree
         { InOpt = receive (InOpt, child_node);  // receive an individual InOpt from its child
           CurrentOpt = min(CurrentOpt, InOpt);  // update the CurrentOpt, if InOpt is better
         }
    If ( MyRank == root_node )                   // if my node is the root of the tournament tree
         broadcast (CurrentOpt);                 // the root broadcast the CurrentOpt
    Else send (CurrentOpt, parent_node);         // send the OurrentOpt to its parent node
}
void termination_judgment()
{   send(stable(α, κ), root_node);               // send stable status to the root node
    If (MyRank == root_node);                    // the root node gather status of each node
    { Termination[0 to k-1] = gather(stable(α, κ));
      If (all elements in Termination == 1)      // if all demes are stable
           broadcast(stopflag(true));            // broadcast the termination command
    }
    StopFlag = receive(stopflag, root_node);     // modify the StopFlag
}
```

Fig. 4.11. A sketch of DEBEA in each node.

4.5.1 Migrations

In DEBEA, each CPU node runs an EBEA for a semi-isolated population, called *deme*. Two types of migrations are produced for each deme, *stepping-stone* and *global* migrations. Both types of migrations are performed at every generation. A unidirectional *ring* network structure is

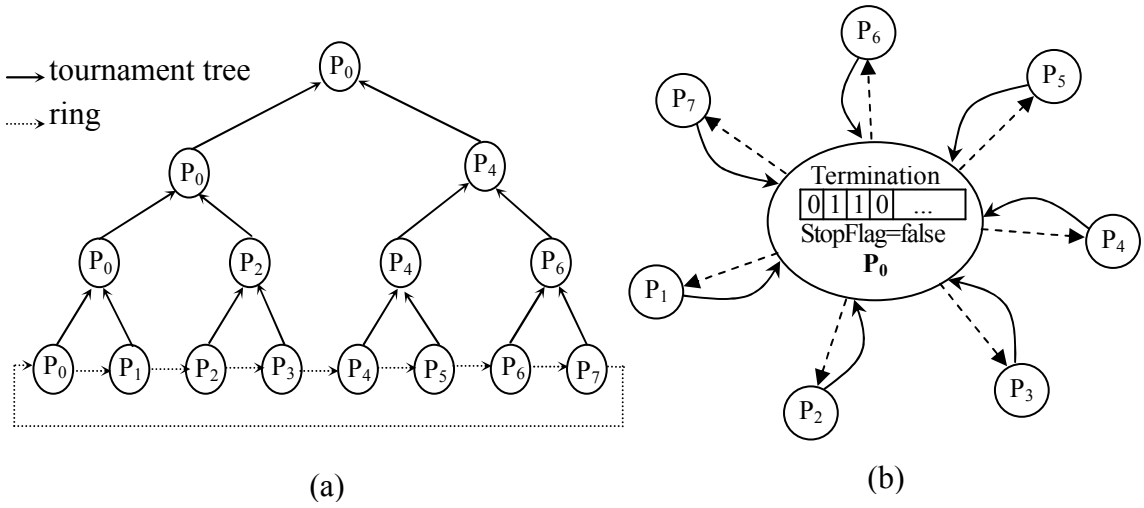


Fig.4.12. (a) The illustration of *ring* and *tournament tree* network structures for the migrations in DEBEA.
(b) The communication for termination criteria in DEBEA.

used in the stepping-stone migration, while both *tournament tree* and *star* network structures are used in the global migration. Fig. 4.12(a) illustrates the *ring* and *tournament tree* network structures for the migrations in DEBEA.

In the stepping-stone migration, each EBEA randomly selects *popsize*/10 individuals to migrate to its neighboring node in the ring network. Each node put the immigrations into a pool, which then includes the old individuals, offspring and the immigrations. The EBEA selects the best *popsize* individuals from among all individuals in the pool for propagation.

The global migration consists of two phases, *collecting* and *broadcasting*. In the collecting phase, a *tournament tree* connection is used in order to balance the load of both computation and communication. DEBEA collects the best individual from the leaves to the root through the tournament tree. Each leaf of the tournament tree sends the best individual in its deme to its parent node. Each internal node receives a migration, compares it with the best of its own population, and then sends the better of them to its parent node. Finally, the root *broadcasts* the best individual to each node and then the best individual joins the deme in each EBEA.

4.5.2 Termination

As shown in Fig. 4.12(b), the *termination criteria* adopted in DEBEA requires global convergence, i.e., each local EBEA runs independently until all EBEAs of the system are stable. The *stable function* introduced in Section 4.4.3 is used as a termination criterion in DEBEA. A *root* node keeps a *termination array* to collect the current value of the stable function from each node. If all the values are equal to 1, then the root broadcasts a *termination command, StopFlag=true,* to all other nodes. If any EBEA receives the command, then it outputs the best solution and stops.

Features of DEABE can be summarized as follows:

- All the network configurations employed in DEBEA can be easily and efficiently implemented on *the PC cluster.*
- Asynchronous communications are used for all communications in DEBEA for efficiency.
- The total number of messages passed is O(p) for each generation, including migrations and termination judgments, where p is the number of CPU nodes used.

4.6 Experimental Results

In this section we describe the experimental results that have been carried out on a *SUN Ultra 1* and a dedicated *PC-cluster* for EBEA and DEBEA, respectively. The algorithms have been integrated with the CUDD package [Som01a, Som01b]. We perform two series of experiments as described in the following subsections. For EBEA, only two parameters are required in the experiments, namely, the *stable function* and the *population size*.

4.6.1 Performance of EBEA

In the first series of experiments, we compare the results of EBEA with those of the latest published BDD minimization algorithms, *Scatter search* [Hun02] and *Exact algorithm* [Dre00]. The results are shown in Table 4.1. Our program is implemented in C on a Sun Ultra 1 with 64 Mbytes memory. This is the same machine but with smaller capacity of memory than that used in

the experiments [Hun02], in which 300 Mbytes memory is used. The data given in the columns *Scatter* and *Exact* of Table 4.1 is directly transcribed from their experimental results. For all circuits, *popsize* is set to be n/4 for the experiments, where n is the number of input variables. Also, we perform ten independent runs and choose *stable(5,1)=1* as the termination criterion. The columns *Min #* and *Max #* show the minimum and maximum results of BDD size among ten runs. The column *No. Opt* shows the number of runs that yield the optimal result. The two rightmost columns show the average and the maximum run times of our EBEA required for the ten runs.

Table 4.1. *EBEA* compared with *scatter search* [Hun02] and *exact algorithm* [Dre00], where parameter setting for EBEA is: popsize=n/4 and termination criterion is satisfied if *stable(5,1)*=1. The columns *Min #* and *Max #* show the maximum and minimum results of BDD size among ten runs. The column *No. Opt* shows the number of runs that obtain the optimal result. The two rightmost columns show the average and the maximum run time of our EBEA required for the ten runs.

Circuit	Inputs	Outputs: # of BDD Nodes					CPU Run Time (Seconds)			
		Exact	Scatter	EBEA			Exact	Scatter	EBEA	
				Min #	Max #	No. Opt			Average	Max
alu4	14	350	564	350	355	6	163.0	23.30	5.69	8.74
cc	21	46	46	46	46	10	753.3	5.47	4.66	6.47
cm150a	21	33	33	33	33	10	3858.8	10.96	3.20	4.32
cm162a	14	30	30	30	31	9	4.2	4.07	2.88	3.48
cm163a	16	26	26	26	26	10	7.7	3.71	2.34	2.63
cmb	16	28	28	28	28	10	0.1	5.16	1.84	1.88
comp	32	95	103	95	98	9	47605.4	151.64	8.18	9.98
cordic	23	42	42	42	42	10	23.8	14.22	6.23	8.55
cps	24	971	971	971	974	8	46130.4	56.35	17.03	24.96
cu	14	32	32	32	32	10	6.5	3.94	2.27	2.68
i1	25	36	36	36	36	10	198.7	7.48	3.54	3.94
lal	26	67	67	67	67	10	4595.4	8.13	3.97	4.32
mux	21	33	33	33	33	10	3872.7	10.15	3.00	3.10
parity	16	17	17	17	17	10	0.1	7.59	1.73	1.78
pcle	19	42	42	42	42	10	60.1	5.64	2.30	2.76
pm1	16	40	40	40	40	10	3.8	3.38	2.31	2.65
s1488	14	369	384	369	381	4	90.0	15.12	5.67	9.26
s344	24	104	104	104	104	10	11519.2	9.72	6.09	9.97
s349	24	104	104	104	104	10	11546.3	9.84	5.41	7.20
s382	24	119	119	119	121	5	6637.6	9.96	5.70	8.65
s400	24	119	119	119	121	5	6846.8	9.98	6.31	8.66
s444	24	119	119	119	121	6	6934.0	8.30	5.47	8.71
s526	24	113	113	113	113	10	8809.1	11.55	5.70	7.61
s820	23	220	266	220	221	3	17145.3	21.72	6.90	8.96
s832	23	220	274	220	221	5	17953.8	21.11	7.44	9.08
sct	19	48	48	48	48	10	60.6	6.22	3.13	3.66
t481	16	21	21	21	21	10	1.2	4.17	7.02	9.37
tcon	17	25	25	25	25	10	3.7	1.15	1.76	1.81
ttt2	24	107	107	107	108	9	7087.2	11.07	5.37	7.34
vda	17	478	478	478	488	6	641.6	21.87	6.23	8.79

Although the Exact algorithm can always get the exact minimum size, its run time explodes as the number of input variables increases. Scatter search could not find the optimal variable order in 5 of 30 benchmark circuits that are manageable by the Exact algorithm. On the other hand, EBEA performs more efficiently and effectively for BDD minimization.

We see that EBEA is able to find the optimal variable orders with very high probability. As shown in Table 4.1 for EBEA, all the optimal orders are found in ten runs; Furthermore, among 30 circuits, 19 circuits achieved the optimal order in each of the 10 runs. The remaining 11 circuits can still get the optimal order in some of the 10 runs. For the example of circuit *comp*, EBEA finds the optimal order, with the optimal size 95 (=*Min #*), in 9 (=*No. Opt*) of 10 runs. The only one remaining run finds a *nonoptimal* size 98 (=*Max #*), which is still smaller than 103 found by Scatter search.

For run time, EBEA can efficiently find a better solution and can outperform other algorithms in most cases. For tests with popsize=n/4, all the tests are completed *within* 10 seconds, except for the benchmark *cps* with 24.96 seconds. For Scatter search, however, its run time for 12 of 30 circuits is longer than 10 seconds. It takes 151.64 seconds for the benchmark *comp* and 56.35 seconds for the benchmark *cps*.

To compare the tradeoff between run time and quality, we also change the *popsize* parameter to observe the impact in the resultant BDD size. Table 4.2 shows the experimental results for popsize=n/2. Although it takes about twice the run time, it not only increases the probability of finding the optimal solution, but also makes the *near-optimal* solutions close to the exact one.

Table 4.2. *EBEA* compared with *scatter search* [Hun02] and *exact algorithm* [Dre00], where parameter setting for EBEA is: ***popsize*=n/2** and termination criterion is satisfied if ***stable(5,1)*=1**.

Circuit	Inputs	Outputs: # of BDD Nodes					CPU Run Time (Seconds)			
		Exact	Scatter	EBEA			Exact	Scatter	EBEA	
				Min #	Max #	No. Opt			Average	Max
alu4	14	350	564	350	355	7	163.0	23.30	11.10	19.90
cc	21	46	46	46	46	10	753.3	5.47	7.03	8.52
cm150a	21	33	33	33	33	10	3858.8	10.96	5.35	7.34
cm162a	14	30	30	30	31	10	4.2	4.07	5.04	5.12
cm163a	16	26	26	26	26	10	7.7	3.71	4.49	4.99
cmb	16	28	28	28	28	10	0.1	5.16	3.41	3.45
comp	32	95	103	95	95	10	47605.4	151.64	15.32	15.55
cordic	23	42	42	42	42	10	23.8	14.22	9.58	14.21
cps	24	971	971	971	973	9	46130.4	56.35	30.80	41.72
cu	14	32	32	32	32	10	6.5	3.94	4.13	5.15
i1	25	36	36	36	36	10	198.7	7.48	7.09	7.62
lal	26	67	67	67	67	10	4595.4	8.13	9.57	9.60
mux	21	33	33	33	33	10	3872.7	10.15	5.05	7.34
parity	16	17	17	17	17	10	0.1	7.59	3.25	3.33
pcle	19	42	42	42	42	10	60.1	5.64	5.16	6.45
pm1	16	40	40	40	40	10	3.8	3.38	3.74	5.05
s1488	14	369	384	369	374	6	90.0	15.12	11.65	20.88
s344	24	104	104	104	104	10	11519.2	9.72	10.31	14.16
s349	24	104	104	104	104	10	11546.3	9.84	9.76	14.10
s382	24	119	119	119	121	8	6637.6	9.96	10.61	11.49
s400	24	119	119	119	121	7	6846.8	9.98	10.33	14.24
s444	24	119	119	119	121	8	6934.0	8.30	10.99	11.61
s526	24	113	113	113	113	10	8809.1	11.55	10.53	14.96
s820	23	220	266	220	221	6	17145.3	21.72	13.53	17.49
s832	23	220	274	220	221	7	17953.8	21.11	13.53	17.59
sct	19	48	48	48	48	10	60.6	6.22	6.82	8.77
t481	16	21	21	21	21	10	1.2	4.17	13.90	18.86
tcon	17	25	25	25	25	10	3.7	1.15	3.30	3.36
ttt2	24	107	107	107	107	10	7087.2	11.07	10.22	11.68
vda	17	478	478	478	483	7	641.6	21.87	12.72	16.45

4.6.2 Performance of DEBEA

In the second series of experiments, we compare the performance of DEBEA with that of EBEA in terms of the ability to achieve the same target *solution quality.* DEBEA and EBEA are applied to 10 large circuits in the LGSynth91. We give a target, goal size, to each of the benchmark circuits. The parameter setting for this experiment is *popsize*=n and the termination criterion is set to *stable(5,1/5)*=1. There are eight CPUs cooperating in a PC cluster for DEBEA. If the algorithm discovers the goal size, then it stops and reports the result. If it has already satisfied the termination criterion but the goal size has still not been found, the algorithm stops and starts another independent run.

Table 4.3. A comparison of run time for EBEA and DEBEA to find advanced results for larger benchmarks. *Goal_Size* is the size for each circuit that the algorithm has to discover; Given_Size is the best size we had discovered before the experiment. The *Speedup* column shows the speedup factors achieved by DEBEA with 8 CPUs compared to EBEA. The column *inputs* shows the number of input variables for each benchmark circuit. We test the run time for 10 benchmarks in three Goal_sizes, the Given_Size and two relaxed sizes, Given_Size×1.005 and Given_Size ×1.01.

Circuit	inputs	Given_ Size	Goal_Size								
			Given_Size×1.01			Given_Size× 1.005			Given_Size × 1		
			EBEA	DEBEA	Speedup	EBEA	DEBEA	Speedup	EBEA	DEBEA	Speedup
bigkey	486	1565	345.98	319.13	1.08	346.02	319.95	1.08	345.63	314.89	1.10
C432	36	1064	332.38	29.26	11.36	370.64	31.99	11.59	2802.53	33.56	**83.51**
C499	41	25866	594.18	578.86	1.03	725.41	583.25	1.24	2150.77	620.35	3.47
C5315	178	1721	628.50	713.74	0.88	1198.51	1001.14	1.20	20260.34	2938.17	6.90
C7552	207	2167	165964.80	63059.88	2.63	349160.45	65468.05	5.33	504368.16	67763.85	7.44
des	256	2881	4179.97	1569.17	2.66	12806.36	1979.71	6.47	76919.39	2826.00	**27.22**
pair	173	2368	4140.85	1148.31	3.61	5770.04	1519.99	3.80	16474.15	2093.27	7.87
rot	135	2690	5067.45	1289.52	3.93	**5356.09**	1268.30	4.22	**47520.30**	1300.41	**36.54**
s5378	199	1857	874.45	924.26	0.95	3167.53	766.09	4.13	4638.67	1097.37	4.23
sbc	68	903	12.94	7.16	1.81	23.01	15.62	1.47	680.99	48.65	**14.00**

In Table 4.3, *Goal_Size* is the size for each circuit that the algorithm has to discover; Given_Size is the best size we had discovered before the experiments. The *Speedup* column shows the speedup factors achieved by DEBEA with 8 CPUs compared to EBEA. The *inputs* column shows the number of input variables for each benchmark circuit. We test the run time for 10 benchmarks in three Goal-Sizes, i.e., the Given_Size and two relaxed sizes, Given_Size× 1.005 and Given_Size×1.01.

In general, the smaller Goal_Size the longer the time required to achieve it for both EBEA and DEBEA. In some cases for EBEA, the run time increases dramatically as the GoalSize decreases. For the example of the circuit *rot* with *Given_Size=2690*, the run time for EBEA increases form 5356.09 to 47520.30 seconds as we decrease the Goal_Size from 2704 (=Given_Size×1.005) to 2690 (=Given_Size×1). However, in the same situation the run time for DEBEA increases modestly, from 1268.30 to 1300.41 seconds. It is important to note that there exists an *acceleration anomaly* [Enr02, Kum94] in this experiment. For the circuits, *C342*, *des*, *rot*, and *sbc*, whose Given_Sizes are not easily discovered, the speedups are 83.51, 27.22, 36.54

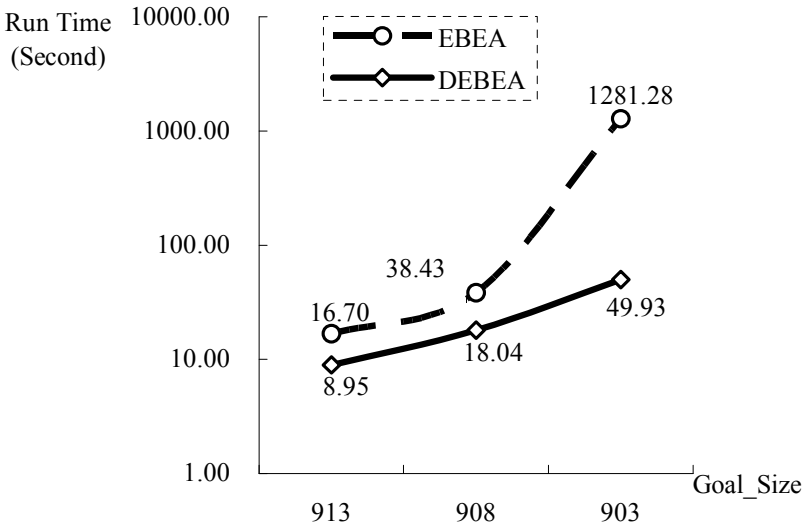


Fig. 4.13. The average run time of 10 runs for the benchmark circuit *sbc*. Notice that the y-axis is drawn with a logarithmic scale. The average speedups are 1.87, 2.13, and 25.66 for the experiments with goal sizes 913, 908, and 903, respectively.

and 14, respectively, for the tests with Goal_Size=Given_Size×1. These speedups are all greater than 8, which is the number of processors used to perform DEBEA.

To further verify the *acceleration anomaly*, we choose the benchmark circuit *sbc* and do the same experiment 10 times. The average run time for 10 runs is given in Fig. 4.13. Notice that the y-axis is drawn with a logarithmic scale. The average speedups are 1.87, 2.13, and *25.66* for the experiments with Goal_Sizes of 913, 908, and 903, respectively. DEBEA consistently achieves a superlinear speedup for the experiment with Goal_Size=903. This shows that DEBEA has a great ability to find more superior results for some *hard* circuits.

The reasons for acceleration anomaly have been well studied in [Alb02]. The authors conclude the sources for the anomaly as follows:

- the higher chances of finding an optimum by using more processors, due to the intrinsically heuristic multipoint nature of parallel evolutionary algorithms;
- splitting the global large population into smaller subpopulations that fit into the processor caches provides faster algorithms than using a single main memory;
- the operators work on much smaller data structure, and they do so in parallel, which is an additional source of speedup.

4.7 Conclusions of This Chapter

In this study, we have presented a powerful model for BDD minimization, an elitism-based evolutionary algorithm *EBEA* and its distributed model *EBDEA*. The experimental results demonstrate the robustness of our algorithms in comparison with *Scatter search* [Hun02] and the *Exact* algorithm [Dre00]. We not only efficiently find all the exact optimal variable orders for the circuits that are manageable by the Exact algorithm, but also discover best-ever results for almost all larger benchmark circuits in LGSynth91. A *stable function* is used for termination criterion to reduce the computation time for the redundant generations. Furthermore, taking advantage of the cooperation of demes' EBEA as well as the flexible reconfiguration and high communication rate of PC-cluster, super-linear performance is achieved by DEBEA in terms of the ability to find the minimized results that are not easily discovered by EBEA.

We conclude this chapter with some comparisons of BDD minimization algorithms. *Exact minimization algorithms* [Dre00] are not too practical because of their time and space complexity. The heuristic algorithm [Dre01] generates a result speedily, but most of the results are not good enough. *Scatter search* [Hun02] offers a reasonable compromise between the quality and time, but even for small circuits it could not efficiently find the optimal results. EBEA is able to supervise the degree of convergence of a population. This not only helps reduce redundant search, but also provides the ability to find the desired quality of solutions. DEBEA is an appropriate method for obtaining *solutions approaching the exact minimization of BDDs*. Using DEBEA, advanced results can be derived within a reasonable run time, even for large-scale functions. Experimental results show that the proposed algorithms improve on all the previously best-known results in the literature. Table 4.4 lists the best BDD size found by DEBEA comparing to the previously published best-known sizes for benchmark circuits with greater than 32 variables in the LGSynth91. Our results can be seen as a new "lower bound" on the BDD size. This can serve as a *benchmark* to evaluate the quality of other approaches. We hope that the algorithms and termination strategy proposed in this study will be helpful to solve other related

optimization problem in the future.

Table 4.4. The best BDD sizes found by DEBEA compared to previously published best-known sizes for benchmark circuits with greater than 32 variables in the LGSynth91. Note that DEBEA is able to obtain the best results for all circuits. The previously best-known results improved by DEBEA are highlighted in **bold** type.

Circuit	Inputs	DEBEA	[Lin01]	[Hun02]	[Dre97]	Circuit	Inputs	DEBEA	[Lin01]	[Hun02]	[Dre97]
apex6	135	490	490	492	490	**mm30a**	**123**	**11065**	**11504**	-	-
apex7	49	214	214	-	-	mm9a	39	1111	1111	-	-
b9	41	97	97	-	-	mm9b	38	1527	1527	-	-
bigkey	486	1565	1565	-	-	**mult16a**	**33**	**111**	**116**	-	-
C1355	41	25866	25866	25866	25866	mult16b	47	93	93	-	-
C1908	33	5526	5705	5526	5526	**mult32a**	**65**	**223**	**235**	-	-
C2670	**233**	**1782**	**1784**	**1846**	**2888**	my_adder	33	82	82	-	-
C3540	50	23828	23828	23829	23828	**pair**	**173**	**2331**	**2370**	**2439**	-
C432	36	1064	1132	-	1064	**rot**	**135**	**2620**	**2837**	**2773**	-
C499	41	25866	25866	25974	25866	**s13207.1**	**700**	**2908**	**-**	**-**	-
C5315	**178**	**1721**	**1744**	**1856**	**1727**	s1423	91	1677	1677	-	-
C7552	**207**	**2107**	**5249**	**4395**	**2284**	**s15850.1**	**611**	**9974**	-	-	-
C880	60	4053	4053	4053	4053	**s38417**	**1664**	**155827**	-	**158909**	-
cht	47	90	90	-	-	**s38584.1**	**1464**	**12822**	-	-	-
clma	415	725	725	-	-	s420.1	34	81	81	-	-
clmb	415	561	561	-	-	**s5378**	**199**	**1848**	**1873**	**1955**	-
count	35	81	81	-	-	s641	54	381	381	-	-
dalu	75	689	689	689	-	s713	54	381	381	-	-
des	**256**	**2881**	**2928**	**2934**	**-**	s838.1	66	161	161	-	-
dsip	452	2456	2456	-	-	**s9234.1**	**247**	**2524**	**2560**	-	-
example2	85	265	265	-	-	**sbc**	**68**	**903**	**904**	-	-
frg2	**143**	**846**	**849**	**854**	**-**	too_large	38	302	302	302	302
i4	**192**	**193**	**-**	**195**	**-**	unreg	36	82	82	-	-
i8	133	1276	1276	1276	1276	**x1**	**51**	**398**	**399**	**406**	-
i9	88	908	908	-	-	x3	135	490	490	491	-
k2	45	1243	1243	-	-	x4	94	320	320	321	-