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**Faculty of Sciences**  
**Scientific Studies and Research**  
**Series Mathematics and Informatics**  
**Vol. 19 (2009), No. 2, 241 - 256**

**NEW HYBRID GENETIC ALGORITHM WITH ADAPTIVE  
OPERATORS AND VARIABILITY TARGET FOR OPTIMIZING  
VARIABLE ORDER IN OBDD**

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**Abstract.** Reduced Ordered Binary Decision Diagrams are one of the most powerful data structure for boolean manipulation on switching functions as top process in digital circuits design. The size of ROBDDs is very sensitive to the ordering choices of input variables. A new genetic algorithm is described for optimizing the variable order. It uses adaptive operators and includes a mechanism based on information energy for controlling the variability of the population. Experimental investigations of the performance of this genetic algorithm are described.

1. INTRODUCTION

The OBDD size is given by the number of its nonterminal nodes. A smaller number of nodes imply a smaller circuit design, whereas a bad ordering can lead to an exponential growth in the size of OBDD.

The existing variable ordering methods [10, 12, 18] include static variable ordering techniques and dynamic variable ordering techniques. Most of static techniques are used to determine good initial variable orders before constructing the OBDD of a function and they are usually based on a breadth-first or depth-first traversal of a circuit [11, 13] from its outputs to inputs. Dynamic techniques are based on a process of improving the variable order and the size of an already built OBDD [4, 19, 22]. The Rudell's sifting algorithm and window permutation algorithm [21, 24] are the most popular dynamic techniques.

In experimental studies, it turned out that methods based on genetic algorithms yield better results than other techniques. Even the runtime for genetic reordering algorithms were brought down to a reasonable level, they are still not competitive to deterministic reordering heuristics like window permutation or sifting [16].

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**Keywords and phrases:** BDD, OBDD Optimisation, GA

**(2000) Mathematics Subject Classification:** 06E30, 94C10, 68W35

Genetic algorithms in finding the best ordering were first introduced in [7] where the main genetic operations are PMX (partially-mapped crossover) and mutation. Simulated annealing used in [1] is a related approach. These two methods yield better results than other techniques, but they are comparably slow (see e.g.[24]) as any other GA based method. In order to speed up the computations, other approaches have been suggested [8, 23] which include treating of sifting as a genetic operation that replaces crossover techniques or advanced tricks for setting the parameters.

Recent research [5, 6, 9] have shown that parallel or distributed genetic algorithms are a feasible way to solve the problem of the best ordering, but the cost of fitness evaluation remain an expensive task which affects the global cost of solution even such algorithms benefits from asynchronous behavior or from the independence of the processes.

This paper focuses on the purely part of genetic reordering algorithms in order to improve the solutions quality. The proposed GA uses three mutation operators and three crossover operators that are applied with given probability distribution. The sifting heuristic method [22] is grafted on the GA, being embedded in a so-called hypermutation operator. Another contribution is a formal framework to increase the quality of solutions by using adaptive operators and a mechanism based on information energy [20] for controlling the population variability. Experimental results prove that using a strategy to modify the probabilities of genetic operators according to prescribed variability policy and adapting the amount of changes produced by these operators to evaluation stages improve OBDD size. Section II treats the importance of variable ordering in OBDDs, section III describes the proposed hybrid genetic algorithm and the formal framework for adapting operators and their application to increase the solutions quality. Section IV presents the experimental results and last section summarizes the work.

## 2. THE IMPORTANCE OF VARIABLE ORDERING IN OBDD

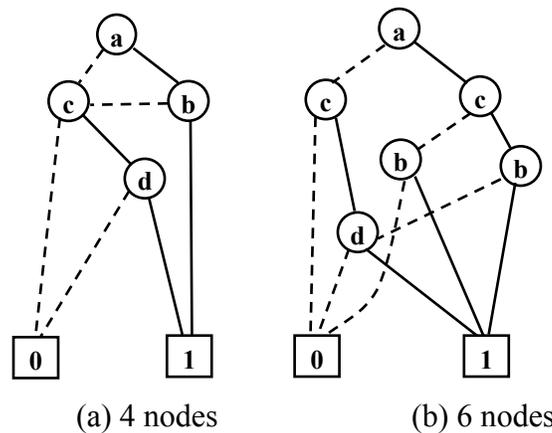
OBDDs have numerous applications- e.g. in formal verification of digital circuits and other finite state systems- have been found and manipulation algorithms or BDD derived data types have improved time and memory performance [4].

Let  $f : B^n \rightarrow B^m$ ,  $B = \{0,1\}$  be a switching function and  $\pi$ - a total order on a fixed set of boolean variables  $x_1, x_2, \dots, x_n$ . An OBDD with respect to order  $\pi$  is a single rooted direct acyclic graph that satisfies the following properties [3]:

- a) there are exactly two terminal nodes labeled by boolean constants 0 and 1, respectively.
- b) each non-terminal node is labeled by a variable  $x_i$ , and has two outgoing edges, called 0-edge and 1-edge. In each inner node, two subfunctions are usually computed according to Shannon decomposition [18].
- c) the order in which the variables appear on a path in the graph is consistent with the variable order  $\pi$ .
- d) further reduction rules could be applied [3] to obtain a canonical representation for  $f$ , a so-called reduced (R)OBDD. Usually, the widely used term OBDD (or simply BDD) refers to a ROBDD.

In the problem of optimizing the variable order in OBDD's, a boolean function  $f$  which describes a digital circuit is represented as a reduced OBDD.

OBDDs share some bad properties with all kinds of switching functions representations: the size of OBDDs strongly depends on the order of input variables (figure 1) and can vary from linear to exponential. The process of improving the variable ordering in OBDDs is a NP- complete problem [2].



**Fig. 1.** The influence of the variable ordering for  $f(a,b,c,d)=a \cdot b \cdot c \cdot d$  with order  $a, b, c, d$  (a) and order  $a, c, b, d$  (b); 0- edges are dashed.

Another critical aspect is related to large amount of memory or computing time consumption needed by the algorithm for optimizing the circuit in case of certain complex functions. There are a variety of methods to find the optimal variable ordering for BDDs but none can fulfill both time and space requirements of the circuit.

The variable reordering problem of OBDDs is a typical combinatorial problem with a huge search space of possible solutions. If an OBDD for a function  $f$  and a variable ordering  $\pi$  is needed, we don't have an efficient procedure to compute the size estimation of OBDD for a certain  $f$ , so we have to construct the OBDD. This can be efficiently done merely in the case when

the size of the resulting OBDD is polynomially related to the size of the initial OBDD [19]. Hereby, heuristics that choose several candidates for a “good” ordering cannot avoid the construction of the OBDDs for their evaluation.

Fortunately, for most functions in real-life applications, we can find a variable order that keeps the size of the corresponding OBDD tractable. Hence, for most practical applications, OBDD are efficient for manipulating switching functions.

In this approach, six genetic operators are used: three for mutation and three for crossover, which include a variant of the alternative crossover [16]. In addition, a GA’s hybridization technique is proposed by using a partial application of sifting [22] as a regular hypermutation operator. Adaptive operators and a strategy to adjust the probabilities of genetic operators according to a variability target in order to improve OBDD size are proposed.

### 3. A GENETIC ALGORITHM FOR THE VARIABLE ORDERING PROBLEM

Further, the main components of the proposed GA are summarized.

The GA’s main directions of improvement the OBDD size are: (i) more operators are applied with given probability distribution, three for mutation and three for crossover. (ii) sifting technique is grafted on the GA by a hypermutation operator and (iii) the use of a control mechanism based on information energy [20] in order to adapt the population variability.

**III.1. Solution representation.** Each individual represents a specific OBDD variable order in permutation form [15] assuming the initial variables input order is the natural one. Every gene represents one input variable by an integer value in range  $[1, n]$ , without duplicates, according to the position of the variable in the stated order.

**III.2. Initial population.** Initial population  $P$  is randomly generated. Additionally, the individual obtained by applying sifting for identical permutation  $1, 2, \dots, n$  is also included. Population size is empirically indicated in table 1.

n	<20	21-200	201-300	301-400	>400
Popsiz	50	60	75	90	120

**Table 1.** Population size.

*Survival selection.* The selection is deterministic and elitist [14]. At the end of each stage current population competes with the new individuals and those with better fitness survives in the limit of  $|P|$  for the next stage.

*Stop condition.* Algorithm stops if the variation of the ratio  $[\phi_m(k) - \phi_m(k-1)] / \phi_m(k) < tol$ , where  $\phi_m(k)$  is the average of the fitnesses

at stage  $k$ ,  $tol$  is a prescribed tolerance, and no further improvement for average fitness is observed for a fixed  $n_{add}$  number of iterations.

**III.3. Fitness function.** The fitness function computes for each chromosome its number of nodes in the corresponding OBDD. Fitness is computed by using *Nanotrav* tool included in CUDD package [24].

#### III.4. Mutation.

*Operators.* Three mutation operators are used: simple mutation (mutual exchange which means the exchange of the positions of two randomly selected genes), group mutation- a group of genes is moved from one position to another (group length, first and last position- chosen randomly) and inversion- in which two cutpoints are randomly selected and the ordering in the enclosed segment is reversed.

*Adaptive operators.* As the algorithm converges, the disruption needs to be small in order to preserve good schemata. In order to apply less disruptive mutation we have to control the cutting segment length for each mutation type. A big enough cutting segment gives a more different individual, which is to prefer in early stages of the algorithm. Thus, the length of the cutting segment is controlled by a linear decreasing function: it decreases from  $1/3$  of the input length at the first iteration to 1 when the number of iterations reached  $it\_max$  (1).

$$f(t) = at + b, f(0) = nrvar / 3, f(it\_max) = 1. \quad (1)$$

where  $it\_max$  is an estimation of maximum number of iterations and  $nrvar = \text{input length} = \text{chromosome length}$ .

*Selection and application.* A randomly chosen individual from population bears mutation with probability  $p_m$ . If a mutation operation is decided, one of the three mutation operators is randomly selected according to a given probability distribution. This probability distribution remains fixed over the whole evolution process.

#### III.5. Crossover.

*Operators.* The algorithm uses three crossover operators. *Partially matched crossover* (PMX) [14] selects a matching section between two cutpoints and uses exchange operations to make first parent's matching section assimilate the second ones. The second is *order crossover* (OX) in which every element between two randomly selected cutpoints is copied from the first parent, and the elements outside the cutpoints are filled with the missing genes from the other parent, preserving its order [14]. The third crossover operator is a variant of *alternating crossover* [16] but instead of taking one gene alternately from each parent (more disruptive), a group of genes is used.

*Adaptive operators.* In order to encourage the growth of the constructive blocks, their formation and preservation as the evolution advances, the distance between the cutting points is adapted to the number of iterations. The length of the cutting segment (matching section for PMX) for all crossover types is controlled by a linear decreasing function. This length also, will decrease with the number of generations from one third of the chromosome length at the beginning to 1 when  $it\_max$  is reached (1).

*Selection and application.* The matting pool is given by the first 50% most efficient individuals. One individual is chosen for crossover with probability  $p_c$ . Its mate is randomly chosen also from the matting pool. For each pair of parents one of the three crossover operators is applied according to a given distribution probability which remains constant over the entire evolution.

**III.6. Hypermutation.** The main function of hypermutation is to graft sifting heuristics on the GA. One arbitrary chosen individual from population bears hypermutation with probability  $p_H$  which remains constant during the evolution process. When hypermutation is applied to an individual, two randomly cutpoints that forms a segment are chosen. Swap steps are restricted to the genes within the segment, the best position that gives the minimum number of nodes for one arbitrary chosen gene is kept, and a new individual is generated. An adaptive mechanism is applied for hypermutation, too. The length of the segment is also adapted to the number of iterations: it is equal to 15% of the chromosome length at iteration 1 and decreases up to 5% when  $it\_max$  is reached.

### III.7. Tuning the genetic operator's application.

Another mechanism to improve performance of the proposed GA is to use a variability policy in order to find the best strategy for applying genetic operators. The variability of population generally decreases as the algorithm converges and the interval between the best and the worst fitness shrinks.

Let  $P$  be the current population of  $x_1, x_2, \dots, x_m$  chromosomes at the beginning of a given evolution stage. For each chromosome its fitness  $fit(x_i)$ ,  $i = 1, \dots, m$ , is computed.

Since the first iteration, best and worst fitness are computed for each population, after evaluation step:  $f_m = \min\{fit(x_i) / i = 1, \dots, m\}$

and  $f_M = \max\{fit(x_i) / i = 1, \dots, m\}$ .

The interval  $[f_m, f_M]$  is divided in  $p$  equal lengths subintervals  $I_k$ , where  $k=1, \dots, p$ ,  $p \approx |P|/10$ .

Let  $F_k$  be the number of fitness values which belong to  $I_k$ ,  $k=1 \dots p$  and  $F'_k = F_k / |P|$ . Obviously,  $\sum_{k=1}^p F'_k = 1$ .

The “energy” of the current population [20] is defined as:

$$E_c = \sqrt{\sum_{k=1}^p (F'_k)^2} . \tag{2}$$

It gives a measure of population variability. It holds:  $1/\sqrt{p} \leq E_c \leq 1$ .

Thus, a small  $E_c$  indicates a high variability and this should be associated with the beginning of the algorithm evolution and a high  $E_c$  indicates a small variability recommended being at the end of the run.

In order to find an appropriate policy to vary the probabilities for operators application four types of variability target functions  $E_{ob}$  are considered, each depending on the number of iterations  $t$  (except first):

a. constant:

$$E_{ob} = B \in [1/\sqrt{p}, 1]. \tag{3}$$

b. linear increasing:

$$E_{ob}(t) = at + b, E_{ob}(t) = 1/\sqrt{p}, f(it\_max) = 1. \tag{4}$$

c. periodic:

$$E_{ob} = (A_1 - A_2) |\cos \omega t| + A_2, \quad 1/\sqrt{p} \leq A_2 < A_1 \leq 1, \quad \omega = 2, 3, \dots \tag{5}$$

d. exponential periodic:

$$E_{ob}(t) = e^{-\lambda/t} |\cos \omega t|, \text{ with } \lambda = 1/2 \ln p . \tag{6}$$

Let  $\lambda = (E_{ob} - E_c)/T$  be an adjustment parameter, where  $T= 2, 3, \dots$  is also a parameter. Parameter  $\lambda$  adjusts the speed wherewith the target value  $E_{ob}$  is reached by the current value of the information energy  $E_c$ .

The probabilities for mutation and crossover are adjusted using the equations:

$$\begin{aligned} p_m &= p_m - \alpha \lambda \\ p_c &= p_c + \beta \lambda, \end{aligned} \tag{7}$$

where  $\alpha, \beta \in [0, 1]$ . Those  $p_m$  and  $p_c$  values which exceed 0 or 1 are forced to 0 or 1, respectively.

Consider  $E_{ob}$  a generic target of variability. The way to adapt  $p_m$  and  $p_c$  is given by the rules (7): remark that if current energy  $E_c < E_{ob}$ , then  $\lambda > 0$  so  $p_c$  is growing and  $p_m$  is decreasing in order to lower the variability. If current

energy  $E_c > E_{ob}$ , then  $\lambda < 0$  and, as a result, a lower  $p_c$  and a higher  $p_m$  are obtained, which will increase variability.

#### 4. PERFORMANCE EVALUATION

In experiments a subset of LGSynth91 benchmarks is used, obtainable from [25]. For OBDD manipulation the package used was CUDD [24]. The experiments were conducted on a Dual Core system, with 2,4 GHz processors, 2G RAM available memory and Linux. Number of runs per circuit test was 10 for each type of experiment.

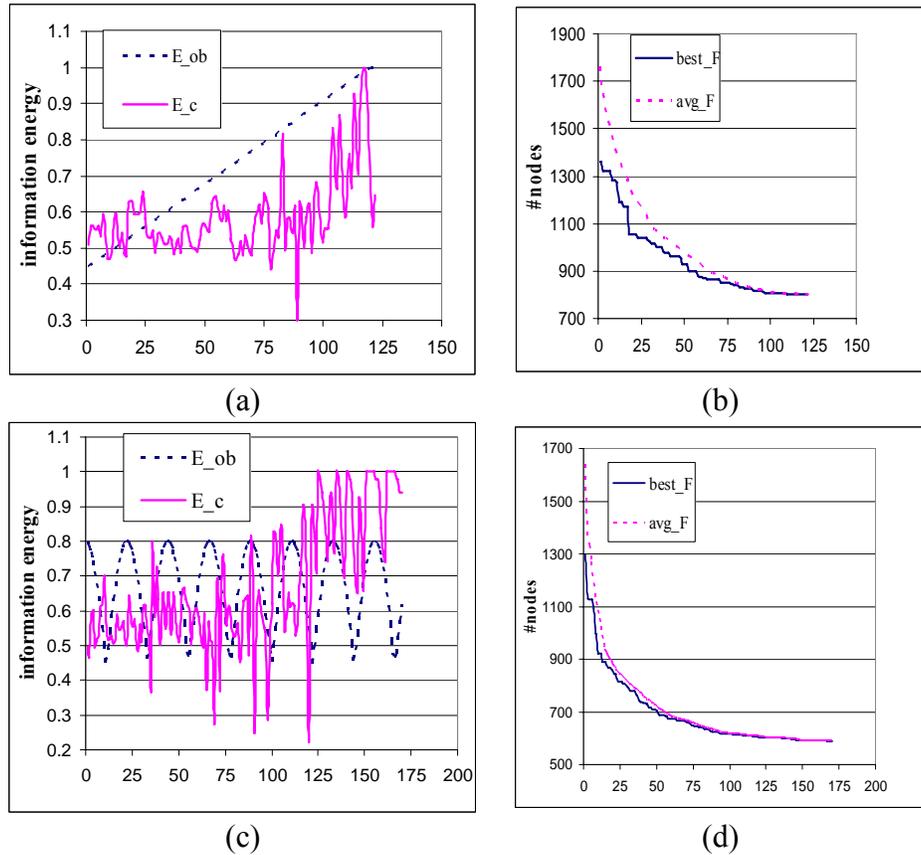
**IV.1. Setting of parameters.** In the first series of experiments, various population sizes, stop criteria, parameters values were tested in order to find adequate values. Consequently, population size is indicated in table 1. Adequates distribution of probability for PMX, AX, OX are 0.2, 0.4 and 0.6 respectively and for simple mutation, inversion and group mutation are 0.2, 0.3 and 0.5, respectively. Hypermutation is applied with probability  $p_H = 0.1$  and is not controlled by the target variability mechanism. A recommended value for  $tol$  is 0.001 and for  $n_{add}$  is 20. Other recommended values for parameters:  $\gamma = 1$  for  $E_{ob}$  constant;  $A_1 = 0.9$ ,  $A_2 = 0.45$  for  $E_{ob}$  periodic,  $\omega = 3$  and  $T = 4$  for  $E_{ob}$  periodic and  $E_{ob}$  exponential periodic.

**IV.2. Performance estimation.** The second series of experiments were conducted in order to find the best policy for variability target. Table 2 shows the corresponding values for best ever fitness reported  $F_{best}$  [22, 24] in literature, followed by the input and output number of nodes for each benchmark. The minimum number of nodes obtained for each benchmark is given in column  $F_{min}$  and the variability target policy that produced it in column  $F_{type}$ .

<i>Name</i>	<i>F<sub>best</sub></i>	<i>In</i>	<i>Out</i>	<i>F<sub>min</sub></i>	<i>F<sub>type</sub></i>	<i>F<sub>min</sub> - F<sub>best</sub></i>	<i>(F<sub>min</sub> - F<sub>best</sub>) / F<sub>best</sub></i>
<i>apex6</i>	498	135	99	589	periodic	91	0.182731
<i>C499</i>	25866	41	32	26153	exp_per	287	0.011096
<i>vda</i>	478	17	39	478	exp_per	0	0
<i>misex3</i>	478	14	14	478	periodic	0	0
<i>dalu</i>	689	75	16	714	periodic	25	0.036284
<i>cordic</i>	42	23	2	42	constant	0	0
<i>ttt2</i>	107	24	21	107	periodic	0	0

**Table 2.** Best variability policy.

Absolute and relative fitness errors are also given. For *ttt2*, *misex3* and *cordic* benchmarks, where the same minimum was obtained for more variability target policies, the best policy was chosen according to the number of  $F_{min}$  occurrences (not shown here). The obtained values seem to prove that the best variability policy is the periodic (5) one. Certainly, constant and linear target variability policies do not improve the performances significantly by comparing with periodic and exponential periodic policies. Periodic variability target seems to give slightly better results than the exponential periodic variability target. A comparison between linear and periodic variability target policies for benchmark *apex6* is illustrated in figure 2. ( $avg\_F$  = average of fitnesses).



**Fig. 2.** Comparison between  $E_{ob}$  linear ((a)-(b)) and  $E_{ob}$  periodic ((c)-(d)) for *apex6* benchmark.

Table 3 gives the average, standard deviation and unitized risk for absolute error distribution  $F_{min}-F_{best}$  and for each type of target variability. In

order to observe which policy performs better, in table 4 same data for relative frequencies  $(F_{min}-F_{best})/F_{best}$  are given.

Name		<i>apex6</i>	<i>C499</i>	<i>vda</i>	<i>misex3</i>	<i>dal</i>	<i>cordic</i>	<i>ttt2</i>
<i>constant</i>	avg	160.0000	3930.6999	2.8000	13.9000	217.6999	2.1000	3.2000
	$\sigma$	27.3464	3730.7937	0.9742	20.3597	36.4336	2.6089	2.2876
	$\sigma$ /avg	0.1709	0.9491	0.7062	1.4647	0.1673	1.2423	0.7148
<i>linear</i>	avg	179.5999	2772.7001	5.3000	16.2000	173.8999	4.4000	1.5000
	$\sigma$	51.9529	2620.1159	4.4988	19.7414	83.1630	4.8620	1.4317
	$\sigma$ /avg	0.2892	0.9449	0.8488	1.2186	0.4782	1.1050	0.9544
<i>periodic</i>	avg	123.3000	2681.8999	2.4000	11.7000	161.7000	3.9000	2.5
	$\sigma$	25.3566	2519.5214	1.2806	17.9451	65.1408	4.6804	2.5446
	$\sigma$ /avg	0.2056	0.9394	0.5335	1.5337	0.4028	1.2001	1.0178
<i>exp_periodic</i>	avg	134.6000	2205.1000	1.9000	15.2000	145.6000	3.8000	3.1000
	$\sigma$	20.2593	1737.8807	1.8676	19.0812	63.0957	3.6848	2.5735
	$\sigma$ /avg	0.1505	0.7881	0.9829	1.2553	0.4333	0.9696	0.8301

**Table 3.** Average, standard deviation and unitized risk of  $F_{min}-F_{best}$  for each variability target

Name		<i>apex6</i>	<i>C499</i>	<i>vda</i>	<i>misex3</i>	<i>dal</i>	<i>cordic</i>	<i>ttt2</i>
<i>constant</i>	avg	0.3212	0.1033	0.0058	0.0290	0.3103	0.0214	0.0299
	$\sigma$	0.05491	0.1522	0.0029	0.0425	0.0430	0.0213	0.0206
	$\sigma$ /avg	0.1709	1.47296	0.5101	1.4647	0.1387	0.9979	0.6912
<i>linear</i>	avg	0.3606	0.1265	0.0110	0.0338	0.2523	0.0119	0.0214
	$\sigma$	0.1043	0.1089	0.0094	0.0413	0.1207	0.14263	0.0118
	$\sigma$ /avg	0.2892	0.8610	0.8488	1.2186	0.4782	11.9816	0.5516
<i>periodic</i>	avg	0.2160	0.1398	0.0050	0.0244	0.2346	0.1357	0.0233
	$\sigma$	0.0512	0.1254	0.0026	0.0375	0.0945	0.1158	0.0237
	$\sigma$ /avg	0.2374	0.8967	0.5335	1.5337	0.4028	0.8532	1.0178
<i>exp_periodic</i>	avg	0.2702	0.0852	0.0054	0.0014	0.1864	0.1843	0.0289
	$\sigma$	0.0228	0.0671	0.0039	0.0386	0.0961	0.1224	0.0240
	$\sigma$ /avg	0.0844	0.7881	0.7256	1.2150	0.5155	0.6643	0.8301

**Table 4.** Average, standard deviation and unitized risk of  $(F_{min}-F_{best})/F_{best}$  for each variability target

Table 4 confirms that the periodic and exponential periodic policies are better than the others. For the first two benchmarks values in table 3 and 4 fits  $F_{type}$  from table 2; for *vda* periodic variability policy has a slight advantage over exponential variability policy. Instead, for the last benchmark, linear policy wins as table 3 shows. Overall, a periodic variability target is the best candidate in order to optimize genetic operator's effect. In the following only this policy is used.

Further, the influence of periodic function parameters  $A_1, A_2$  (5) is studied. Three sets of 10 runs are made (*apex*). Because periodic function varies between  $A_2$  and  $A_1$ , in the first set of runs we lower the upper limit, in the second we rise the inferior and in the last both to the average distance between them. Table 5 shows that there are no further improvements for  $F_{min}$ , hence, the distance between  $A_1, A_2$  should be kept at maximum.

$A_1, A_2$	$A_1=0.6,$ $A_2=0.45$	$A_1=0.9,$ $A_2=0.6$	$A_1=0.55,$ $A_2=0.7$
$F_{min}$	599	612	607

**Table 5.** Setting parameters for periodic function

In table 6 is presented for each benchmark, for periodic variability target, average number of iterations until algorithm stop  $it_{stop}$ , average number of fitness evaluations  $avgF$ . In order to evaluate the cost of policy application, the given values includes the benchmarks for which periodic variability target was not the best one.

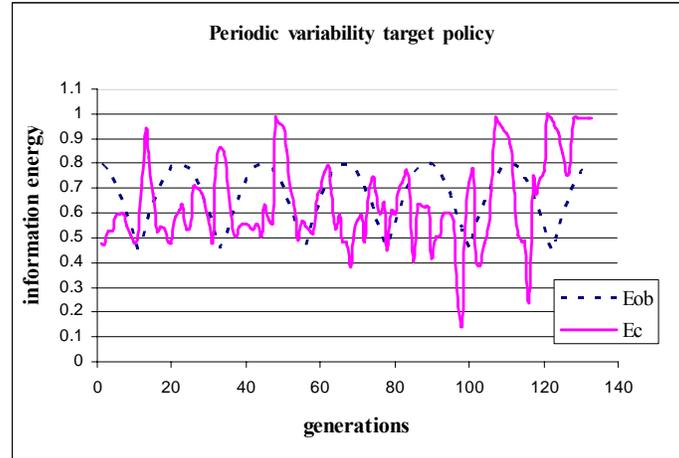
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<i>Name</i>	<i>Periodic</i>	
	<i>it stop</i>	<i>avgF</i>
<i>apex6</i>	182.2	4212.7
<i>C499</i>	122.6	3310.6
<i>vda</i>	62.1	1644.7
<i>misex3</i>	61.6	1623.4
<i>dalú</i>	148.1	3250.0
<i>cordic</i>	89.2	2147.3
<i>ttt2</i>	71.7	1672.7

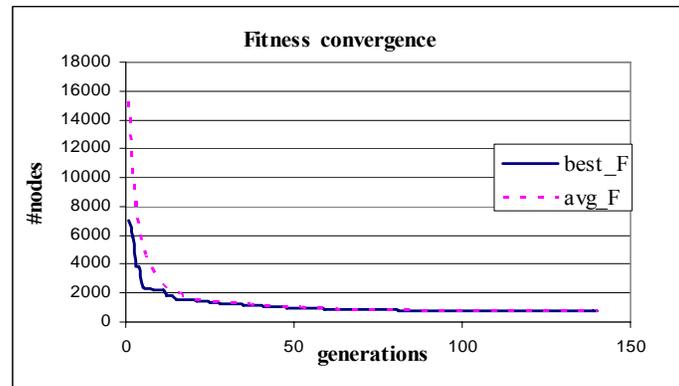
**Table 6.** Costs for periodic variability target

Costs are also related to structural benchmark complexity in terms of computational time.

Figure 3 illustrates the algorithm behavior with periodic variability target and adaptive operators for one benchmark (*dalú*) run. It can be observed that the current energy (2) of the algorithm cannot follow with accuracy the objective energy. The process of current energy adaptation to objective energy has, however, a normal oscillatory trend. When current energy is down, a lower amount of mutation is compensated by a higher rate of crossover operations (7). Lower peaks for current energy observed around iterations 100, 120 are because, for some period, mutation probability is 1. At the end of the run a high value for current energy fits the idea that population variability is low. Figure 4 presents for this runtest the best  $best_F$  and the average fitness  $avg_F$  according to the number of generations. A very good convergence can be observed.



**Fig. 3.** Example of periodic variability target behavior (*dalu benchmark*).



**Fig. 4.** Best fitness and average fitness convergence for *dalu benchmark*.

**IV.3. The effect of hypermutation.** Third set of experiments studies the effect of hypermutation within periodic variability target policy. *Apex6* benchmark was selected for tests, as it gives the worst result compared to  $F_{best}$ . Hypermutation was applied with different probabilities  $p_H$ . Average time, minimum number of nodes  $F_{min}$  obtained, the average, standard deviation and unitized risk for  $F_{min}-F_{best}$  are presented in table 7. High values of hypermutation probability lead to better fitnesses. Thus, a good policy is to apply hypermutation with a high rate. Unfortunately, higher  $p_H$  values lead to a growing computational time as second row in table 7 indicates. Tests on other benchmarks confirm this result. In order to observe the postoptimization effect of hypermutation, we applied hypermutation at the end of the runs, for the first best five chromosomes. Half of their genes were shifted within a window length equal to the chromosomes length.

$p_H$	0.05	0.1	0.15	0.2	0.25
<i>time</i>	100.240	103.298	131.664	137.405	145.824
<i>F_min</i>	592	589	574	569	564
<i>F_min - F_best</i>	94	91	76	71	66
<i>avg.</i>	152.5	152.1999	134.3000	128.5000	123.3000
$\sigma$	34.3203	31.7000	37.6269	38.2057	25.3566
$\sigma/avg$	0.2250	0.2082	0.2801	0.2973	0.2056

**Table 7.** The effect of hypermutation for *apex6* circuit with periodic variability target policy.

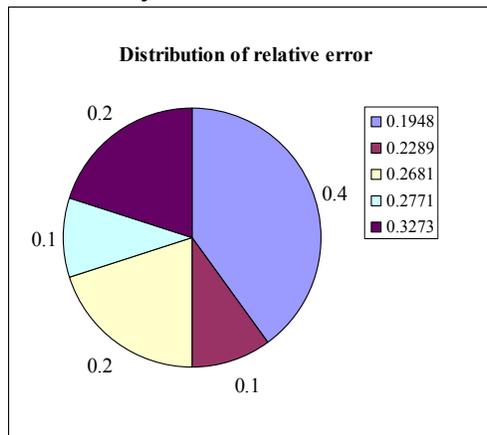
No further improvement was obtained except a single case ( $p_H= 0.05$ ) where the gain was of two nodes.

In order to illustrate the method behavior, circuit *apex6* is considered with periodic variability target and the following parameters:  $A_1= 0.45$ ,  $A_2=0.8$ , popsize  $|P|=50$ ,  $tol= 0.001$ ,  $n_{add}= 20$ ,  $p_m= 0.3$ ,  $p_c=0,4$ ,  $p_H=0.1$ . Distribution of the relative error  $(F\_min-F\_best)/F\_best$  is presented in table 8 and the associated graph in figure 5.

err.	0.1948	0.228916	0.2681	0.2771	0.3393
rel.freq	0.4	0.1	0.2	0.1	0.2
average= 0.2476			std.dev=0.0509	unitized risk=0.2056	

**Table 8.** Average, standard deviation and unitized risk for  $(F\_min-F\_best)/F\_best$

The resulted average error is 0.2476. The graph of this distribution is shown in figure 5. The second objective is to get an idea on the stability of the method. The value of the standard deviation obtained for the above-mentioned sample is 0.0509, the unitized risk is 0.2056, and this shows that the method gives good results systematically.



**Fig. 5.** Distribution of relative error  $(F\_min-F\_best)/F\_best$

## 5. FINAL REMARKS

This paper presents a new hybrid GA for optimize variable ordering in OBDDs. It contains new techniques for adapting and for controlling the genetic operators' behavior based on variability target policies. The hybrid GA contains three main improvements: firstly, it uses three mutation operators and three crossover operators applied with given probability distributions. Secondly, a hypermutation operator grafts the sifting technique on the GA. Third, the algorithm contains a control mechanism based on information energy for adapting the population variability. In order to evaluate the GA's performance, experiments were made to determine the adequate algorithm's parameters values, to evaluate the best variability target policy and to study the effect of hypermutation. Experimental results show that the proposed method performs very well [15] and has further development potential.

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