

# System Level Diagnostics over the PMC Model

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## Abstract

System level diagnostics is targeted to complex computer systems. The basis of this diagnostics is defined by formal diagnostic models. The paper presents diagnostic process over the symmetric diagnostics model. A new Boolean syndrome decoding algorithms have been developed and implemented for the one-step diagnostics of  $t$ -diagnosable regular systems over this model. New Boolean expressions for the system model were defined for regular systems based on simplification of test syndrome decoding. The developed algorithms were tested on several examples of computer architectures and the results were compared with existing and published another syndrome decoding algorithms. The presented algorithms consume less time for larger computer systems in comparison with current algorithms.

## Categories and Subject Descriptors

B.8.1 [Reliability, Testing, and Fault-Tolerance]: System diagnostics

## Keywords

$t$ -diagnosable system, PMC model, one-step diagnostics, system level diagnostics

## 1. Introduction

At the present time system diagnostics is one of the important testing topics targeted to large computer systems. Typical representatives of such systems are the large scale distributed computer systems and loosely coupled multi-processor and multicomputer systems. Each unit - a processor of the system is a complex device and therefore it is a source of defects due to manufacturing, environment

conditions, life time, etc. Testing and diagnostics of possible faults in such systems is solved at the system level. The main objective of the system level diagnostics is the identification of unit's state (faulty or fault-free states). The system-level diagnostics concept was introduced by Preparata, Metze and Chien [1]. The links among processors can be used also for testing connected other processors, later named also as diagnostic links. A system graph model called PMC model was defined for systems which can be decomposed into units (processors) that are capable of testing each other. The goal is to identify the set of faulty processors in the system based on a given collection of test outcomes produced by the system units.

In general, let us assume that a system  $S$  consists of complex blocks (units)  $u_0, u_1, \dots, u_{N-1}$ , where  $N$  is the number of system units. It is supposed that self-testing of each system unit  $u_j$  (tested unit) is initialized by linked adjacent unit  $u_i$  (testing unit). When a self-test is completed, the tested unit  $u_j$  provides test results to testing unit  $u_i$ . Each system unit can be faulty or fault-free, and it is assumed that this state does not change during the diagnostic process. The testing unit can produce correct or incorrect test result, independent of the state of the tested unit. The set of all testing process results, called a syndrome [12], consists of the binary outcomes related to state of each tested unit in the system. Determining the status of the system units from the syndrome is known as the syndrome decoding process. Some diagnosis algorithms have been developed for identification of actual states of all system units. The main difficulty of the syndrome decoding process is the fact that any unit in the system can be in a faulty state. Subsequently, such unit may generate a correct or incorrect test result irrespectively of the actual state of the tested unit.

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If states of all system units are identified in a single step of the syndrome decoding process, the system is referred to as one-step diagnosable system. One-step diagnostics can be done only if the number of faulty units is not above the parameter  $t$  defined by the expression:  $N > 2.t + 1$ , where  $N$  is the number of units in  $t$ -testable system and  $t$  is the threshold of the number of faults. If each system unit is tested by  $t$  other units then the system is called  $t$ -diagnosable system [9].

Some modifications of the PMC model were defined, e.g. Boolean formalization [8], extended properties of model in regular computer structures [2], asymmetric extension of BGM model [16].

The thesis was targeted to simplify and minimize time dependency of the syndrome decoding process performed by algorithms based on Boolean formalization in selected computer structures. The paper is organized as follows. The next section (Section 2) describes a small background to the basic of the PMC model and the Boolean representation of the testing status. Section 3 describes motivation and objectives of the thesis and Section 4 and Section 5 present main contributions to the system level diagnostics for selected types computer structures. The last section (Section 6) concludes the paper.

## 2. The PMC model

The first diagnostics model is the PMC model with symmetric test results evaluation. It assumes that a test performed by a fault-free unit is reliable and that performed by a faulty unit is completely unreliable [6]. Then diagnosed system can be represented by an oriented system graph  $G = (U, E)$ , where a set of nodes  $N$  represents system units and a set of edges  $E$  represents the test relations between system units. The edge orientation is based on unit types (testing or tested unit). The edge  $(u_i, u_j) \in E$  exists if and only if units  $u_i$  and  $u_j$  are interconnected and unit  $u_j$  (tested unit) is tested by unit  $u_i$  (testing unit) with binary outcome  $\gamma_{ij}$ . This outcome represents the state of unit  $u_j$  without knowledge of unit  $u_i$  state. The outcome value  $\gamma_{ij}$  depends on evaluation by testing unit  $u_i$  ( $\gamma_{ij} = 0$  for fault-free state and  $\gamma_{ij} = 1$  for faulty state). Results from all tested units are constituted into one binary sequence called test syndrome or simple syndrome, later marked  $\sigma$  [12].

In the system level diagnostics, the output of each diagnostic algorithm under the PMC model is a division of the system unit set  $N$  into subset  $U_f$  containing units declared as faulty, subset  $K$  of units declared as fault-free and subset  $S$  of suspect units (units with unidentified status) [7]. Effectiveness of diagnostic methods depends on correctness and completeness of the used algorithm for identifying faulty units from syndrome  $\sigma$ . The diagnostics is referred to as correct if the diagnosed status of each unit corresponds to its actual status. The diagnostics is complete if all units are classified as fault-free or faulty and subset  $S$  is empty [8].

### 2.1 Boolean expressions for faulty units diagnostics

The PMC model was extended by other Boolean variables and expressions for identifying faulty units in  $t$ -diagnosable system. One general deterministic algorithm was developed over the extended PMC model. Thus the PMC model was enriched by evaluation of each vertex of the system graph by one binary variable which gains the value 0 or 1 [8].

Let the PMC model be represented by system graph  $G = (U, E)$ , where  $U = u_0, u_1, \dots, u_{N-1}$  and edge  $(u_i, u_j) \in E$  exists if and only if unit  $u_i$  is tested by unit  $u_j$  with binary outcome  $\gamma_{ij}$ . Each edge in  $G$  is evaluated by one syndrome outcome  $\gamma_{ij}$  and each tested unit  $u_j$  is evaluated by one binary variable  $x_j$ . The variable added to each unit in graph  $G$  expresses its state in dependence on the status of both tested and testing units. Let  $x_i$  and  $x_j$  be variables added to arbitrary system unit  $u_i$  and  $u_j$ ,  $u_i, u_j \in U, (u_i, u_j) \in E$ , then for the received syndrome element  $\gamma_{ij}$  the expressions 1 - 4 can be defined (the operator  $\neg$  means logical negation of a variable, the "+" and

"+" symbols represent the logical operations AND, OR).

$$\neg x_i \cdot \neg x_j \rightarrow \neg \gamma_{ij} \quad (1)$$

$$\neg x_i \cdot x_j \rightarrow \gamma_{ij} \quad (2)$$

$$x_i \cdot \neg x_j \rightarrow \neg \gamma_{ij} + \gamma_{ij} \quad (3)$$

$$x_i \cdot x_j \rightarrow \gamma_{ij} + \gamma_{ij} \quad (4)$$

Thereafter the problem of finding the logical values  $x_i, i = 0, 1, \dots, N - 1$ , which compose the Boolean vector  $R = (x_i)$  is transformed into Boolean expression solving. The Boolean expressions 1 - 4 can be simplified to 5 and 6 describing the relationship between the states of the testing unit  $u_i$  and of the tested unit  $u_j$  (faulty or fault-free).

$$x_i + x_j + \neg \gamma_{ij} \quad (5)$$

$$x_i + \neg x_j + \gamma_{ij} \quad (6)$$

The solution process is based on the transformation of the binary outcomes of syndrome  $\sigma$  into the Boolean expression in the normal conjunctive form (NCF). The basic totals correspond to each outcome  $\gamma_{ij}, (u_i, u_j) \in E, i, j \in 0, 1, \dots, N - 1$  and they are defined by 7.

$$x_i + x_j \iff \gamma_{ij} = 1, \quad x_i + \neg x_j \iff \gamma_{ij} = 0 \quad (7)$$

The expression 7 presents the situation where the tested unit or the testing unit or both may be faulty. The defined Boolean expressions can be assigned to each interconnection in the system graph. The Boolean expressions of the whole system can be rewritten into the NCF form and assigned to each syndrome of the tested system. Then, the syndrome decoding process is based on solving the Boolean function 8, where  $\#E$  is the number of edges.

$$\prod_{0 \leq k < \#E} B_k = 1, \text{ where} \quad (8)$$

$$B_k = (x_i + x_j) \iff \gamma_{ij} = 1$$

$$B_k = (x_i + \neg x_j) \iff \gamma_{ij} = 0$$

For the diagnostics of faulty or fault-free units in system under the presented extension of the PMC model consists of finding the combination of logical values assigned to Boolean vector  $R = (x_i), i = 0, 1, \dots, N - 1$  for which Boolean function  $B = 1$ . Then algorithm, named SYDEB (SYndrome DEcoding based on Boolean function solution), consists of the following steps [13]:

1. Generation of function  $B$  from actual syndrome  $\sigma$ .
2. Generation of all combinations of the Boolean variables for the solved function  $B$ .
3. Exclusion of all the generated combinations for which  $B \neq 1$ .
4. If only one Boolean vector  $R = (x_0, x_1, \dots, x_{N-1})$  remains as the solution of  $B = 1$ , then the state of all units in the system can be identified in one step.
5. If more than one combination of logical values remains, the identification of faulty units is executed sequentially.

Complexity of SYDEB is  $O(2^N)$  due to the generation of all combinations of the Boolean variables in vector  $R$ .

This means that its usage is appropriate just in systems with approximately tens of processing units only [3]. In extension of the listed approach by a selective choice of the input set according to the property of the PMC model is reduced to the value  $O\binom{N}{t}$  [3].

### 3. Motivation and Objectives

The complexity of the syndrome decoding algorithm SYDEB can be modified for some selected system structures with effective applications in system level diagnostics, e.g. for regular structures. The complexity of system diagnostics can be decreased by reducing the number of Boolean variables in function  $B$  based on other aspects related to the regular structures defined in [14]. A regular system should be divided into smaller special parts depending on test outcomes. Using this aspect a new structure, called Z-aggregate, was defined in some heuristic syndrome decoding algorithms [14], [15].

The main objectives of the thesis are targeted to define new or modified Boolean expressions and Boolean function solution for selected computing structures, to develop new effective algorithms for one-step faulty units identification using new Boolean expressions and transformation of Z-aggregates to the Boolean formalization. The PMC model was selected as the basic system model for structure representation.

### 4. The PMC model for regular structures

Simplification of the PMC model can be defined on the properties of regular system structure. Let  $S$  be a system with regular structure (e.g. hypercube, 3D-toroid, 3D-cube, etc.), which is represented by a  $k$ -regular oriented graph  $G = (U, E)$ , where  $U = u_0, u_1, \dots, u_{N-1}$ ,  $N$  is the number of units and  $E = (u_i, u_j) \mid u_i$  tests  $u_j$  with outcome  $\gamma_{ij}$ ,  $i, j = (0, 1, \dots, N-1), i \neq j$ . We propose the following assumptions for regular structures testing based on definitions presented in [2]:

- Adjacent units perform bidirectional tests, in other words, if  $(u_i, u_j) \in E$  then also  $(u_j, u_i) \in E$ .
- The system graph  $G$  is  $k$ -regular, i.e. all vertices in  $U$  have the same degree  $k$  (every unit tests, and is tested by exactly  $k$  neighbours).
- Minimum diagnosability level is defined as  $t = k$ . By higher levels of system regularity and number of units the estimated minimum diagnosability level increases [6].

Then we transfer these properties into new diagnostic definitions for regular structures represented by the PMC model and syndrome  $\sigma$  [14]:

- if  $\gamma_{ij} = 0 \wedge \gamma_{ji} = 1$ , then  $u_i$  is faulty;
- if  $\gamma_{ij} = 0 \wedge u_i$  is fault-free, then  $u_j$  is also faulty;
- if  $\gamma_{ij} = 0 \wedge u_j$  is faulty, then  $u_i$  is faulty;
- if  $\gamma_{ij} = 1 \wedge \gamma_{ji} = 1$ , then unit  $u_i$  or  $u_j$  is faulty.

Based on these new properties, new Boolean expressions can be defined and reduced for syndrome decoding algorithms. Both are described in the following subsections.

### 4.1 Reduced Boolean expressions

It is assumed that in regular structures bidirectional links exist between two units; thus, both can be used for diagnostics. Therefore generation of Boolean expressions of the final function  $B$  can be simplified [4] by Definitions 1, 2.

**DEFINITION 1.** Let  $G = (U, E)$  be a system graph of a  $k$ -regular system with  $N$  units where  $U = u_0, u_1, \dots, u_{N-1}$ ,  $E = (u_i, u_j)$ ,  $u_i$  tests  $u_j$  and syndrome  $\sigma = (\gamma_{ij})$ ,  $u_i$  tests  $u_j$  with binary outcome  $\gamma_{ij}$ . Then  $B = B_{ij}$ ,  $i, j = (0, 1, \dots, N-1)$  is a Boolean function for faulty units diagnostics and for each couple  $(u_i, u_j), (u_j, u_i) \in E$  the following rules exist according to the values of  $\gamma_{ij}$  and  $\gamma_{ji}$ :

- if  $\gamma_{ij} = 0 \wedge \gamma_{ji} = 0 \implies B_{ij} = (x_i + \neg x_j) \wedge B_{ji} = (x_j + \neg x_i)$ ;
- if  $\gamma_{ij} = 0 \wedge \gamma_{ji} = 1 \implies B_{ij} = (x_i + \neg x_j) \wedge B_{ji} = (x_j + x_i)$ ;
- if  $\gamma_{ij} = 1 \wedge \gamma_{ji} = 0 \implies B_{ij} = (x_i + x_j) \wedge B_{ji} = (x_j + \neg x_i)$ ;
- if  $\gamma_{ij} = 1 \wedge \gamma_{ji} = 1 \implies B_{ij} = (x_i + x_j) \wedge B_{ji} = (x_j + x_i)$ ;

**DEFINITION 2.** The rules described in definition 1 can be simplified by integration of  $B_{ij}$  and  $B_{ji}$  into one Boolean expression  $B_{\langle ij \rangle}$ . Then the following expressions are valid:

- if  $\gamma_{ij} = 0 \wedge \gamma_{ji} = 0 \implies B_{\langle ij \rangle} = (x_i \cdot x_j + \neg x_i \cdot \neg x_j)$ ;
- if  $\gamma_{ij} = 0 \wedge \gamma_{ji} = 1 \implies B_{\langle ij \rangle} = (x_j)$ ;
- if  $\gamma_{ij} = 1 \wedge \gamma_{ji} = 0 \implies B_{\langle ij \rangle} = (x_i)$ ;
- if  $\gamma_{ij} = 1 \wedge \gamma_{ji} = 1 \implies B_{\langle ij \rangle} = (x_i + x_j)$ .

Reduction of the number of Boolean function results is in 50% complexity in comparison with the Boolean function used in the SYDEB algorithm.

### 4.2 Z-aggregates in regular structures

Transformation of Z-aggregates from the existing heuristic algorithm into the Boolean algorithm SYDEB can simplify the diagnostics process. Let  $G = (U, E)$  be system graph of  $k$ -regular system with  $N$  units. Then for an arbitrary syndrome  $\sigma$ , a subgraph  $G_0 = (U_0, E_0)$  of  $G$  with a set of edges  $E_0$  is defined by 9 [15].

$$E_0 \subseteq E, E_0 = (u_i, u_j) \in E \mid \gamma_{ij} = 0 \wedge \gamma_{ji} = 0 \quad (9)$$

If sub-graph  $G_0$  can be divided into  $r$  strongly connected subgraphs  $G_{Zq}$ , where  $r$  is an arbitrary number, then each subgraph  $G_{Zq}$  will define a set of strongly connected nodes  $U_{Zq}$  according to expression 10 and this set is called a Z-aggregate. It is supposed that each node from set  $U$  will occur in one set  $U_{Zq}$  at the most.

$$G_{Zq} = (U_{Zq}, E_{Zq}) \quad (10)$$

$$G_0 = \bigcup_{q=0}^{r-1} G_{Zq}$$

New properties were defined for  $k$ -regular systems modeled by the PMC model based on the Z-aggregates.

**DEFINITION 3.** Let  $U_{Z_0}, U_{Z_1}, \dots, U_{Z_{r-1}}$  be groups of Z-aggregates defined over syndrome  $\sigma$  using system graph  $G = (U, E)$ , where  $r$  is positive integer number and  $U_f$  is a group of faulty units. Then for each couple of units  $u_{Z_{qi}}, u_{Z_{qj}} \in U_{Z_q}, i, j = 0, 1, \dots, U_{Z_q} - 1, q = 0, 1, \dots, r - 1$ , the following properties are valid:

1. Actual faulty state is identical for all units from  $U_{Z_q}$ . It means if  $u_{Z_{qi}}, u_{Z_{qj}} \in U_{Z_q}$  for  $i \neq j$  and  $u_{Z_{qi}} \in U_f$ , then  $u_{Z_{qj}} \in U_f$ .
2. If  $u_{Z_{qi}}, u_{Z_{qj}} \in U_{Z_q}$  for which  $(u_{Z_{qi}}, u_{Z_{qj}}) \in E$  and the test outcome is  $\gamma_{Z_{qi}Z_{qj}} = 1$ , then each unit from  $U_{Z_q}$  is faulty. It means that for  $\forall u_{Z_{ql}} \in U_{Z_q}$  is valid:  $u_{Z_{ql}} \in U_f, l = 0, 1, \dots, U_{Z_q} - 1$ .
3. If  $u_{Z_{qi}} \in U_{Z_q}$  and  $u_{Z_{ql}} \in U_{Z_p}, p = 0, 1, \dots, r - 1, l = 0, 1, \dots, U_{Z_p} - 1, q \neq p$ , and  $(u_{Z_{qi}}, u_{Z_{ql}}) \in E$  with test outcome  $\gamma_{Z_{qi}Z_{ql}} = 0$ , then all units from  $U_{Z_p}$  are faulty.

The mentioned properties are the basis for reduction of the number of variables in Boolean function  $B$ . The new properties have been defined for representation of faulty state of units in Z-aggregates in the final function  $B$  introduced in the next definition.

**DEFINITION 4.** Let be  $\sigma$  a test syndrome of the system  $S = (U, E)$  and  $X = x_0, x_1, \dots, x_{N-1}$  be the vector of Boolean variables in function  $B$  expressed in the NCF form, which is generated by the deterministic algorithm SYDEB. Let exist a group of Z-aggregates  $U_Z$  related to the syndrome  $\sigma, U_Z = U_{Z_q}, q = 0, 1, \dots, r - 1$ . Then  $X$  can be transformed to  $X_Z = x_i \mid x_i$  representing the state of unit  $u_i, u_i \in U_{Z_q},$  for  $i = 0, 1, \dots, N - 1, q = 0, 1, \dots, r - 1 + x_{Z_q} \mid x_{Z_q}$  representing the state of units from  $U_{Z_q}, q = 0, 1, \dots, r - 1$ .

According to definition 4, Boolean variables  $x_i$ , for  $i \in 0, 1, \dots, N - 1$ , which represent actual state of units integrated in one Z-aggregate ( $U_{Z_q}$ ) have identical values. Therefore in Boolean function  $B$  these variables are replaced by one variable only marked by  $X_{Z_q}$ . Then the number of the Boolean variables can be minimized in the new developed algorithm. Then time complexity of solving the examined Boolean function in the syndrome decoding process for regular system structure is also reduced.

Roughly, the new syndrome decoding algorithm for systems with regular structure, named SYDEB-Z, is based on the following steps:

1. The system graph for  $k$ -regular system is divided into subgraphs defined by Z-aggregates related to test syndrome  $\sigma$ .
2. Boolean function  $B$  is calculated for the whole system including Z-aggregates. All units in the same Z-aggregate are represented by the same Boolean variable in calculated function  $B$ .

3. Solution of  $B = 1$  in the context of  $t$ -diagnosability is solved like in primary SYDEB algorithm.

The main disadvantage of this algorithm is generating Z-aggregates for each test syndrome  $\sigma$ . It means it has to be executed for each test run.

### 4.3 System decomposition method

Test syndrome decoding by the basic SYDEB algorithm is based on solving Boolean function in the CNF form. Each variable  $x_i$  of the function represents actual state of unit  $u_i, i = 0, 1, \dots, N - 1$ . New rules for decomposition of systems, e.g. a multiprocessor system defines the basics of the new algorithm for one-step diagnosis in  $t$ -diagnosable systems. The system decomposition is realised over the related graph model by finding cycles with the same length by using graph edges. Then Boolean function can be divided according decomposition of the system structure.

Identification of faulty units in the system after Boolean function  $B$  decomposition runs independently for particular subsystems. The resulting set of faulty units is identified by composition of particular solutions of all subsystems. The next subsection describes a method for system decomposition as the basis of the new diagnostic algorithm. The proposed decomposition method assumed the bidirectional interconnection links in system and mutual testing between adjacent units.

Let  $S$  be a system, which is represented by an oriented graph  $G = (U, E)$ , where  $U = u_0, u_1, \dots, u_{N-1}$ ,  $N$  is the number of units and  $E = (u_i, u_j) \mid u_i$  tests  $u_j$  with the outcome  $\gamma_{ij}, i, j = (0, 1, \dots, N - 1), i \neq j$ . We make the following assumptions for the proposed decomposition:

1. Adjacent units perform bidirectional tests, in other words, if  $(u_i, u_j) \in E$  then also  $(u_j, u_i) \in E$ .
2. When  $\epsilon$  is the length of the shortest cycle in a system graph  $G(U, E)$  of system  $S$ , the edge cover set of graph  $G$  has to be completely covered by cycles with length  $\epsilon$ .

Assume that system graph  $G(U, E)$  of system  $S$  can be divided into  $h$  smaller subsystems  $S_d, d = 0, 1, \dots, h - 1$  with identical structure. The result of the system graph decomposition is a set of non disjoint subgraphs  $G_d$  that are related to a set of units  $U_d \subset U$ , edges  $E_d \subset E$  and test syndrome  $\sigma_d \subset \sigma$  for all subsystems  $S_d$ . The following rules are valid for the graph decomposition:

1. All subgraphs cover the graph by edges and identify all cycles there with the same length  $\epsilon$ .
2. The number of units  $U_d$  is identical in each subgraph  $G_d$ . Each unit belongs to at least one subgraph  $G_d$ , for  $d = 0, 1, \dots, h - 1$  and expression 11 has to be fulfilled.

$$U = \bigcup_{d=0}^{h-1} U_d \quad (11)$$

3. Edges of each subgraph  $G_d = (U_d, E_d)$  create a bidirectional cycle. Each edge belongs to at least one

subgraph  $G_d$ , for  $d = 0, 1, \dots, h - 1$  and expression 12 has to be fulfilled.

$$E = \bigcup_{d=0}^{h-1} E_d \quad (12)$$

4. A partial syndrome  $\sigma_d$  for the subsystem  $S_d$  is a subset of the test outcome  $\gamma_{rs}$  from  $\sigma$  for which expression 13 is valid.

$$\sigma_d = \gamma_{rs} | u_r, u_s \in N_d, (e_r, e_s) \in E_d \quad (13)$$

The decomposition of the system  $S$  is based on structure of such system and can be described by set  $A$  defined by expression 14, where  $S$  = system structure,  $\sigma$  = current syndrome and  $U_f$  = set of faulty units.

$$A = (S, \sigma, U_f) \quad (14)$$

Then decomposition of the system is represented by decomposition of set  $A$  into subsets  $A_i$  according to 15. The division of system  $S$  is realized by decomposition of graph  $G$  to non-disjunctive subgraphs  $G_i = (N_i, E_i)$ ,  $i = 0, 1, \dots, h - 1$ .

$$A = A_i \quad (15)$$

$$A_i = (S_i, \sigma_i, U_f), i = 0, 1, \dots, h - 1$$

The primary SYDEB algorithm was modified to the new algorithm, named SYDEB-D, uses the above-mentioned system decomposition and consists of two basic phases. The first one is a preparatory phase for creating special index and mapping tables of a system generated from a decomposed system structure. It is applied on the system only once, before system running. The index table transforms the Boolean function generating process and their solution into a simple process of searching solution in this table. The mapping table performs reindexing of system units and outcomes of actual syndrome into the index table range according to defined system decomposition.

The second phase is applied to the system during its run and syndrome decoding and identification of faulty units is done.

## 5. Experimental results

Effectiveness of the developed algorithms SYDEB-Z (SYDEB with Z-aggregates) and SYDEB-D (SYDEB with Boolean function decomposition) for test syndrome decoding was evaluated by experiments in  $t$ -diagnosable regular systems with different sizes, which were simulated by software implementation (2-dimensional grid, 3-dimensional toroid). The main disadvantage of the primary SYDEB algorithm is its exponential time dependency on the number of units in the system. Both new developed and implemented algorithms minimize its time consumption whereas the other parameters of the SYDEB algorithm are the same. Therefore, time complexity, correctness and completeness of the syndrome decoding process by new proposed algorithms were monitored in the performed experiments. The results were compared with experimental results of two published algorithms (the primary SYDEB [13] algorithm and heuristic EDARS algorithm [5] for regular structure).

Time complexity of all four algorithms (SYDEB, EDARS, SYDEB-Z, SYDEB-D) were measured in the experiments. It was realized over the following regular structures, which were simulated by software implementation:

- 2-dimensional grid [10] with degree of regularity  $k = 4$  (Figure 1, 2).
- 3-dimensional toroid [11] with degree of regularity  $k = 6$  (Figure 3, 4).

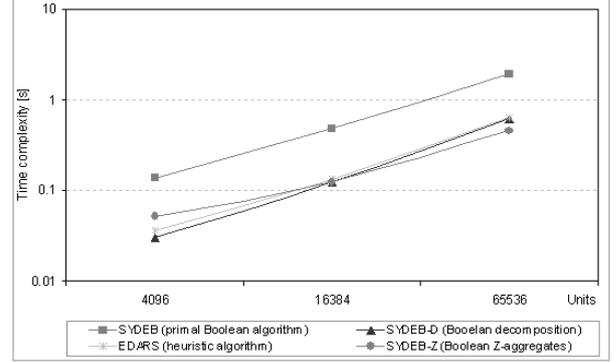


Figure 1: Time complexity in 2-dimensional grid.

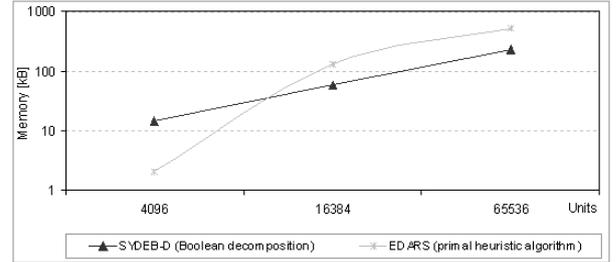


Figure 2: Memory consumption in 2-dimensional grid.

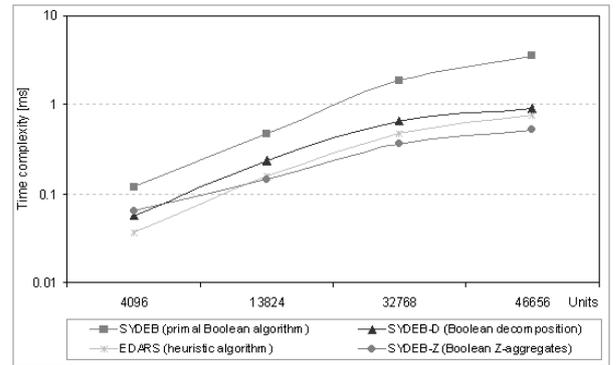


Figure 3: Time complexity in 3-dimensional torus.

The presented experiments performed over selected systems have shown that two new presented algorithms for syndrome decoding in one-step  $t$ -diagnosable systems have approximately the same results as the EDARS algorithm. Both algorithms achieved 100% correctness and completeness of syndrome decoding process during practical experiments.

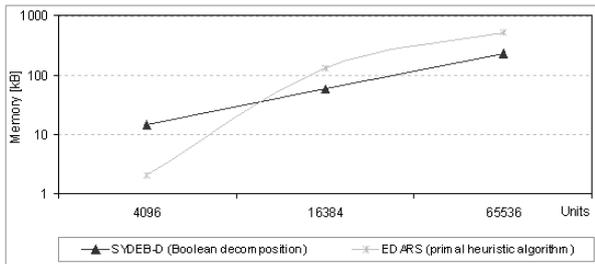


Figure 4: Memory consumption in 3-dimensional torus.

## 6. Conclusions

The work contributes to the system level diagnostics based on the PMC model. New rules were defined for the PMC model for defined system structures. Two innovative and effective algorithms of one-step system level diagnostics SYDEB-Z and SYDEB-D have been developed and implemented using simplified Boolean expression for faulty units identification from a test syndrome in  $t$ -diagnosable systems. The first algorithm, SYDEB-Z, is based on an idea from the heuristic algorithm EDARS; the idea of Z-aggregates was transformed into Boolean function generation in systems with regular structure, where the number of Boolean variables can be significantly reduced.

For the second algorithm, SYDEB-D, new implementation approaches were defined in the form of index and mapping tables for decreasing the time for decoding of several syndromes. Its main advantage is using for other systems with regular structure. It is specific by its implementation simplicity and deterministic solution in comparison with both SYDEB and EDARS algorithms. Against the primary SYDEB algorithm, syndrome decoding process is performed without the need to generate and solve Boolean function  $B$ . This task is realized by defined decomposition of a system structure with defined index and mapping table, which has been prepared before diagnostics algorithm run.

Both algorithms were tested over selected examples of regular computer structures and the results have been compared with two existing algorithms EDARS and SYDEB. The experiments have shown effectiveness of both algorithms for syndrome decoding process mainly for more complex and large systems.

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