

Soft fault diagnosis based on the Pearson correlation

Marek Korzybski, Marek Ossowski

Faculty of Electrical, Electronic, Computer and Control Engineering, Technical University of Lodz, Stefanowskiego street 18/22, 90-924 Lodz, Poland, e-mail: marek.korzybski@p.lodz.pl

Faculty of Electrical, Electronic, Computer and Control Engineering, Technical University of Lodz, Stefanowskiego street 18/22, 90-924 Lodz, Poland, e-mail: marek.ossowski@p.lodz.pl

Abstract The paper deals with the diagnostic algorithm enabling location and identification of soft faults in analogue circuits. It bases on the spectrum analysis of the circuit response to the rectangular input signal. The classifier applied in the location process uses Pearson product-moment correlation coefficient of the examined circuit with the models of all potential faults. The identification is based on the formulas constructed with use of one of the evolutionary methods: gene expression programming. The algorithm represents SBT (Simulation Before Test) technique and requires multiple analysis of circuit under test. They enable us to build a fault dictionary. The numerical example shows the effectiveness of the proposed algorithm.

Keywords fault diagnostic in analog circuits, parametric faults, dictionary diagnostic methods, gene expression programming, correlations, the fast Fourier transform..

I. INTRODUCTION

The fault diagnosis of the analog circuits is the area of great importance in the process of design, manufacturing and exploitation of electronic devices. Despite the over thirty years of the research development, there is still a need of new universal, quick and effective, diagnostic methods. There are two main causes of such a situation. The first one is the difficulty of diagnosing the analog circuits, due to the non-linear characteristics and tolerances of the system's elements. The second - new challenges, like limited access to the systems' interiors.

The challenges appearing before the modern diagnostics of analog circuits are, apart from the before-mentioned limited access to systems' interiors, the high speed of diagnostic methods used during the production process, effectiveness and accuracy enforced by the increasing demand for reliability of finished products, and more frequently occurring global failures, which are the effect of the production process of electronic systems.

The proposed algorithm includes some of the above-mentioned requirements: for measurements, it uses only the output of the tested system, and it belongs to the group of SBT methods, which are known for not being time-consuming.

II. BASIC INFORMATION ABOUT THE ALGORITHM

The algorithm presented in this paper is provided to localize and identify parametric faults in dynamic analog circuits. Meeting the requirements of the methods used for testing the systems with limited access to their interiors, the proposed algorithm uses the measurements taken from one node – output of the system. Obtaining the necessary number of measurement points was achieved by the examination of changes in the value of multiple harmonic responses of the system to the rectangular test signal, similar to [1]. The influence of the decrease of harmonic values, along with the increase of their number, on the result of the procedure was achieved by the examination of the relative changes in their value:

$$\delta A^{(i)} = \frac{A^{(i)} - A_{nom}^{(i)}}{A_{nom}^{(i)}} \quad (1)$$

where: $\delta A^{(i)}$ is the relative harmonic change number i , $A^{(i)}$ is the actual value of the i^{th} harmonics of the voltage, $A_{nom}^{(i)}$ is the value of the i^{th} harmonics of the voltage in the unfaulty circuit.

The classifier of the proposed method is based on the Pearson correlation coefficient calculated for relative changes of the harmonics of the output signal of the faulty circuit, and the fault dictionary, which is similar to the work [2] on catastrophic faults. The Pearson correlation coefficient of the two variables – x and y , is defined below:

$$P_{xy} = \frac{\sum_{i=1}^{i=n} (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{i=n} (x_i - \bar{x})^2} \sqrt{\sum_{i=1}^{i=n} (y_i - \bar{y})^2}} \quad (2)$$

where: x_i and y_i are sample variables, and n is the number of analyzed samples.

The signatures of the created fault dictionary, apart from the relative changes of the harmonics of the signal, include the functions allowing the fault identification. They are appointed by the heuristic method of gene expression programming. Its operation is explained for instance in [3].

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IV. REFERENCES

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