Reducing the parameter count through a Sensitivity Analysis performed on a mathematical model used for estimating energy consumption in a Passive House

Silvia Cristina Stegaru\textsuperscript{a}*, Mihail – Bogdan Cărăuşiu\textsuperscript{b}, Emil – Ioan Slușanschi\textsuperscript{a}, Nicolae Țăpuș\textsuperscript{a}

\textsuperscript{a}University Politehnica of Bucharest, Faculty of Automatic Control and Computers, Bucharest 060042, Romania
\textsuperscript{b}University Politehnica of Bucharest, Faculty of Power Engineering, Bucharest 060042, Romania

Abstract

Energy efficiency in the buildings sector is one of the main research areas on which the European Union has focused its efforts. Reducing energy consumption has become a priority, as well as its estimation and prediction. There are a number of different models used to achieve the latter, from white-box models (fully informed) to black-box models (all necessary information is inferred from data), as well as hybrid approaches. However, these existing gray-box models rely on mathematical models which can easily be over-parameterized. We have implemented a gray-box model and propose an improved Sensitivity Analysis method which we have used to identify the correlated parameters. Moreover, upon analyzing the results of this analysis, we propose a simplification applied on the mathematical model, without actually modifying it.

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1. Introduction

The buildings sector represents the largest end-use energy consumer, responsible for a share of 40% across the EU territory [1,2,3]. The large amount of energy consumption in this case is due to space heating and cooling, which

* Corresponding author.
E-mail address: silvia.stegaru@cs.pub.ro.
accounts for more than 50% for a typical building. In addition to this, the final energy required for space heating represents the largest percentage, estimated at 55% from total [1]. In order to achieve the proposed new energy reduction goals by 2030 and 2050, the European Union needs to take into consideration efficient strategies which imply work on improving this area.

A Passive House is a construction standard, which manages to maintain a high comfort level with a small energy consumption, and without an active cooling systems [1,2]. This can be achieved through a combination between a special type of architecture, compact shape, very good insulation level with minimal thermal bridges, high air tightness, optimal use of external and internal heat gains, as well as a high efficient mechanical ventilation and heat recovery unit (MVHR) [1,2]. Applying this standard in combination with a very efficient HVAC system based on renewable energy sources, the energy demand for heating can be reduced by 80% compared to conventional buildings, and by 75% compared with new buildings [1]. In order to be accredited as Passive, a building must fulfill the following energetic requirements: less than 15 kWh/m2/year energy requirement for heating and less than 120 kWh/m2/year total primary energy requirement.

Using the Passivhaus construction standard, a duplex of Passive Houses were built in the campus of University Politehnica of Bucharest. The buildings comply with the construction and energetic requirements stipulated by the standard, and they are equipped with two heat exchangers (earth-to-air and air-to-air) in order to minimize the energy consumption and to reduce the peak energy demand [4]. The study presented in this paper is performed on the Passive House in the University campus, using data collected by the monitoring system. We will investigate how the Sensitivity Analysis can be used to improve the performance of a previously implemented energy consumption application for a Passive House [5].

2. Related work

In recent years, the problem of finding the best mathematical approach for estimating and prediction of the energy consumption in buildings has been intensively researched. Transient mathematical models are essential for developing control and operational strategies in order to decrease the energy consumption in the buildings sector. The shortcoming of using purely physical models (white-box models) is represented by the need of a comprehensive description of the building’s materials, detailed HVAC system, operating schedule, etc. On the other side, the black-box models, which are purely data driven approaches, use statistical models to estimate the energy consumption in a building. The latter type of models is represented by the Artificial Neuronal Networks – ANN, which require large amount of training data in order to offer satisfying results [6]. The general trend is to improve on the good parts of the previous two methods, by implementing a hybrid approach, namely a gray-box model.

Braun et al [7] have developed such a hybrid model, a simplified 3R2C (3 Resistance and 2 Capacitances) thermal network in order to represent each of the building’s components (roof, ground floor, exterior and interior walls). Wang and Xu developed a series of simplified gray-box models [8,9,10,11] in which they have modeled the interior component as a 2R2C thermal network. In all these approaches, the building was reduced to only one thermal zone.

However, the gray-box model approaches can easily be over-parameterized, and the extra-parameters could influence the time to converge to a solution, as well as finding the solution itself. Given these aspects, it is important to identify which of the proposed parameters of the model actually build up towards a solution, and which of the parameters are correlated with one another. For this, we propose implementing a Sensitivity Analysis in order to assess the degree of proportionality between the parameters. Although the method is not new and it has been successfully used in various domains, there are very few examples of the method implementation within the buildings sector. In [12] a Sensitivity Analysis was performed on a building envelope in order to quantify the effect of the construction type and window size on the thermal performance of an office building. The authors of [13] have studied the influence of the building’s parameters on the optimum energy consumption in residential buildings using the Polish climate data. The authors of this paper have used the Sensitivity Analysis to observe the most important parameters which influence the energy performance of buildings from a macroeconomic point of view. In [14], the method is used in a comprehensive analysis on the energy performances and comfort levels in residential buildings. They presented the influence of the thermal characteristics of the building envelope on the energy required for heating, and they have also analyzed the most critical parameters which influence the PMV comfort index.
3. Implementation

The implementation of the software application consists of:

- A mathematical model, used for doing an initial rough estimation and providing the general outline of the function graph.
- A Genetic Algorithm, which estimates the constant, unknown parameters of the mathematical model.
- A Sensitivity Analysis algorithm, which analyzes the chromosomes of the GA in order to identify which of the parameters in the mathematical model are actually connected, directly or inversely, to one another.

In the next subsections, we will detail each of the above, with a focus on the Sensitivity Analysis. The inputs to the model are provided by sensors placed within the Passive House, and collected at an hourly rate.

3.1. The mathematical model

In order to simplify the problem, we have considered the house a single space, with 4 sections: interior, exterior, ceiling, and floor. The mathematical model used to estimate the energy consumption is made up of four 3R2C cells, one for each section, and one R cell for the windows. The 3R2C model is a modified version of the one presented in [7] that describes the simplified description of the Passive House. Fig 1 depicts the placement of the components within the circuit, as well as underlines the differences between the unknown parameters (R1, R2, R3, C1, and C2).

The inputs are comprised of 9 parameters which reflect the energy requirement: Tz, the exterior temperature - Ta, ground temperature – Tg, the solar radiation absorbed by the roof and exterior (Qsol,c, Qsol_e), radiative internal gains (Qg,r,c, Qg,r,e), convective internal gains (Qg,c) and solar radiation transmitted through the windows (Qsol,w). However, the mathematical model also includes a series of parameters which cannot be computed from the available data. These latter parameters are constant, which means that once they are computed they can be reused in all consequent computations. Because computing these parameters is a complex problem which might not have a viable solution, we have used a Genetic Algorithm to search for the best estimate which could provide results under the admissible threshold.

3.2. The Genetic Algorithm

Genetic Algorithms are typically used for solving NP-complete problems [15,16,17], such as the problem presented in Section 3.1. Consequently, the scope of the GA is to minimize the error from the mathematical model computation, and lower it under the desired threshold.

![Fig. 1. 3R2C model components placement within the circuit](image)

GAs are inspired from the process of natural selection described by the evolutionary theory. Given this context, we must first identify the traits of interest, which will become the search goal of this algorithm. In our case, these traits are the 3R2C parameters for the interior, which will form the basic chromosome (BC): {R1, R2, R3, C1, C2}.

The main steps of the algorithm are:

- Initialize a population of randomly initialized BCs, within their respective ranges.
- Solve the mathematical model for each of the BCs spawned within this round.
Compute a fitness factor to decide which BCs are closer to the desired threshold from the population. This formula represents the standard deviation between the computed consumed energy and the measured consumed energy.

Perform genetic operators (mutation and cross-over) within an acceptable probability in order to ensure diversity and convergence toward the minimum. The influence of such operators has been studied in [18].

Keep the best solution(s), which are called “survivors”, and re-start from the initializing of the population step, until an ending condition is met. The ending conditions are the following: (i) a maximum number of iterations has been reached, and (ii) the desired threshold has been reached.

Given these conditions, the GA either provides a solution under the imposed threshold, or stops searching after the maximum number of iterations is reached. The latter is a necessary condition, because finding a solution depends on the computed limits for the five traits in the chromosome, the maximum error accepted, as well as on other variables given as input to the GA (population size, survivor number etc.). As such, if the system is poorly specified, the program might not terminate, or the time required for it to terminate might be unfeasible. In order to increase the performance of this algorithm, we have researched ways to lower the time necessary to find a solution. A very reliable method is to do a Sensitivity Analysis on the parameters in order to identify which of them are correlated; the results of this analysis specify which of the subset of parameters we should do the actual search on, thus limiting the search spaces and reducing the total time of the search.

3.3. Sensitivity Analysis

The Sensitivity Analysis is used to increase performance of an algorithm by means of reducing the number of parameters we need to identify. For our program, we have used the Morris method [19] augmented with the Campolongo improvement [20] in order to assess the correlation factors between pairs of parameters. Consequently, for each run of the algorithm we have varied only one parameter at a time, keeping the others constant, and we have applied this principle for each of the parameters. For each consequent run, we calculate the mean and standard deviation for each set of parameters, after which we use them to compute the elementary effect. This matrix of values represents the sensitivities we need in the form of number between \([-1, 1]\) for each parameter pair. A value of 1 means that the two parameters in the pair are directly proportional with one another, whereas a value of -1 represents inverse proportionality; zero represents no correlation between the two. Evidently, if we pair a parameter with itself it will always result in a perfect direct proportionality of 1.

Given the fact that for our problem the search intervals are continuous, we needed to improve the approach programmatically. This is a necessary step, we have modified the algorithm because it is not possible to test all values in the continuous set and we needed to preserve the randomness of the initializations, while also taking into account a uniform step size between the search intervals of two consecutive runs. As such, we have divided the continuous space into a fixed number of smaller intervals, which represent the search spaces for the respective runs of the program.

4. Results

In our case, applying the modified Sensitivity Analysis algorithm yielded in the results presented in Table 1. One can observe that all values on the main diagonal are equal to 1 because the parameters are pairs with themselves. Moreover, the matrix is symmetrical, since the pair \(\{R1, R2\}\) will always yield the same value as the pair \(\{R2, R1\}\). What is interesting is that all the resistors are highly correlated amongst themselves. The correlations between resistor-capacitors and capacitor-capacitor are under 0.5 and therefor negligible.

The results are compelling and have motivated us to create an improved chromosome to remedy the problems with the high direct proportionality between resistors. The mathematical model remains the same since our assumptions about it have been validated [5]. However, because the percentage is in close proximity of the perfect direct proportionality value, we have decided to consider them as having the same value. The 3R2C model changes as shown in Fig 2.
After implementing the reduced chromosome \(\{R, C_1, C_2\}\), we have applied the sensitivity analysis in the same conditions mentioned in the previous paragraphs. The benefit of reducing the chromosome size is in the simulation time: instead of searching for 5 parameters, we now have to search for only 3, reducing the search time to \(\frac{3}{5}\)ths of the initial runtime of the algorithm.

Table 1. Results of the Sensitivity Analysis applied to the Basic Chromosome

<table>
<thead>
<tr>
<th>Pairs</th>
<th>R1</th>
<th>R2</th>
<th>R3</th>
<th>C1</th>
<th>C2</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>1</td>
<td>0.8042</td>
<td>0.8014</td>
<td>-0.4614</td>
<td>-0.4614</td>
</tr>
<tr>
<td>R2</td>
<td>0.8042</td>
<td>1</td>
<td>0.8028</td>
<td>-0.4628</td>
<td>-0.4628</td>
</tr>
<tr>
<td>R3</td>
<td>0.8014</td>
<td>0.8028</td>
<td>1</td>
<td>-0.46</td>
<td>-0.46</td>
</tr>
<tr>
<td>C1</td>
<td>-0.4614</td>
<td>-0.4628</td>
<td>-0.46</td>
<td>1</td>
<td>0.28</td>
</tr>
<tr>
<td>C2</td>
<td>-0.4614</td>
<td>-0.4628</td>
<td>-0.46</td>
<td>0.28</td>
<td>1</td>
</tr>
</tbody>
</table>

Fig. 2. Reduced 3R2C model components placement within the circuit. The resistors all have the same value.

The results of using the reduced chromosome can be viewed in Table 2. Since the three resistors have the same value, it is normal to notice a perfect direct proportionality between them. We can also observe that the elementary effects values between the two capacitances remain the same. Interestingly enough the approximately -0.4 correlation between resistors and capacitances has more than halved its initial value. This, however, is a normal result, since the initial direct proportionalities between resistors were not perfect; practically, the program has considered an approximately 0.2 uncertainty regarding which of the parameters tested were correlated (resistors or capacitances). Since we have forced the program into certainty by implementing the reduced chromosome, the uncertainty regarding resistor-capacitance interactions disappears, a fact which also validates our assumptions. This implication is very important, since it shows that reducing the chromosome has to be done in a gradual, incremental manner, or else premature optimization could lead to fallacies in the model due to the uncertainties described.

Table 2. Results of the Sensitivity Analysis applied to the Reduced Chromosome

<table>
<thead>
<tr>
<th>Pairs</th>
<th>R1</th>
<th>R2</th>
<th>R3</th>
<th>C1</th>
<th>C2</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>-0.183</td>
<td>-0.183</td>
</tr>
<tr>
<td>R2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>-0.183</td>
<td>-0.183</td>
</tr>
<tr>
<td>R3</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>-0.183</td>
<td>-0.183</td>
</tr>
<tr>
<td>C1</td>
<td>-0.183</td>
<td>-0.183</td>
<td>-0.183</td>
<td>1</td>
<td>0.28</td>
</tr>
<tr>
<td>C2</td>
<td>-0.183</td>
<td>-0.183</td>
<td>-0.183</td>
<td>0.28</td>
<td>1</td>
</tr>
</tbody>
</table>

5. Conclusions

In this paper, we have presented a reliable method for increasing performance of a parameter estimation program for estimating energy consumption within a Passive House, by eliminating redundant operations. Applying the analysis on the basic and reduced chromosome has proven that the performance penalty resulting from parameter correlations can be eliminated.
Moreover, this optimization does not require the modification of the underlying mathematical model developed, its main focus being on inspecting the correlations between constant parameters utilized within the model. As such, the method can be successfully applied to other, similar applications in order to increase performance.

We have also discussed the implications of the results obtained and argued in favor of incremental modifications to the chromosomes, starting from the highest absolute value obtained in the elementary effects table. This observation has allowed for the understanding of the correlation uncertainty which could appear within the initial analysis results.

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