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# Application of Genetic Algorithms for Approximation with Energy-Based Models 

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#### Abstract

This paper shows the approximation of the values of material constants referring to energy-based models of hyperelastic materials by means of pseudorandom methods. As opposed to conventional approaches to these sorts of issues, this paper introduces the application of evolutionary algorithms for this purpose. The attention has been focused particularly on genetic algorithms. The whole process of validation described in the paper was based on the Mooney model modified by Wegner [1]. The chosen measure of adjustment is the mean square error value of the stress, referring to the positions of the points on the theoretical curve, compared with corresponding experimental values obtained by Treloar [1,4]. Five models, including the assumption of material compressibility, have been taken into consideration.


Keywords: energy-based models, hyperelastic materials, rubber-like materials, compressibility, genetic algorithms, evolutionary algorithms.

## 1 Introduction

In recent years increased interest in different aspects of energy-based modelling has been observed [1-6]. It is understandable when the advantages of energy-based models referring to theoretical analysis of chosen materials are taken into consideration. Presenting their mechanical properties by means of properly formulated mathematical model, including right and correctly defined material constants, allows to estimate the stability of the equilibrium state and to simulate [2] their behaviour in variable external conditions.

Formulating the proper mathematical model of hyperelastic material in which material constants have been determined in a right way requires making proper initial assumptions as well as presenting the core of modeled phenomenon in the clearest possible way. These conditions have been fulfilled in the mechanical
properties models taking incompressibility of chosen materials into consideration [3].

The objective of this paper is to present a method of optimal values of material constants computation for chosen energy-based models approximating mechanical properties of hyperelastic materials determined in tests. The method enables comparison and estimation of their approximation objectively. The pseudorandom evolutionary algorithms have been used for this purpose. Particular attention has been paid to genetic algorithms.

## 2 Analysis

### 2.1 Preparation

The numerical tool which enables investigating a given energy-based models describing mechanical properties of hyperelastic materials has been created using MATLAB software. The aforementioned investigation is based on determining the capability of given energy-based models to approximate material characteristics obtained experimentally. On the basis of defined adjustment measures, numerical compilation of parameters describing material constants of chosen material model, is demanded. The compilation is made in order to find the values, for which an energy-based model approximate experimentally obtained material characteristics in the most precise way possible.

The values of mean squared errors of the positions of points on the theoretical curve, compared with corresponding experimental values obtained by Treloar [1,4] is a measure of adjustment. MSE values have been made dependent on strain value in the direction of force that caused them, taking into account transverse strains impact at the same time.

### 2.2 Energy-based modelling

### 2.2.1 Initial assumptions

The energy-based modelling is a method of complex machanical problem solving based on the assumption that the correctness of mechanical energy dissipation in a chosen object depends mainly on fulfiling the law of conservation of energy. The mathematical and computing difficulty in it seems to be the assumption that some of the existent materials can be perfectly incompressible. Inaccuracies subsequented from the abovementioned assumption are easly seen among others in researches connected with the dissipation process where the necessity of fulfiling the assumption of incompressibility introduces additional complications while solving the problem [1]. The abovementioned assumption leads also to an incorrect material description. That results from omitting the energy that is needed for a volume change, whereas it is stored in the volume deformation of all bodies, even those that seem to be practically incompressible.

By matching proper value of a bulk modulus ( K ) which is the element of volume energy of a strain energy, and also one of the three material constants whose values are searched by the created algorithm, it is possible to describe materials which show practical incompressibility in a simple way. That leads to avoiding computational difficulties connected with evaluating strains in whichever part of material as well as avoiding problems connected with fulfiling the condition of constant volume of deforming part of the element [1].

### 2.3.2 Energy-based models

One of the first and still basic strain energy function related to incompressible materials is Mooney function [1-6,9] given by Equation (1):

$$
\begin{equation*}
U=C_{1}\left(I_{1}-3\right)+C_{2}\left(I_{2}-3\right) \tag{1}
\end{equation*}
$$

where:
$\mathrm{C}_{1}, \mathrm{C}_{2}$ - material constants determined in tests:

$$
\begin{equation*}
\frac{\partial U}{\partial I_{1}}=C_{1} \quad \frac{\partial U}{\partial I_{2}}=C_{2} \tag{2}
\end{equation*}
$$

However, this function does not take material compressibility into consideration, which makes difference in many cases. Rubber, which is hyperelastic material, is characterized by nonzero compressibility as well. This fact has been taken into account in many models following the example of Mooney model by introducing J value [1] defining the volume of given material. The value $J$ is equal to square root of the third invariant which describes the volume of each finite element into which the chosen material has been divided and is given by the Equation (3):

$$
\begin{equation*}
J=\sqrt{I_{3}}=\lambda_{1} \lambda_{2} \lambda_{3}=\frac{d \underline{s}_{1}}{d s_{1}} \cdot \frac{d \underline{s}_{2}}{d s_{2}} \cdot \frac{d \underline{s}_{3}}{d s_{3}} \tag{3}
\end{equation*}
$$

where:
$\lambda_{i}-$ relative length of the deformed edge of rectangular element,
$\mathrm{ds}_{\mathrm{i}}$ - length of the undeformed edge of the element,
dsi - length of the deformed edge of the element.
One of the featured of aforementioned models is the Mooney model modified by Wegner [1] given by Equation (4):

$$
\begin{equation*}
U=C_{1}\left(I_{1}-3 \sqrt[3]{I_{3}}\right)+C_{2}\left(I_{2}-3 \sqrt[3]{I_{3}^{2}}\right)+\frac{1}{2} K \frac{\left(\sqrt{I_{3}}-1\right)^{2}}{\sqrt{I_{3}}} \tag{4}
\end{equation*}
$$

On the basis of this model the numerical tool described below has been created. Also the following models $[1,8]$, which differ from each other only by the form of
volume energy of the strain energy function and which are given by Equation (5) Equation (8):

$$
\begin{gather*}
U_{I}^{(v)}=K(J-1)^{2},  \tag{5}\\
U_{I I}^{(v)}=K(J \ln J-J+1),  \tag{6}\\
U_{I I}^{(v)}=\frac{3}{4} K[\sqrt[3]{J}(J-4)+3],  \tag{7}\\
U_{I V}^{(v)}=K(J-\ln J-1) \tag{8}
\end{gather*}
$$

have been subjected to the genetic algorithm.

### 2.3 Algorithm

### 2.3.1 Processing

The optimization algorithm consists of two parts. An operating of each of them is related to using different methods. The first part is founded on enumerative method which is the binary searching method (bisection method) and, connected with it, Bolzano-Cauchy theorem which makes the given equations roots existence dependent on signs of the endpoints of a closed interval of given continuous function. The second part uses the simplicity of genetic algorithms subjecting the population of possible results to processes of replication, crossing-over and mutation.

In the preliminary stage of search for optimal values of material constants minimizing a nonlinear objective function determining the approximation error, the division of the considered class of values of material constants is made by iterative method, until the values are close to optimal or, which is seldom, until material constants of an ideal model with a zero approximation error are found.

On the basis of the graphic presentation of the mean squared errors dependence on received values of material constants, the distribution of constants sets into two groups is achieved. Each of these groups determines proper fitting of the theoretical curve to the experimental one in one of two strain ranges - from small to medium and from medium to large one. The initial populations of models obtained in this way, determined by close to optimal material constants sets are then subjected to optimization processes according to created genetic algorithm.

The genetic processing begins from determining individuals which will be included in so called mating pool - the first generation subjected to further processing of genetic algorithm. This generation is made of two populations originating from the ones created before and conditioning the satisfying adjustment of the theoretical curve to the experimental one in one of two strain ranges. With the
biggest probability, individuals determining the smallest values of the mean squared error, are qualified to the initial generation, which means giving the best adjustment of the two mentioned curves. The number of individuals enclosed in a mating pool is conditioned upon the program user.
All the sets of material constants are then submitted to binary coding. Within the limits of each set one chromosome consisting of three combined with each other binary codes is created. Large sets of genes obtained in this way undergo then processes of replication, crossing-over and mutation.

Before the genetic material exchange, the individuals have to be joined in pairs. A single individual is randomly chosen from each population enclosed in a mating pool. This individual becomes one of the parents in newly created pair. This procedure is applied to all the individuals in the mentioned pool.

In order to accomplish all subsequent genetic operations on material constants values in a proper way all coded forms of material constants are remembered as sequences of symbols. Function 'strcat' is used to achieve it. The final notation is as follows:
CHROMOSOME = STRCAT(C1,C2,K).

It means that binary coded values of subsequent material constants, each of which is remembered in a separate matrix row, is recorded now as one sequence of symbol constants. According to that, the individual for the following set of material constants: $\mathrm{C}_{1}=0.0062, \mathrm{C}_{2}=0.1308$ and $\mathrm{K}=2$, which was initially equal to:

$$
\text { CHROMOSOME }=\left[\begin{array}{l}
C 1 \\
C 2 \\
K
\end{array}\right]=\left[\begin{array}{l}
0.0062 \\
0.1308 \\
2.0000
\end{array}\right]=\left[\begin{array}{l}
000000000111110 \\
000010100011100 \\
000000000000010
\end{array}\right],
$$

is going to have the following form:

$$
\left.\begin{array}{c}
\text { CHROMOSOME_NEW }= \\
=\left[\left[\begin{array}{llll}
0000000001 & 11110
\end{array}\right][000010100011100][000000000000010]\right.
\end{array}\right] .
$$

The sequences included in the matrix are treated, at this stage of processing, as sets of symbols (zeros and ones) only, not as binary codes, and the fact that some of the material constants had initially non-integer values is considered again not before decoding a new generation obtained as a result of crossing-over. It is made by dividing obtained values of particular material constants by 10000 .

The function defining the way of crossing-over, by properly defined cutting place, chooses therefore one of the coded values of material constants, which will then be cut. Subsequently a place of cutting the chosen sequence of symbols is determined, for each individual whose genetic material is supposed to be exchanged. Assuming that a chromosome includes $l$ characters and randomly chosen cutting point is described by $k$, the all signs placed on the positions from $k+l$ to $l$ are exchanged between individuals. Using the example of the individual presented
before and assuming that the algorithm has randomly chosen the value of $k$ as equal to 25 , the cutting of the sequence will take place lengthwise the second material constant. All gens from the cutting point till the end of the sequence of symbols describing the second material constant and all the following sequences are then exchanged between individuals. The described process is shown in the following scheme:

$$
\begin{gathered}
\text { CHROMOSOME_NEW }= \\
=[000000000111110][000010100011100][000000000000010] .
\end{gathered}
$$

The chosen material constant has been marked red and the cutting point blue.
The next stage of the processing is another conversion of obtained sequences of characters into binary codes and decoding newly obtained genotypes. The material constants values obtained in this way make it possible to estimate mean squered errors of the curves adjustment for a proper model. As a result the estimation of correctness and utility of each material model, by confronting obtained results with the previous generation, is possible.

The whole process can last for any time. The number of generations is chosen by a programme user.

## 3 Results

As a result of implemented method of validation, very promissing outcomes have been obtained. The values of mean squered errors characterising best sets of material constants and obtained by the algorithm values of $\mathrm{C}_{1}, \mathrm{C}_{2}$ and K have been tabulated below.

| form of volume energy in an investigated energy-based model | outcomes |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
|  | C1 | C2 | K | MSE |
| $U^{(v)}=\frac{1}{2} K \frac{\left(\sqrt{I_{3}}-1\right)^{2}}{\sqrt{I_{3}}}$ | 0.0102 | 0.114 | 2 | 0.01399 |
| $U_{I}^{(\nu)}=K(J-1)^{2}$ | 0.0059 | 0.127 | 1 | 0.02592 |
| $U_{I I}^{(\nu)}=K(J \ln J-J+1)$ | 0.0050 | 0.123 | 1 | 0.00955 |
| $U_{\text {III }}^{(\nu)}=\frac{3}{4} K[\sqrt[3]{J}(J-4)+3]$ | 0.0258 | 0.048 | 1 | 0.05819 |
| $U_{I V}^{(\nu)}=K(J-\ln J-1)$ | 0.0288 | 0.043 | 1 | 0.06689 |

Table 1. Values of mean squared error and material constants obtained for investigated energy-based models

The figure placed below presents the adjustment of the theoretical curve to the experimental one in the whole investigated range of strains for the initial model, defined by the Equation (4) on which the whole algorithm was based - Mooney model modified by Wegner.


Figure 1. Comparision of results obtained for Mooney model modified by Wegner with experimental data obtained by Treloar

In case of this energy-based model as well as in case of the all other investigated models, the differences in adjustment of a theoretical curve to the experimental one, that is in MSE values, oscillate between 5 and $8 \%$ depending on the chosen number of generations, however, these differences decrease with increasing number of generations.

The application of genetic algorithms for this kind of measurements ensures also time saving. In comparision to conventional methods, the computation time has been reduced by $45 \%$ average, in cases of all the investigated models.

## 4 Conclusions

Rubber-like materials can be described in a satisfying way using Mooney model and different types of its modification. The basic investigated function on which the algorithm was built and which is given by Equation (4) gives one of the best obtained results as well as the modified model given by Equation (6) while the values of MSE are a chosen measure of adjustment.

The algorithm created which uses the mechanism of genetic material exchange enables the above mentioned results to be obtained in a much faster way in comparison to conventional enumerative methods.

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