The cellular automata parameters identification with use of parallel evolutionary algorithm

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Abstract

The goal of the paper is to present methodology of cellular automata rules parameters identification. The cellular automata rules parameters are identified on the basis of comparing the state of the cellular automata with referenced one. The identification is performed with the use of a parallel evolutionary algorithm.

Keywords: cellular automata, evolutionary algorithm, identification

1. Introduction

The cellular automata (CA) are used from years in many different areas of science. The combination of CA and the Finite Element Method (CAFE) in multiscale engineering problems are recently presented in papers [2]. The cellular automata can be applied to biological tissue modeling [4]. The most important problem in applications of cellular automata is proper description of rules. The researchers try to obtain rules on the base of phenomenological equations describing behavior of the real system. The goal of the paper is identification of rules parameters with the use of an artificial intelligence optimization method. The parallel evolutionary algorithm [1] is used in presented approach. The example of identification of rules parameters are shown in the paper.

2. Problem formulation

The result of identification is cellular automata which mimics some processes or phenomena. The observations from nature (e.g. observation of the damaged bone reconstruction) are input values for identification problem. The state of structure represented by cellular automata in different time moments allows to formulate an objective function. The aim of the identification is to find optimal parameters of cellular automata rules. The identification is formulated as minimization problem. The cellular automata with one floating point value for each cell are considered. The beginning state of the cellular automata should be the same as observed one in experiment in first time step. The final and mid states of the cellular automata and states observed during experiment are used to compute the objective function value:

$$F(\mathbf{p}) = \frac{1}{nsteps} \sum_{step=1}^{nsteps} \left(\frac{1}{nfeature} \sum_{feature=1}^{n} \left| \frac{v_{feature_{step}} - \hat{v}_{feature_{step}}}{\hat{v}_{feature_{step}}} \right| \right) \qquad (1)$$

where *nsteps* is a number of steps used for comparing cellular automata, *nfeature* is a number of features used to compare reference and analysed cellular automata, $v_{feature}$ is a feature value for analysed cellular automata, $\hat{v}_{feature}$ is a feature value for reference cellular automata, **p** is a vector containing cellular automata parameters.

3. Cellular automata

As the creator of cellular automata is considered John von Neumann [3]. However, in the 1970s John Conway invented a two-state, two-dimensional cellular automaton, and he called it, Game of Life¸ which became very widely known. Rules of Conway's CA are as follows: if a cell has 2 black neighbors, it stays the same. If it has 3 black neighbors, it becomes black. In all other situations it becomes white. In all other situations it becomes white. Despite its simplicity, the system achieves an impressive diversity of behavior, fluctuating between apparent randomness and order. In 2002 Wolfram published A New Kind of Science [5], which extensively argues that the discoveries about cellular automata are not isolated facts but have significance for all disciplines of science. In mathematics and computability theory, an elementary cellular automaton is a one-dimensional cellular automaton where there are two possible states (labeled 0 and 1) and the rule to determine the state of a cell in the next generation depends only on the current state of the cell and its two immediate neighbors. It is one of the simplest possible models of computation, but there is an elementary cellular automaton which is capable of universal computation. Cellular automaton structure is based on concrete data. Can not exist in one CA of two cells, which do not have all the elements of the same. The construction of all cells must be identical (they must have the same neighbors, the same sets of states, etc.). The construction elements of the machine can also significantly affect its quality. Each CA has a space that is created by the same cell, and call it a grid. Each cell stores its own state - depending on the state space. Cells are different, they are independent and each cell can be uniquely identified by its location on the grid. In a basic way affect the structure of the grid: dimension of space, depending on the size of the test problem (mesh 1D, 2D, 3D, nD); regularity condition, which speaks of the grid is completely full by the same cells (triangular, square, hexagonal, cubic, etc. for nD); number of neighbors (depending on both the above).

The neighborhood in the theory of cellular automata is the environment the cell. Neighbors can be defined in different ways. If we denote the directions on a compass rose: N, S, E, W and intermediate directions NW, NE, SE, SW, a von Neumann

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neighborhood is a collection of four cells: N, S, E, W. This neighborhood used for a triangular and square grid. Using these marks, the neighborhood Moore will be a set of all eight (in 2D mesh) cells around a central cell.

4. Parallel evolutionary algorithm

The evolutionary algorithms are global optimization techniques. The most important advantage of these algorithms is possibility of finding the global optimum. The evaluation of hundreds or thousands the objective function values during optimization is main drawback of the evolutionary algorithms. Parallelization of computations speeds up optimization process. The time cost of optimization can be reduced by introducing island or distributed population techniques. The modified evolutionary algorithm operates on subpopulations and each of them evaluates separately. The exchange of chromosomes between subpopulations occurs from time to time during migration step. The evolutionary algorithm operates on a population of chromosomes. The design parameters of optimization process play the role of the genes. The genes can be expressed as a floating value numbers which simplifies coding for problems where design variables are also formulated as floating point numbers.

5. Numerical example

The three dimensional cellular automata 100x100x25 with cubic cells are used in a numerical example. The cellular automata with constant boundary values are used. The cells can obtain binary values. The behaviour of the cells is similar to remodeling of the bone process, however rules are simplified and many aspects are no taken into account. The identification process should find 4 parameters used in cell rules. The cells are changed with use of transition rules:

1) if the cell is on
   if the number of neighbourhoods with sate on is bigger than *parameter1*
      if random value [0,20) is bigger than *parameter2* than change state to off
2) if the cell state is off
   if the number of neighbourhoods with sate off is bigger than *parameter 3*
      if random value [0,20) is bigger than *parameter4* then change state to on

where *parameter1-4* are searched values in identification process.

The number of active cells where used to compare the reference and obtained for a set of chromosomes defined parameters states of cellular automata. The reference state of the cellular automata was obtained during numerical experiment (so the exact values of starting and final state are known). The fitness function depends on the difference of numbers of active cells (*nfeature=1*) in three steps; 100, 150 and 200 (*nsteps=3*). The sample view of starting and states in step 100, 150, 200 for one cross section of the cellular automata are shown in Figure 1. The fitness function was based on average values obtained on the base of (1) from 10 cellular automata runs (due to randomness presented in cell rules).

The evolutionary algorithm with the floating point coding was used during computations. The uniform and Gaussian mutations and the simple crossover where used. The number of subpopulations was equal to 4 and total number of chromosomes was 60. The number of genes was 4.

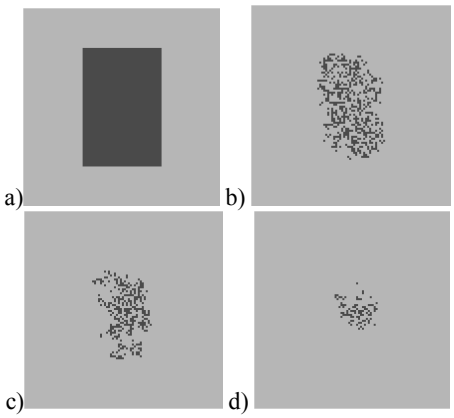

Figure 1: The view of cross section of cellular automata (*z=10*) a) starting, b) step 100, c) step 150, d) step 200

The change of the objective function value during optimization is shown in Figure 2.

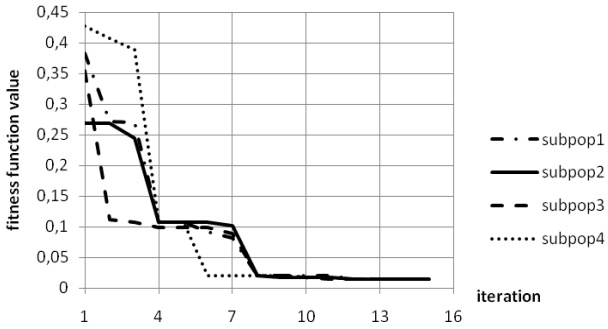

Figure 2: The fitness function value for subpopulations in function of number of iterations

6. Final conclusions

The parameters obtained after identification process were different than set used for reference cellular automata. It shows that there exist problems with uniqueness of solution. The use of set of features is planned in the future research to avoid these problems. The application of presented methodology to identification of parameters of cellular automata used in multiscale CAFE simulation of bone remodelling will be tackled in the future research.

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