Analysis of global properties for dynamical systems by a modified digraph cell mapping method

Xiaole Yue*, Wei Xu, Ying Zhang, Lin Du

Department of Applied Mathematics, Northwestern Polytechnical University, Xi'an 710072, PR China

ABSTRACT

A modified procedure is proposed in this paper to solve the limitations of digraph cell mapping method in accurately analyzing the global properties of dynamical system, such as fractal basin boundaries. Firstly a rough cell structure is applied to the generalized cell mapping (GCM) method to obtain the general global properties of dynamical systems with digraph algorithm, and then a procedure based on the composite cell coordinate system method is proposed to increase the calculation accuracy. In order to further increase the calculation speed, a simple and feasible parallel strategy is applied during the creation process of one-step transition probability matrix for the GCM method. Meanwhile, the memory consumption can be greatly reduced by storing the one-step transition probability matrix as finite separate data files. The accurate global properties of two examples, a nonlinear oscillator with fractal basin structure and the Lorenz system, are demonstrated to show the effectiveness of our proposed improvement strategy.

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1. Introduction

The researches of complex dynamical systems have always received a great deal of attention of many scholars [1–12], such as crisis, bifurcation, response, first-passage problem, optimal control, dynamic behavior, etc. Different analytical or numerical procedures are proposed to deal with these issues. Among these methods, cell mapping method is an efficient numerical tool not only for deterministic dynamical systems but also for stochastic dynamical systems, which was first proposed by Hsu [13] and called the simple cell mapping (SCM) method. Then it was extended to the version of the generalized cell mapping (GCM) method [14]. All these developments and applications have been gathered in a monograph [15]. For the GCM method, Hsu presented a theory of subdomain-to-subdomain global transient analysis of dynamics in [16]. The introduction of the theory of partially ordered sets and the theory of digraphs offered the GCM method a new way to analyze the multifaceted complex behavior of nonlinear systems [17].

Many improvements have appeared since the cell mapping method was proposed. For the SCM method there was interpolated cell mapping [18], adjoining cell mapping [19], Poincare-like simple cell mapping [20]. Based on the digraph theory, the generalized cell mapping method using digraph was proposed by [1,2], which can obtain the unstable invariant set of dynamical systems. By introducing two new concepts, the digraph cell mapping method was proposed by [21,22], which can obtain the stable and unsta-

ble manifolds of dynamical systems. Zou and Xu [23] proposed another modified method without using the digraph algorithm for the GCM method. Through the combination of point mapping and cell mapping, a few improved algorithms were presented such as point mapping under cell reference method [24–26], expanded point mapping method [27] and composite cell coordinate system method [28] etc. For the global analysis of dynamical systems, there are some other extension methods similar to cell mapping method using digraph, such as the set oriented method [29–31] and the symbolic dynamics method [32,33]. They can obtain the global properties such as attractors, saddles and invariant sets. But they don't contain some useful information including basins of attraction and basin boundaries.

In order to increase the calculation speed, the parallel computing method was introduced into the cell mapping method [34], where a parallel strategy was proposed and applied to a two-dimensional system. For a higher-dimensional dynamical system, the parallelized multi-degrees-of-freedom cell mapping method was developed by Eason and Dick [35], which mainly focused the attractors and the basins of attraction. Recently, Xiong et al. [36,37] proposed a parallel cell mapping method for global analysis of nonlinear dynamical systems, which can be applied to the high-dimensional systems.

To accurately predict the long-term behavior and global analysis of nonlinear dynamical systems by using the GCM method, some adaptive refinement techniques were put forward [30,38,39], which mainly focused the stationary densities, attractors and invariant measures. Further, Guder and Kreuzer [40] computed a series of sets that approximates the basin of attraction by the

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* Corresponding author.
  E-mail address: xiaoleyue@nwpu.edu.cn (X. Yue).

adaptive subdivision. However, how to obtain some other important global properties is still a challenge, such as fractal basin boundaries, saddles embedded in them, and invariant manifolds of saddles. Although they can be shown schematically by the GCM method, some accurate computing methods should be considered to precisely represent them.

In this paper, all the global properties, such as attractors, basins of attraction, basin boundaries, saddles and invariant manifolds, will be determined firstly by the GCM method and then the accurate results will be obtained based on the composite cell coordinate system method. Meanwhile, the ability of the proposed procedure to deal with the complex dynamical properties, such as fractal basin boundary, will be shown. Otherwise, a simple and feasible parallel strategy is applied to increase the calculation speed.

This paper is organized as follows. In Section 2, the review of generalized cell mapping method is firstly introduced. And then the detailed implementation of our proposed procedure will be discussed. Section 3 respectively provides a two dimensional dynamical system with fractal basin boundary and the Lorenz system to illustrate the effectiveness of our proposed procedure. Finally, some conclusions are given in Section 4.

2. The method

2.1. The digraph cell mapping method

In order to review the GCM method, we can refer to the work [17]. For an n-dimensional dynamical system

$$\dot{\mathbf{x}} = \mathbf{F}(\mathbf{x}, t), \mathbf{x} \in \mathbf{D} \tag{1}$$

where $\mathbf{x}$ is the state vector, $\mathbf{D}$ is the interesting bounded region in the state space $\mathbf{R}^n$ and $\mathbf{F}$ is a vector value function. By dividing the bounded region $\mathbf{D}$ into finite number of cells, the GCM method transforms the system (1) to the cell mapping system

$$\mathbf{p}(m+1) = \mathbf{P} \cdot \mathbf{p}(m) \quad or \quad \mathbf{p}(m) = \mathbf{P}^m \cdot \mathbf{p}(0) \tag{2}$$

where $\mathbf{P}$ is the one-step transition probability matrix with the $(i, j)th$ element p_{ij}, the computation of which is as follows. For a cell j, S points are uniformly selected within it. Then there will be S trajectories generated by simulating the system (1) with the time length ΔT. If S_i points fall in cell i from cell j, then the one-step transition probability $p_{ij} = S_i/S$. Once the one-step transition probability matrix $\mathbf{P}$ is calculated, the global properties of system (1) can be obtained based on the digraph algorithm. If we want to analyze the qualitative properties, we just need consider the generalized cell mapping to a digraph, where $p_{ij} > 0$ means that there exists a directional arc connecting the vertices j and i. By further analysis of the strongly connected sub-digraph of the digraph [21,22], the global qualitative properties of dynamical systems can be obtained, which contain attractors, basins of attraction, basin boundaries, saddles, stable and unstable manifolds etc.

2.2. The proposed method

2.2.1. Creation of one-step transition probability matrix

Two important issues for the GCM method are respectively long calculation times and huge memory demands. To reduce computer memory consumption of the GCM method, the analysis process can be divided into two independent portions: creation of one-step transition probability matrix $\mathbf{P}$ and qualitative analysis. Actually, most of calculation times of GCM method are spent in the process of creating one-step transition probability matrix. Therefore, we mainly consider how to reduce the computing times in this portion. The implementation procedure of parallel strategy is shown as follows, which is easily realized with high efficiency.

As the generation of every trajectory is separately from any other trajectory, it is very easy to parallelize the creation process of one-step transition probability matrix. Suppose that the interesting region $\mathbf{D}$ is divided into N cells, there are S trajectories are generated from each cell to determine the one-step transition probability of this cell. Denote the total times of computing the matrix $\mathbf{P}$ are T_1. As the computational processes of one-step transition probability of each cell i, $i = 1, 2, \ldots, N$ are independent, the calculation times will be reduced to $T_2 = T_1/N_p$ if there are N_p threads to simultaneously compute the one-step transition probability of all the N cells. Meanwhile, each thread will generate a data file after computing and so the information of the N_p threads needs not to be exchanged. Therefore, the calculation times are completely dependent on the number of threads, which can be nearly N_p times faster in theory compared with the conventional approach. In this work the number of thread N_p is 24 on a graphic workstation.

When all the cells are computed, the data of matrix $\mathbf{P}$ are obtained and stored as N_p separate file. Then by reading these files into memory, the qualitative properties can be calculated by digraph algorithm. In order to read these data quickly, the data of matrix $\mathbf{P}$ is stored in binary format in the creation process of one-step transition probability matrix. Because the one-step transition probability matrix is not stored during the global analysis process, the memory consumption can be greatly reduced.

2.2.2. Determination of global properties

Another challenge that should be considered is the accuracy of global properties for the GCM method. For this question, we adopt a procedure based on the composite cell coordinate system method [28] to deal with. First, a rough cell structure of region $\mathbf{D}$ is used, the global properties of dynamical system can be obtained by using the digraph algorithm, including attractors A_i', corresponding basins of attraction B_i', basin boundaries B', saddles S', stable manifold SM' and unstable manifold UM', where $i = 0, 1, 2, \ldots, N_a$ and N_a is the total number of attractors. A_0' and B_0' represent respectively the sink cell and its basin of attraction. The detailed processes to determine the accurate global properties are as follows.

2.2.2.1. Attractors.
An attractor is already a stable invariant set. The set of the obtained attractor A_i' should contain the true attractor. Thus the new set constituted by the iterative trajectory after some times from this attractor will tend to the true attractor. In order to obtain the more accurate attractor, we divide each cell of attractor A_i' into finite sub-cells. For each sub-cell, a trajectory is generated with its center as the initial value. Record the point of this trajectory after some times into an array. When all the cells of attractor A_i' are computed, the points in this array constitute a new set. If the value of measure between the new set and the previous set is less than a given error, the iteration stops and the new set is the true attractor, denoted as A_i.

2.2.2.2. Basins of attraction and basin boundaries.
The accurate basin of attraction B_i, $i = 1, 2, \ldots, N_a$ should contain the whole basin B_i' and parts of the corresponding basin boundary. Thus the basin of attraction B_i' needs not to be divided. The basin of attraction B_0' may not be the true basin of infinity. It may be a part of basin of attraction B_i', $i = 1, 2, \ldots, N_a$. To determine this, we just need consider the location of the trajectory after iteration from the center of one cell within basin B_0'. If the trajectory locates the basin B_i' then this cell is the point of the true basin of attraction B_i; otherwise, it is the true basin of infinity.

For each cell within basin boundary B', divide it into finite sub-cells. For each sub-cell, some given sample trajectories are evenly generated within it. If these trajectories after iteration are all located in the same basin of attraction B_i', then the sub-cell is the