

Global Analysis for Nonlinear Dynamical System Based on Parallel Subdomain Synthesis Method

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Abstract: The generalized cell mapping (GCM) method is an excellent numerical technique to reveal global structures hidden in dynamical responses of system, and the method has shown the powerful performance of global analysis in various model-based system which may be deterministic, stochastic or fuzzy. However, unaffordable memory requirement becomes a bottleneck for the cell mapping method when global analysis is carried out in a chosen domain of the state space with a specific computer in order to depict complex invariant sets with high resolution, and/or in high dimensions. In the work, a subdomain synthesis method with parallel computing based on clustered GPUs Architecture is thus developed to conquer the traditional ticklish problem encountered in global analysis. Several examples from low to high dimensions are illustrated to show the power of the proposed method.

Keywords: global dynamics, cell mapping method, subdomain synthesis, clustered GPUs computing

1. Introduction

Recall that the idea of space discretization has been introduced to GCM method developed originally by Hsu in the 1980s to investigate the global structures of nonlinear dynamical systems such as attractors, boundaries of basin as well as manifolds [1]. The discretization divides a continuous state space \mathbf{R}^N into a set of small and countable hypercubes called *cells*. The probabilities of the system residing in the cells are described by a Markov chain in the cell space as

$$\mathbf{P} \cdot \mathbf{p}(n) = \mathbf{p}(n+1) \quad (1)$$

where $\mathbf{p}(n)$ denotes the probabilistic vector describing the probability of each cell at n th step. $\mathbf{p}(n)$ indicates the probability vector of the response at n -step mappings. \mathbf{P} is a constant matrix with traditional $N_c \times N_c$ size that represents the one-step transition probability of the system.

It is known that the majority of executing time of the GCM is spent on the construction of the \mathbf{P} matrix, which depends predominantly on the number of cells used to discretize on each dimension of the chosen domain in the state space and also on the dimensions of the dynamical system. For a high-dimensional system, therefore, the computational and the storage burden is a great challenge to GCM. In the work, a *subdomain synthesis* method for cell mapping is proposed [2]. By this way, the chosen domain in the state space is divided into smaller subdomains with affordable memory requirements. Then, the cell mapping analysis can be independently carried out on each subdomain, taking advantage of GPUs architecture. The global structure of the system in the complete chosen domain can be finally identified and recovered from the dynamical information revealed in the subdomains.

2. Results and Discussion

One key technique in the proposed subdomain synthesis method is to solve the problem that the loss of invariant sets may occur when the traditional GCM is followed, if the invariant sets are split

into piece due to the domain partition in the state space. Here, the cells in each subdomain is classified as the follows: An *input cell* denotes the cell whose preimage cells are outside the processed subdomain. An *output cell* is the cell whose image cells are outside the processed subdomain. An *intersection cell* is the cell both of whose pre-image and image cells are outside the processed subdomain, as shown in Fig. 1.

In a processed subdomain D_i , suppose that the mapping paths across the partition boundaries from an output cell will surely return back to the processed subdomain through each input cell in finite maps. Then if the output cell is reachable also from the input cell inside the processed subdomain, these reachable cells can be regarded as a self-cycling set, for instance, cells $\{2,5\}$ for the processed subdomain D_1 in Fig. 1. In this paper, the synthesis of these cells, namely $\{2,3,4,5\}$, is called as a *virtual invariant set* in the complete chosen domain. Obviously, the cell set may not be a real strongly connected component of the dynamical system, but contain all possible invariant sets split by the partition boundaries on the chosen domain in the state space. So it is a covering set of the real invariant sets split by the state space partition. Thus, the global structure in the complete chosen domain can be identified and recovered from the virtual invariant sets after all dynamical information revealed in the subdomains are synthesized.

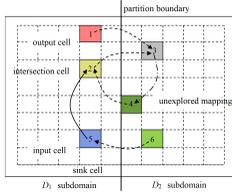


Fig. 1. Schematic representation of subdomain synthesis method

Three examples of application are presented in order to demonstrate the performances of the proposed method. The first example with 2-dimensions is used to validate the basic idea of subdomain synthesis method, and the second one presents 3-dimensional system, devoting to illustrating ability of the method. In the third example, the subdomain synthesis method is applied to a challenging example that is a 12-dimensional rotor system.

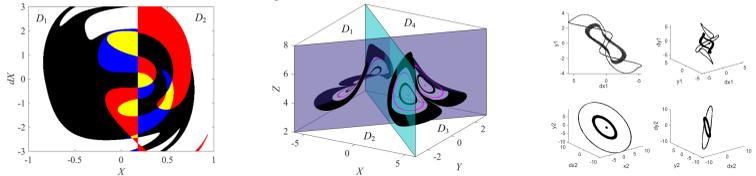


Fig. 2. Global analyses for three examples by the proposed subdomain synthesis method

3. Concluding Remarks

By the proposed method, the memory requirement is usually quite acceptable and much smaller than that of traditional way. The recovery of the global structure from the information of the subdomains takes a relatively little computation. In this way, the proposed method makes it possible to investigate global properties of the high-dimensional and complex systems.

References

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