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A two scaled numerical method for global analysis of high dimensional nonlinear systems

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Abstract This paper first analyzes the features of two classes of numerical methods for global analysis of nonlinear dynamical systems, which regard state space respectively as continuous and discrete ones. On basis of this understanding it then points out that the previously proposed method of point mapping under cell reference (PMUCR), has laid a frame work for the development of a two scaled numerical method suitable for the global analysis of high dimensional nonlinear systems, which may take the advantages of both classes of single scaled methods but will release the difficulties induced by the disadvantages of them. The basic ideas and main steps of implementation of the two scaled method, namely extended PMUCR, are elaborated. Finally, two examples are presented to demonstrate the capabilities of the proposed method. [doi:10.1063/2.1106301]

Keywords nonlinear systems, global analysis, multi-scaled numerical methods, point mapping, cell mapping, point mapping under cell reference

The global structure of a nonlinear dynamical system involves attractors and their basins of attraction, unstable invariant limit sets and their manifolds. The former is of great practical interest because it provides information on the types and the characteristics of possible system responses. The latter is of great scientific importance because it can provide a way to understand the mechanisms of many dynamical phenomena, i.e., intermittency, crises and boundary metamorphoses, as a few names among them. Global analysis is a process to detect and determine all the items composing of the global structure of a nonlinear system in order to get a full picture of the system characteristics.

For global analysis of nonlinear dynamical systems, especially those with strong nonlinearity, numerical methods are almost the only useful tool which is capable to be employed. However, dynamists still face great challenges in the global analysis on high-dimensional nonlinear systems even with numerical methods. For the currently existing numerical methods for global analysis, they can be classified into two classes according to how they hold the state space of the systems, continuous or discrete. The representative method for global analysis that falls into the first class and regards the state space as continuum is the classical point mapping method (or direct numerical simulation). The representative method for global analysis that belongs to the second class and holds the state space as discrete one is the cell mapping method.[1] In different cell mapping methods,[2–8] the state space is divided uniformly in each axial direction into small subsets, called (state) cells, with each cell taken as a state entity. From the idea and the implementation of generalized cell mapping (GCM),[5,6] it is not hard to find that the cell is actually still regarded as a collection (subset) of point states. So a cell having a finite volume owns a scale that is different from the scale of a point with zero volume. It is mathematically confirmed in Ref. 9 that approximation of invariant sets can be always obtained within an error of the cell (subsets) scale used by deriving the information from image of each cell (subset) through one-step mapping. The finer approximation of the invariant sets can be achieved when the refinement or the subdivision techniques[8,9] is adopted.

The features of the two classes of methods for global analysis in single scale will be summarized below. The purposes for summarizing them are the followings. On one hand, it will make the differences in the ways to dig out global structure of nonlinear systems between two classes of methods in two different scales more clearly. On the other hand, the advantages and disadvantages of the two classes of methods in two different scales will be well exposed. On basis of the knowledge readers will be easier to understand the ideas and the ways of implementation of the two scaled method for global analysis of nonlinear systems proposed in this paper. Moreover, as will be demonstrated later, the two scaled method will make some methods in one scale, e.g., PIM-triple method for determining unstable invariant limit sets, more feasible and efficient to be implemented.

For a finite dimensional dynamical system governed by an ordinary differential equation

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

where $x \in D \subset R^N$ is an N-dimensional state vector, $t \in R$ the time variable, and F a vector-valued function of x and t, D denotes the chosen region in the state space within which the global structure of the system will be explored.

Equation (1) is often casted into the form of point map or Poincare map in discrete instants of time

$$x_{n+1} = f(x_n). \tag{2}$$

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Features of the methods for global analysis in point scale. This class of methods takes state space as continuum and generates trajectories from a collection of initial states representing by points in the state space. For each individual trajectory starting from an individual initial point, it will be evolved until it converges into a state according to the given criterion, e.g., for periodicity of an attractor, before the generation of the trajectory will be ended. Then, the dynamics of the initial point (to which attractor it belongs) has been determined.

Such a (discrete) trajectory from an initial point in the chosen region can be mathematically expressed as

$$p = \{f^n x_0 | x_0 \in D, n \in Z^+, M_{\mathrm{c}} < n < M_{\mathrm{L}}\}, \tag{3}$$

where Z^+ stands for the positive integer, M_{c} and M_{L} are the minimal mapping step number to meet the given criterion of convergence and the maximal mapping step number set by a program, respectively. Therefore, the mapping points obtained between the mapping steps of M_{c} and M_{L} are thought to be on the attractor.

The advantage of this class of method is the accurate determination of an individual trajectory from a given initial point and the corresponding attractor in the sense to pertain the accuracy of computer. When using the class of methods for global analysis, trajectories from a collection of initial points in the chosen region are generated one by one and dealt with independently. The collection of the initial points can be denoted as

$$S = \{x_0^i \in D | i \in [1, N_{\mathrm{p}}] \subset Z^+\}, \tag{4}$$

where N_{p} is the total number of initial points in the chosen region used to detect and depict the global structure of the system.

The disadvantage of the method is that the transient part of each trajectory, which takes up a great portion of computational work of the trajectories, is thrown away and the information on the vector field derivable from the flow of the trajectories are not taken use. Due to the way of implementation of this class of method for global analysis, the number of initial points, N_{p}, should be large enough in order to find all possible attractors and depict the basin of attraction with sufficient accuracy in a chosen region in the state space. On the other hand, the length of a trajectory, M_{L}, should be long enough in order to well depict the structure of an attractor, especially for a strange attractor. Both features imply a requirement of increasing computational work.

Features of the methods for global analysis in cell (subset) scale. This class of methods takes state space as discrete one and divides the chosen region in the state space into uniform cells (subsets). That is

$$D = C = \cup C_i, \quad i = 1, 2, \cdots, N_{\mathrm{c}}, \tag{5}$$

where C_i is a rectangular parallelepiped in state space standing for a cell (subset), N_{c} is the total number of cells. The scale of the cells (subsets) can be defined as $d = \max \operatorname{diam}(C_i)$.

For each cell, the one-step image of the cell, which encloses all the images of individual points in the subset, will be first determined and then the complete self-cycling sets,[6] as approximations on the underlying invariant limit sets covered by the cells, will be acquired by removing the cells which contain no point on any of the individual invariant limit sets. This procedure can be expressed by

$$\begin{aligned} V_A = \{C_i \in C | f^{-1}(C_i) \cap C \neq \emptyset \text{ and} \\ f^{+1}(C_i) \cap C \neq \emptyset\}, \end{aligned} \tag{6}$$

where V_A is the approximation of or a covering of invariant limit sets in cell scale, d.

Some methods for the implementation of above procedures are developed on the basis of GCM,[4,5] e.g., the so-called generalized cell-mapping digraph (GCMD) method[7] and improved GCMD.[8] The advantage of this class of method is the sufficient use of the information on the vector field of the studied system derived from the mappings of cells. The disadvantage of the class of methods in global analysis is that: all cells in the chosen region must be dealt with and the size of cells, on the other hand, must be small enough in order to get a reasonable good approximation of the global structure so as not to induce mistake in the number and/or the types of the invariant sets. Due to the way of implementation of this class of method for global analysis, the region covered by cells should be large enough in order to contain the invariant sets to be uncovered in the state space. On the other hand, the size (scale) of the cells, d, should be small enough in order to well depict the structure of the invariant sets. Both features mean a requirement of increasing memory storage.

From above discussion the differences between the methods in point scale and in cell scale for global analysis of nonlinear systems become more obvious. Generally speaking, the methods in point scale are implemented in a local way: dealing with each individual trajectory separately. One trajectory is enough to complete the task of the detection and the description of the corresponding attractor. On contrast, the methods in cell scale are carried out in a global way: determining the approximation of invariant sets from the relation of the images of all cells in the chosen region. A large amount of cells with refinement technique are required in order to first cover and then converge to an invariant limit set. The failure of covering part of the invariant limit set by cells will generally cause the failure to catch the invariant limit set. The methods in point scale provide both the structure in state space and the time varying behavior of invariant limit sets. But the methods in cell scale only provide the structure in state space of invariant limit sets, even when the cell scale is reduced to the scale of a point in the precision of computers.

Difficulties are faced by the single scaled methods for global analysis of high dimensional systems. For the methods in point scale, e.g., point mapping method, the