



A MODIFIED INTERPOLATED CELL MAPPING METHOD

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A modified interpolated cell mapping (MICM) method is developed for global analysis of deterministic dynamical systems with smooth basin boundaries. By improving the algorithm of the interpolated cell mapping (ICM) and including the idea of sampling mappings of cells from the generalized cell mapping (GCM), MICM gives a more complete and precise global analysis of systems than ICM. In addition, based on analysis using MICM, a method using exact mappings is proposed to remedy the inaccuracy and incompleteness of global analysis due to interpolated mappings and the assumption of the sink cell. For the three systems studied in this paper, this method locates identical attractors and basins of attraction as the integration of a grid of points (IGP) method, with a 100-fold improvement in computational efficiency.

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1. INTRODUCTION

It is well known that there may be multiple attracting steady states, called attractors, in a non-linear dynamical system. Since different initial conditions may lead to different attractors, the attractors and their basins of attraction in the region of interest must be delineated to characterize the global behaviour of the system [1]. No analytical method can accomplish such a global analysis effectively. The conventional numerical approach is carried out by the integration of a grid of points method, that takes a grid of starts and iterates each forwards through numerical integration until a steady state behaviour is approximately realized. In this approach, the Poincaré map is used to simplify the location of the attractors and their basins of attraction; in addition, suitably defined neighbourhoods of the attractors must be introduced, since a system does not reach an attractor in finite time. As the number of points is increased, the location of the basin boundaries becomes better approximated. However, the computational effort required can soon become restrictive [2–4]. Thus, two kinds of cell mapping methods were provided to improve computational efficiency.

The first was developed by Hsu and co-workers under the names of simple cell mapping (SCM) and generalized cell mapping methods [5]. Both SCM and GCM divide the region of interest in state space into an array of cells in cell-state space. Each cell is considered to be an indivisible entity of the state of the system. The complement of the region of interest forms a large cell called the sink cell, that is the attractor of cells mapped outside the region of interest. SCM then constructs only one image cell for each cell, but GCM constructs multiple image cells. From the image cells, SCM locates periodic cells (attractors) and transient cells (basins of attraction) by using the concept of cell-state space; GCM locates persistent groups (attractors), single-domicile transient cells (basins of

attraction) and multiple-domicile transient cells (boundary regions) by applying the theory of finite Markov chains. GCM then divides persistent groups and boundary regions into smaller cells to locate attractors and basins of attraction more precisely [6]. In addition, GCM was applied to study random systems [6–8] with improved computational efficiency over Monte Carlo simulation [9].

The second was developed by Tongue and Gu under the name of interpolated cell mapping method [10, 11]. ICM is also called interpolated mapping, since it is not based on the concept of cell-state space [12]. This method takes the first mappings of all nodes (centers of cells) given by numerical integration as reference mappings, and then constructs interpolated mappings of nodes within the periods assigned. The attractors of cells are located by the final mappings of nodes. The applications indicate that ICM locates attractors and basins of attraction more precisely than SCM and GCM [10, 13]. ICM also provides high resolution analysis of dynamical systems by locating the attractors of points not situated at nodes. This method is often applied to determine the fractal-like [14] basins of attraction of systems [11, 15]. In addition, Ge and Lee characterized global behaviour of random systems using ICM and Monte Carlo simulation. This method yields more precise results than GCM when compared with those from Monte Carlo simulation [16].

These cell mapping methods use only the first mappings of cells given by numerical integration to characterize global behaviour of dynamical systems. The computational efficiency of global analysis is thus superior to that using IGP. However, analyses using cell mapping methods have three common limitations. First, the analyses are incomplete due to the basin of attraction of the sink cell, in which the attractors of cells are still unknown after the analyses. Second, the analyses are less accurate than the analysis using IGP since only the first mappings of cells are precisely given by numerical integration and other mappings are approximations. Third, the analyses require more computational memories than the analysis using IGP since cell mapping methods study all cells simultaneously. As the dimensions of systems increase, the computational memories required can soon become restrictive. Thus, cell mapping methods are generally applied to obtain a global picture of low order systems [14]. Furthermore, cell-state space is not an actual feature of dynamical systems, but is only an assumption. From the point of view of state space, a cell is just a small cube in state space. Thus, if a cell resides in a basin of attraction wholly, all initial conditions in the cell eventually lead to an identical attractor. If a cell includes part of basin boundaries, different initial conditions in the cell may lead to different attractors. Such cells are important for global analysis since they point out basin boundaries that define which regions of state space go to which attractors. In addition, the cells in which attractors reside must also be located to indicate the positions of attractors. Therefore, cells can be classified into *attracting*, *basin* and *boundary* cells, to indicate the attractors, basins of attraction and basin boundaries of systems. If a cell mapping method locates the attracting and boundary cells of a system correctly, further analysis can study only these cells with satisfactory accuracy. However, as the dimensions of systems increase, the difficulties of tracking the basin boundaries of the systems by each cell mapping method goes up quickly due to the large amount of computational memory and effort required.

In this paper, a modified interpolated cell mapping method is developed to study the global behaviour of deterministic dynamical systems with smooth basin boundaries. MICM gives more complete and precise global analyses than ICM for the systems studied in this paper. After analysis using MICM, cells are classified into attracting, basin and boundary cells to indicate attractors, basins of attraction and basin boundaries of systems. However, further analysis must be carried out precisely to locate attractors and basins of attraction of systems, since analyses using cell mapping methods are not precise and

complete enough as stated above. Therefore, three methods (high-resolution analysis, refined cell space and exact mappings) are proposed for such further analyses. The first two methods still use interpolated mappings to locate attractors and basins of attraction, but the last uses mappings given by numerical integration. Among these methods, the method using exact mappings gives the most complete and accurate analysis, correctly locating all attractors and basins of attraction of the three systems studied with a 100-fold computational improvement over IGP.

2. A MODIFIED INTERPOLATED CELL MAPPING METHOD

When a deterministic system is studied by ICM, the interpolated mappings of each cell are constructed within the mapping periods assigned, such as 20 periods used in [10], and considered as the mapping sequence of the cell. Studying the mapping sequences successively, ICM locates periodic attractors and their basins of attraction by an assigned attraction criterion, such as a 10^{-3} used in [10]. The cells not attracted by the periodic attractors located are all considered in the basin of attraction of a “strange attractor”, that is the set of attractors not located by the attraction criterion. However, this strange attractor often indicates an actual strange attractor for a periodic system [10, 13]. Although ICM is seemingly the best existing cell mapping method, global analysis using ICM still has three drawbacks. First, an incorrect global analysis may result from an inappropriate assignment of mapping periods and the attraction criterion, as shown in a later analysis. When assigning few mapping periods and a small attraction criterion, ICM may not locate basins of attraction of periodic attractors completely, since some cells may not lead to their attractors within the criterion during the mapping periods [17]. On the other hand, when assigning many mapping periods and a large attraction criterion, ICM may locate spurious periodic attractors in the region of an actual strange attractor as follows. The region of a strange attractor is divided into a finite number of small cubes with a uniform size of the attraction criterion. Then a spurious periodic attractor is located by ICM if a cell is mapped to one of these small cubes more than once within the mapping periods assigned. This is more possible when more mapping periods are used or a larger attraction criterion is assigned. Then various assignments of mapping periods and attraction criteria may yield various global analyses of a system. Thus, different mapping periods and attraction criteria, that may come from several trial analyses, are used by ICM to give precise global analyses of different systems [10, 13, 15, 17, 18]. Second, ICM does not classify cells to delineate the critical cells of global analysis. High resolution analysis of ICM studies points in each cell. Thus, for dynamical systems with smooth basin boundaries, most of the computational effort required is used to study points in basin cells, but precision of analysis is not improved by these studies. Third, ICM does not distinguish multiple strange attractors or limit cycles of a system, and considers them as a strange attractor only; thus, the global analysis of such a system is incomplete.

ICM is applied to the analysis of a forced Duffing’s oscillator, governed by the following equation:

$$\ddot{x} + 0.25\dot{x} + 0.02x + x^3 = 8.5 \cos(t). \quad (1)$$

This system, which was also studied in [10, 19], has a periodic attractor of period three and a strange attractor in the region of interest, $(1.5, 4.2) \times (-3.0, 6.0)$. In Figure 1(a) are shown the attractors and basins of attraction located by ICM with a total of 20 mapping periods and an assigned attraction criterion of 10^{-4} , in which 12.4% of the basin of attraction of the periodic attractor is not located; Figure 1(b) shows those with a total of 50 mapping periods and an assigned criterion of 2×10^{-4} , in which five spurious periodic

attractors are located on the strange attractor. In these figures, the symbols “+”, “×” and “·” denote the basins of attraction of the sink cell, the periodic attractor and the strange attractor. Large and small dots show the periodic attractor and strange attractor located by ICM. Curves show the reference basin boundaries located by IGP, with 909² points studied. Moreover, all global analyses in this paper are carried out using 101² cells in the region of interest unless otherwise specified.

A modified interpolated cell mapping method is then developed to remedy the three drawbacks of ICM when applied to global analysis of deterministic dynamical systems with smooth basin boundaries. Two criteria are used by MICM. The first criterion is a 10^{-5} cell size to locate periodic attractors. This small criterion can avoid locating spurious periodic attractors in the region of a strange attractor. The second criterion is a 10^{-2} cell size to locate the cells attracted by the periodic attractors located. In addition, unlike ICM, which assigns identical mapping periods for all cells, MICM constructs the interpolated mappings of different cells through varied iterations of N_p , typically ten, periods to locate the attractors of cells. After long enough periods, MICM can locate periodic attractors

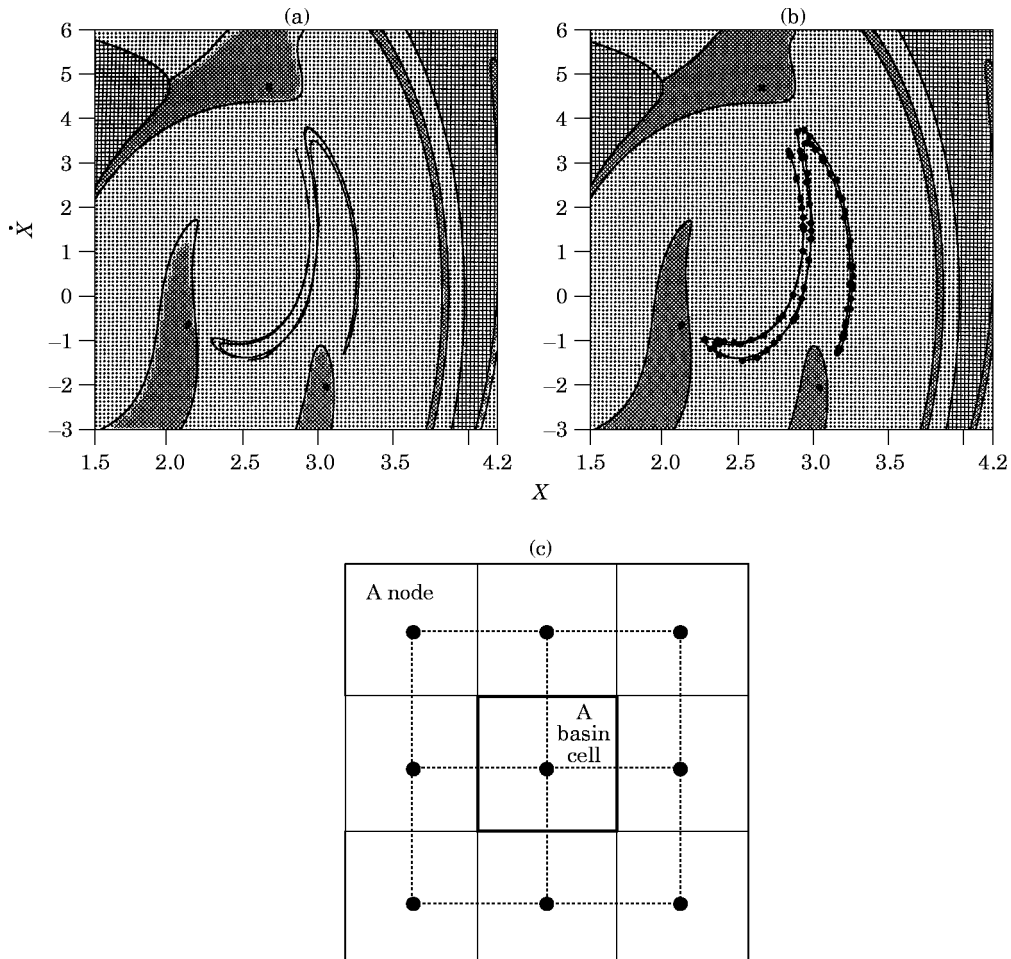


Figure 1. Various global analyses of the system given by equation (1): (a) by ICM with a total of 20 mapping periods and an attraction criterion of 10^{-4} ; (b) by ICM with a total of 50 mapping periods and an attraction criterion of 2×10^{-4} ; (c) a basin cell of an attractor defined by nine nodes leading to the attractor.

with periods of less than N_p and their complete basins of attraction correctly. Thus the first drawback of ICM is remedied. Moreover, MICM classifies cells into the attracting, basin and boundary cells of attractors to indicate attractors, basins of attraction and basin boundaries of a system. This classification of cells reveals the critical cells for further analysis of attractors and basins of attraction; namely, the attracting and boundary cells. Thus the second drawback of ICM is remedied. Furthermore, MICM first regards all the attractors not located by the first criterion as an “undetermined attractor”. The attracting cells of the undetermined attractor are then divided into different sets of attracting cells with each indicating an attractor. Thus the third drawback of ICM is remedied. Global analysis using MICM includes two stages. First, periodic attractors with periods of less than N_p and their basins of attraction are located. Second, the attracting cells of the undetermined attractor are divided into different sets, and then the basin of attraction of each set is located.

For n -dimensional dynamical systems, the algorithm of MICM is stated as follows. In the first stage of analysis using MICM, the first mappings of cells in the region of interest and of cells surrounding the region are constructed by numerical integration to serve as the reference mappings for interpolation. Hence, $(N_c + 2)^n$ cells are studied by MICM, where N_c is the number of the total cells divided in each dimension of the region of interest. Then each cell has a sequence of N_p interpolated mappings at the first N_p periods. When mappings of cells are constructed, a cell is considered in the basin of attraction of the sink cell if it is mapped outside the region of interest. From these mapping sequences, periodic attractors with periods of less than N_p are located by the first criterion assigned above. If no periodic attractor is located, the N_p th mapping of each cell is assigned to the first mapping, and then iterated forward to construct the next iteration of N_p mappings. If periodic attractors are located and a cell leads to a periodic attractor within the second criterion, the cell is considered in the basin of attraction of the attractor. In addition, MICM assumes that a cell eventually leads to a periodic attractor if its N_p th mapping in a mapping sequence reaches a basin cell of the periodic attractor.

Definition 1. If a cell and its adjoining cells [5] all lead to an identical attractor, this cell is a *basin cell* of the attractor.

This assumption is reasonable for the analysis of systems with smooth basin boundaries. It considers only the central part of a region, the corners of which all lead to an attractor, as a region in which all initial conditions eventually lead to the attractor. For example, a basin cell of a two-dimensional system is the central quarter of the region latticed by nine (3×3) nodes (centers of cells) that lead to the same attractor, as shown in Figure 1(c). After each iteration, MICM defines the basin cells of the periodic attractors located; furthermore, except for the cells attracted by the sink cell and the periodic attractors located, all cells are considered to be in the basin of attraction of an “*undetermined attractor*”, that is the set of the final mappings of these cells in the iteration. Then MICM constructs new mappings of only the cells in the basin of attraction of the undetermined attractor. When cells are iterated forwards, some cells reach the periodic attractors located after long enough periods, and thus the basin of attraction of the undetermined attractor decreases. The construction of mappings of cells is eventually halted upon satisfaction of two conditions. First, the number of cells in the basin of attraction of the undetermined attractor does not decrease in an iteration. This indicates that all cells attracted by the periodic attractors located have led to the attractors within the second criterion or reached the basin cells of the attractors. Second, the number of attracting cells of the undetermined attractor does not decrease in the iteration.

1 *Definition 2.* The *attracting cells of an attractor* are the cells in which the final mappings of cells in the basin of attraction of the attractor reside.

The number of attracting cells of the undetermined attractor eventually decreases to a constant value, since all cells will reach their attractors within one cell size after long enough periods. If the second condition is satisfied, the attracting cells of the undetermined attractor can efficiently indicate the regions of the attractors not located by the first criterion. In addition, the sets of attracting cells for the periodic attractors located are defined by the positions of the attractors. The first stage of global analysis is finished here. The basins of attraction of the sink cell and the located periodic attractors have been located completely. If all cells are attracted by the attractors located, global analysis using MICM is also finished. Otherwise, the second stage of analysis is carried out. Note that the undetermined attractor defined by MICM is the set of attractors not located by the first criterion. If multiple attractors belong to the undetermined attractor, these attractors and their basins of attraction must be further located for a complete global analysis. In addition, after the first stage of analysis, MICM ensures that all cells reach the basin or attracting cells of attractors through various long enough periods. On the other hand, ICM cannot ensure this, since identical mapping periods are assigned for all cells, but different cells require various periods to lead to their attractors within an identical distance, the attraction criterion.

In the second stage of analysis using MICM, the idea of sampling mappings of cells from GCM [5] is introduced to divide the attracting cells of the undetermined attractor into different sets of attracting cells. Some of these attracting cells are further iterated forwards by interpolation in extra iterations. In each iteration, all mappings of an attracting cell are assigned to the sampling mappings of the attracting cell. The first set of attracting cells is located as follows. The first registered attracting cell of the undetermined attractor is considered in the first set. If a sampling mapping of this attracting cell reaches another attracting cell, the reached attracting cell is also included in the first set. Only the attracting cells in the first set are continuously examined in extra iterations. The iterations to locate the first set are halted when the number of attracting cells in the first set does not increase. Then other sets of attracting cells are located by the attracting cells not in the existing sets according to the same algorithm. In this analysis, if a sampling mapping of an attracting cell reaches an attracting cell in an existing set, the former attracting cell is also included in the set. Each attracting cell of the undetermined attractor eventually belongs to a set. This simple algorithm divides the attracting cells of the undetermined attractor into different sets with each indicating an attractor; moreover, no extra computational memory is required. Then the basin of attraction of each set is located by checking the final mappings of cells in the basin of attraction of the undetermined attractor. If the final mapping of a cell resides in an attracting cell in a set, this cell is considered in the basin of attraction of the set. Thus, all attractors and basins of attraction are located. MICM then defines the basin and boundary cells of each attractor. Global analysis using MICM is finished here.

Definition 3. If a cell and each of its adjoining cells [5] lead to different attractors, this cell is called a *boundary cell*.

MICM is applied to analysis of the system given by equation (1), with $N_p = 10$. In Figure 2(a), the number “1”, “2” and “3” denote the regions of basin cells of the sink cell, the periodic attractor, and the strange attractor located by MICM; squares denote the boundary cells. Large and small dots denote the periodic attractor and the strange attractor located; curves denote the precise basin boundaries located by IGP. It can be seen that the 1665 boundary cells located with a thickness of two or three cell sizes include the precise basin boundaries. In addition, all the attracting cells of the undetermined

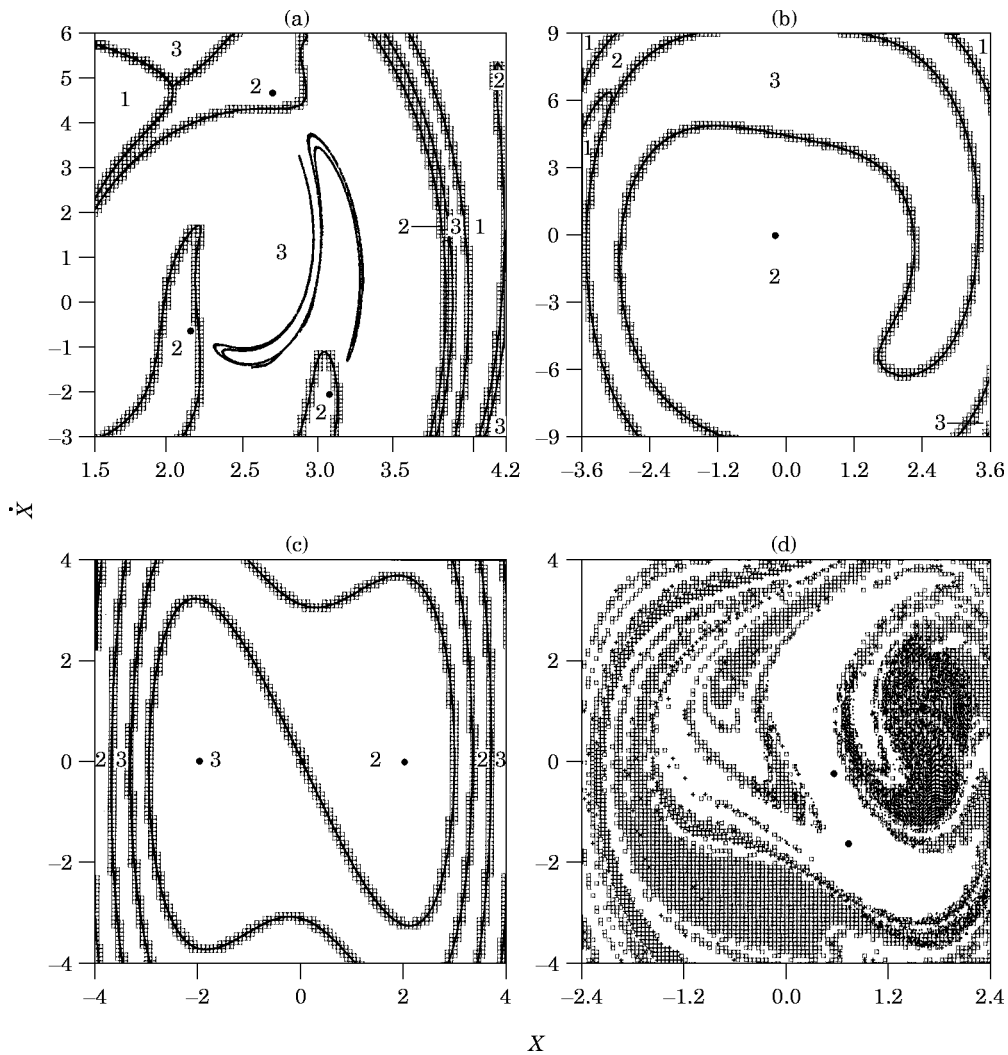


Figure 2. Global analysis using MICM of the system: (a) equation (1); (b) equation (2); (c) equation (3); (d) equation (4).

attractor belong to a set. Note that if MICM does not locate the attractors of the cells surrounding the region of interest, all cells at the edges of the region of interest must be regarded as boundary cells due to the definition 3. Moreover, MICM yields the same global analysis of the system with N_r ranging from 4 to 900. Therefore, global analysis using MICM is more stable than global analysis using ICM for this example.

The ability of MICM to locate all boundary cells correctly is examined by another forced Duffing's system, which was also studied by GCM [7], governed by the following equation:

$$\ddot{x} + 0.1\dot{x} + x + x^3 = \cos(2.5t), \quad (2)$$

with the region of interest $(-3.6, 3.6) \times (-9, 9)$. MICM locates a periodic attractor of period one situated at $(-0.192, 0.229)$ and the undetermined attractor with only one attracting cell situated around $(1.898, 5.092)$. The 1261 boundary cells also include the precise basin boundaries, as shown in Figure 2(b). Then the attracting cell of the

undetermined attractor is examined by numerical integration. The undetermined attractor is indeed a periodic attractor of period one. Although this periodic attractor is not located by the first criterion, this global analysis is still complete, since MICM locates all attractors and their basins of attraction in the region of interest. After this global analysis using MICM, it is necessary to study the single attracting cell of the undetermined attractor. In addition, all cells reach the attracting cells of attractors within 90 periods. However, this is of no consequence in global analyses using MICM. On the other hand, to locate the complete basins of attraction of this system by ICM, 120 periods are required for all cells with an attraction criterion of 10^{-4} , and 150 periods are required for an attraction criterion of 10^{-5} . The information cannot be obtained before several trial analyses.

MICM is then applied to global analysis of the autonomous system governed by the following equation:

$$\ddot{x} + 0.3\dot{x} - 4x + x^3 = 0, \quad (3)$$

with the region of interest $(-4, 4) \times (-4, 4)$. When characterizing the global behaviour of an autonomous system, MICM locates point attractors [1] as periodic attractors of period one, and considers all limit cycles as the undetermined attractor after the first stage of analysis; in addition, the mapping time step duration is at our disposal [5]. Assigning the mapping time step duration to $0.05 \times 100 = 5$ time units, MICM locates an unstable node situated at $(0, 0)$ and two point attractors situated at $(2.00, 0.00)$ and $(-2.00, 0.00)$ for this system. No cell is mapped outside the region of interest. The 1942 boundary cells also include the basin boundaries located by IGP, as shown in Figure 2(c).

From these three analyses, it is found that MICM can locate all boundary cells correctly. The accuracy of analysis using MICM forms a basis for the further analysis of locating exact attractors and basins of attraction. On the other hand, the parameter variation method of ICM (PVICM) [17] defines boundary cells as definition 3. However, PVICM may not locate complete basins of attraction of periodic attractors, since PVICM constructs mappings of all cells within identical periods as ICM. Thus, the boundary cells located by PVICM may not include the entire basin boundaries, although PVICM is more computationally efficient than ICM for parametrical analysis.

Global analysis using MICM also provides information on whether the basin boundaries of a system are smooth. For example, MICM is applied to the analysis of a forced Duffing's oscillator governed by the following equation:

$$\ddot{x} + 0.1\dot{x} - x + x^3 = 3.2 \cos(0.4776t), \quad (4)$$

with the region of interest $(-2.4, 2.4) \times (-4, 4)$. This system with fractal basin boundaries was also studied by high resolution analysis of ICM [18]. Two periodic attractors of period two and their basins of attraction are located by MICM, as shown in Figure 2(d). The symbol “+” and squares denote the basins of attraction of the sink cell and the first attractor, and the symbol “×” and blank areas for that of the second attractor. Small dots denote the first mappings of cells in the basin of attraction of the first attractor. This analysis provides the following information. First, a large amount of the cells in each basin of attraction are not situated continuously. This indicates that this system has fractal-like basins of attraction. Second, the first mappings of some cells in the basin of attraction of the first attractor reside in the basin of attraction of the second attractor. Note that all mappings of a point reside in the same basin of attraction, since each mapping assigned to an initial condition follows the mapping trajectory of the point to the attractor. Let all points in a basin of attraction be a set H . Then $G(H) \subset H$, where G is a point mapping. Therefore, each basin of attraction is a positively invariant set [5]. The phenomenon

obtained by the analysis conflicts with this feature of basins of attraction. Finally, the first mappings of some cells in the basin of attraction of the first attractor are surrounded by the cells in the basin of attraction of the second attractor. Thus, the second mappings of these cells in the basin of attraction of the first attractor are constructed by interpolation of the reference mappings of cells in the basin of attraction of the second attractor. This construction is not reasonable. According to these considerations, MICM cannot be directly applied to global analysis of a system with fractal basin boundaries; however, high resolution analysis of ICM without these considerations will locate fractal-like basins of attraction with some degree of error. This topic is not pursued in this paper.

MICM is finally applied to global analysis of the four-dimensional system, which was also studied by SCM [22], governed by the coupled van der Pol equations as follows:

$$\begin{Bmatrix} \dot{x}_1 \\ \dot{x}_2 \end{Bmatrix} - \mu \begin{bmatrix} 1 - x_1^2 & 0 \\ 0 & 1 - x_2^2 \end{bmatrix} \begin{Bmatrix} \dot{x}_1 \\ \dot{x}_2 \end{Bmatrix} + \begin{bmatrix} 1 + v & -v \\ -v & 1 + \eta + v \end{bmatrix} \begin{Bmatrix} x_1 \\ x_2 \end{Bmatrix} = \begin{Bmatrix} 0 \\ 0 \end{Bmatrix}, \quad (5)$$

with $\mu = 0.1$, $v = 0.1$ and $\eta = 0.04$. The region of study, $-3 \leq x_1, \dot{x}_1, x_2, \dot{x}_2 \leq 3$, is divided into 25^4 cells. The mapping time step duration is assigned to $0.2 \times 50 = 10$ time units with $N_p = 10$. MICM first locates an unstable node situated at $(0, 0, 0, 0)$. In Figures 3(a) and (b) are shown the projections of the undetermined attractor on the x_1 - \dot{x}_2 plane after the first and second iterations. There is no change in the attracting cells and the basin of attraction of the undetermined attractor in the seventh iteration. Thus, the first stage of global analysis is finished there. The attracting cells of the strange attractor are then divided into two sets of 136 and 128 attracting cells, indicating the first and second limit cycles. In Figures 3(c) and (d) are shown the projections of the two limit cycles on the x_1 - \dot{x}_2 and \dot{x}_1 - \dot{x}_2 planes, with dots denoting the two limit cycles located by MICM and curves for those located by IGP. The two limit cycles located by MICM agree well with those located by IGP. In addition, there are altogether 390 625 cells in the region of study, of which 1, 189 772 and 200 852 cells are in the basins of attraction of the unstable node, the first limit cycle and the second limit cycle. There are only 152 cells with attractors incorrectly located when compared with those located by IGP. For $\dot{x}_2 = 0$ and $\dot{x}_1 = 0.24, 0.48$ and 0.72 , the basins of attraction are shown in Figures 4(a)–(d). The symbols “+”, “×” and “.” denote the cells attracted by the unstable node, the first limit cycle, and the second limit cycle, respectively. The basins of attraction located by MICM are more precise than those located by SCM [20]. In addition, the algorithm of ICM [10] cannot distinguish the two limit cycles and their basins of attraction. In Figures 3(a)–(c) it is also indicated that the number of attracting cells of the undetermined attractor decreases as the mappings of cells are iterated forwards. Hence, MICM appropriately finishes the first stage of analysis by checking the number of attracting cells of the undetermined attractor. In analysis using IGP, the two limit cycles are first located. If a cell is mapped near a limit cycle within 0.05, this cell is assumed to be attracted by the limit cycle.

The computational times required for various global analyses of the systems, equations (1–3) are listed in Table 1. The mapping periods used by ICM indicate the periods within which the mappings of all cells are constructed, and those used by MICM and IGP indicate the periods within which the mappings of cells are constructed in each iteration. The two criteria of ICM and IGP are used to locate the periodic attractors and their basins of attraction, respectively. In global analysis using IGP, if a point does not reach a periodic attractor before 100 periods, the point is considered to be in the basin of attraction of a strange attractor. When compared with the analysis using IGP, the number of cells with incorrectly located attractors is indicated by the item “number of cells of error”. It can be seen that analysis using MICM is more precise than analysis using ICM: in addition,

the computational times required for global analysis using MICM and ICM are of the same order. Furthermore, the computational times required for analyses using MICM and IGP of the four-dimensional system given by equation (5) are 8093 and 48 820 seconds. The computational improvement of ICM over IGP is not so apparent as that of analyses of two-dimensional systems, since more computational effort is required to construct an interpolated mapping for higher-dimensional systems [12, 21]. In addition, all computations in this paper were processed on an IRIS Indigo workstation with 16 MB of main memory. The algorithm used for numerical integration is the fourth order Runge-Kutta method. Each mapping time step duration for periodic systems [5], namely one period, is divided into 100 integration steps used in numerical integration.

3. FURTHER ANALYSIS BASED ON GLOBAL ANALYSIS USING MICM

Since global analysis using MICM correctly locates the boundary and attracting cells of systems, as shown previously, the systems can be further studied on the basis of global analysis using MICM. In this section three methods are provided for further analysis of

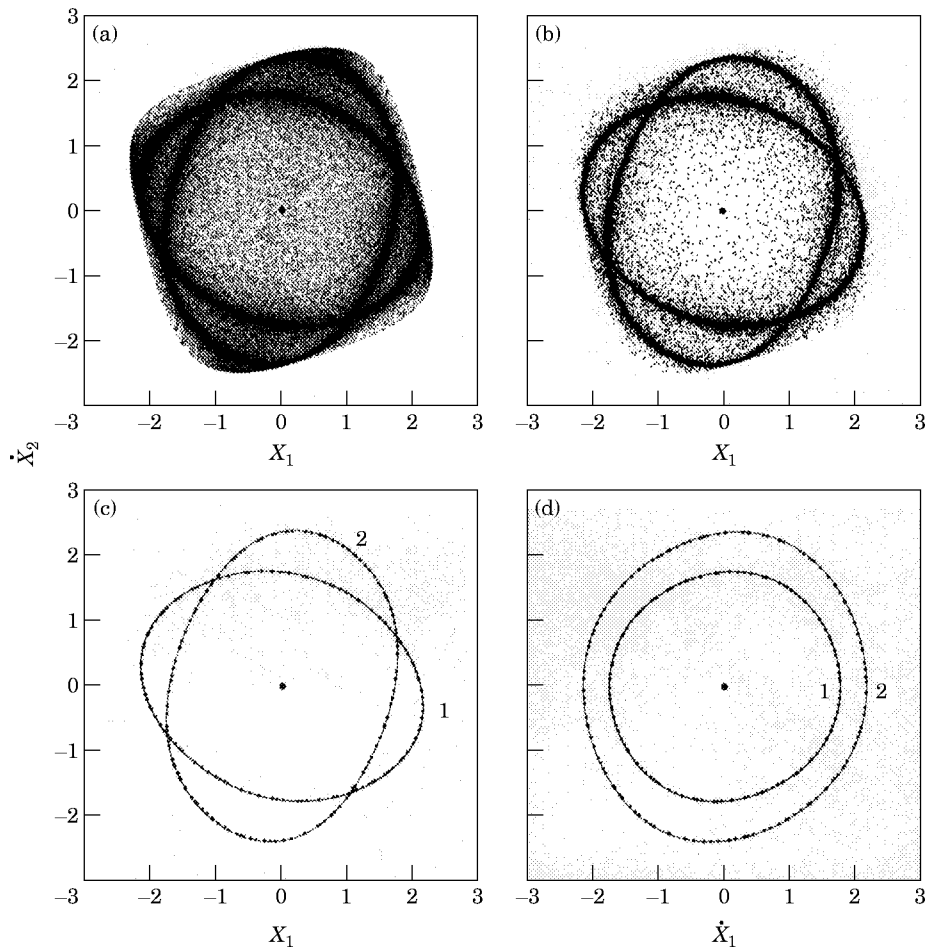


Figure 3. The evolution of the undetermined attractor using MICM for global analysis of the system given by equation (5): (a) after the first iteration; (b) after the second iteration; (c, d) after the seventh iteration with the attracting cells of the undetermined attractor divided into two sets of attracting cells.

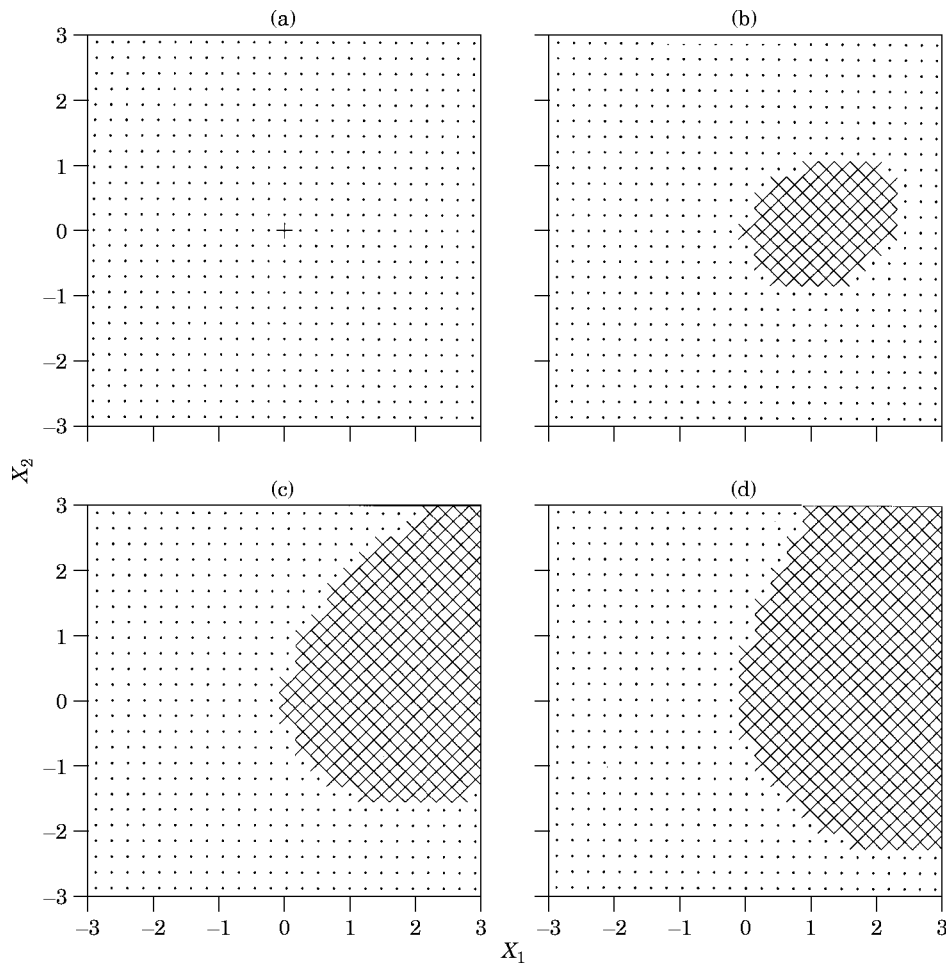


Figure 4. Basins of attraction of the system given by equation (5), located by MICM for $\dot{x}_2 = 0$: (a) $\dot{x}_1 = 0$; (b) $\dot{x}_1 = 0.24$; (c) $\dot{x}_1 = 0.48$; (d) $\dot{x}_1 = 0.72$.

basins of attraction and attractors: high resolution analysis, refined cell space and exact mappings. The first two methods still use interpolated mappings, but the last method uses exact mappings given by numerical integration.

High resolution analysis of ICM is first applied to locate the detailed basin of attraction of the system, equation (1), with 909^2 points studied, a total of 35 mapping periods and an attraction criterion of 10^{-5} . In Figure 5(a), the basin boundaries located by ICM and IGP are shown by the thin and thick curves. The maximum difference between these two basin boundaries is more than one cell size. This reduces the reliability of high resolution analysis of ICM. The errors of the basins of attraction located come from two sources. First, some points do not reach the periodic attractor within 10^{-5} before 35 periods and are considered to be in the basin of attraction of the strange attractor. This error can be remedied by high resolution analysis of MICM with the maximum difference of less than one cell size, as shown in Figure 5(b). In high resolution analysis of MICM, all basin cells of attractors are considered to be criteria of attraction for the attractors located by global analysis using MICM; moreover, only the mappings of points in the boundary cells are given by interpolation of reference mappings used in global analysis until the points are

mapped to the basin cells. If a mapping of a point reaches a basin cell of an attractor, the point is considered to be in the basin of attraction of the attractor. Using the large attraction criteria for attractors and constructing mappings of points in the boundary cells through various long enough periods, high resolution analysis of MICM locates more complete basins of attraction of the periodic attractor than high resolution analysis of ICM, as shown in Figure 5(b). Another source of error results from the fact that the interpolated mappings of points near basin boundaries are not precise enough to locate the attractors correctly. If an interpolated mapping of a point resides in the basin of attraction of another attractor, the attractor of the point is not correctly located. This error cannot be remedied by high resolution analysis of MICM, since identical reference mappings are used by high resolution analyses of MICM and ICM.

To reduce the source of error due to interpolated mappings, the method of refined cell space is proposed. The boundary cells located by global analysis using MICM are further divided into refined boundary cells. The first mappings of the refined cells from numerical integration serve as precise reference mappings of interpolation. If a mapping of a refined cell still resides in a boundary cell, the next mapping is given by interpolation of these reference mappings. If a refined cell is mapped to a basin cell of an attractor, the refined cell is considered to be in the basin of attraction of the attractor. When this method is applied to the location of detailed basins of attraction of the system given by equation (1), with each boundary cell divided into 9^2 refined boundary cells, the detailed basins of attraction located are almost identical to those located by IGP with only the attractors of 51 refined cells incorrectly located. This approach is more precise than high resolution analyses of MICM and ICM, since the reference mappings of refined boundary cells can construct more precise interpolated mappings to locate the attractors of refined cells more correctly.

The method of refined cell space is also applied to locate precise attractors. The attracting cells located by global analysis using MICM are divided into refined attracting cells for precise reference mappings. The mappings of each refined cell are then given by interpolation of these reference mappings. If a mapping of a refined cell reaches a basin cell located by global analysis using MICM, the basin cell is also refined for precise reference mappings. In this approach, the region of study is reduced to only the sets of attracting cells located by global analysis using MICM; moreover, the two criteria, 10^{-5} and 10^{-2} refined cell size, are used to locate periodic attractors and their basins of

TABLE 1
Computational time required (seconds) for various global analyses

System	Method	Mapping periods	Criteria	Time	Number of cells of error
Equation (1)	ICM	20	$10^{-4}, 10^{-4}$	39	229
	ICM	50	$2 \times 10^{-4}, 2 \times 10^{-4}$	48	39
	MICM	4		41	39
	MICM	10		42	39
	MICM	50		48	39
	IGP	10	$10^{-5}, 10^{-4}$	2192	0
Equation (2)	MICM	10		46	18
	IGP	10	$10^{-5}, 10^{-4}$	2748	0
Equation (3)	MICM	10		22	4
	IGP	10	$10^{-5}, 10^{-4}$	308	0

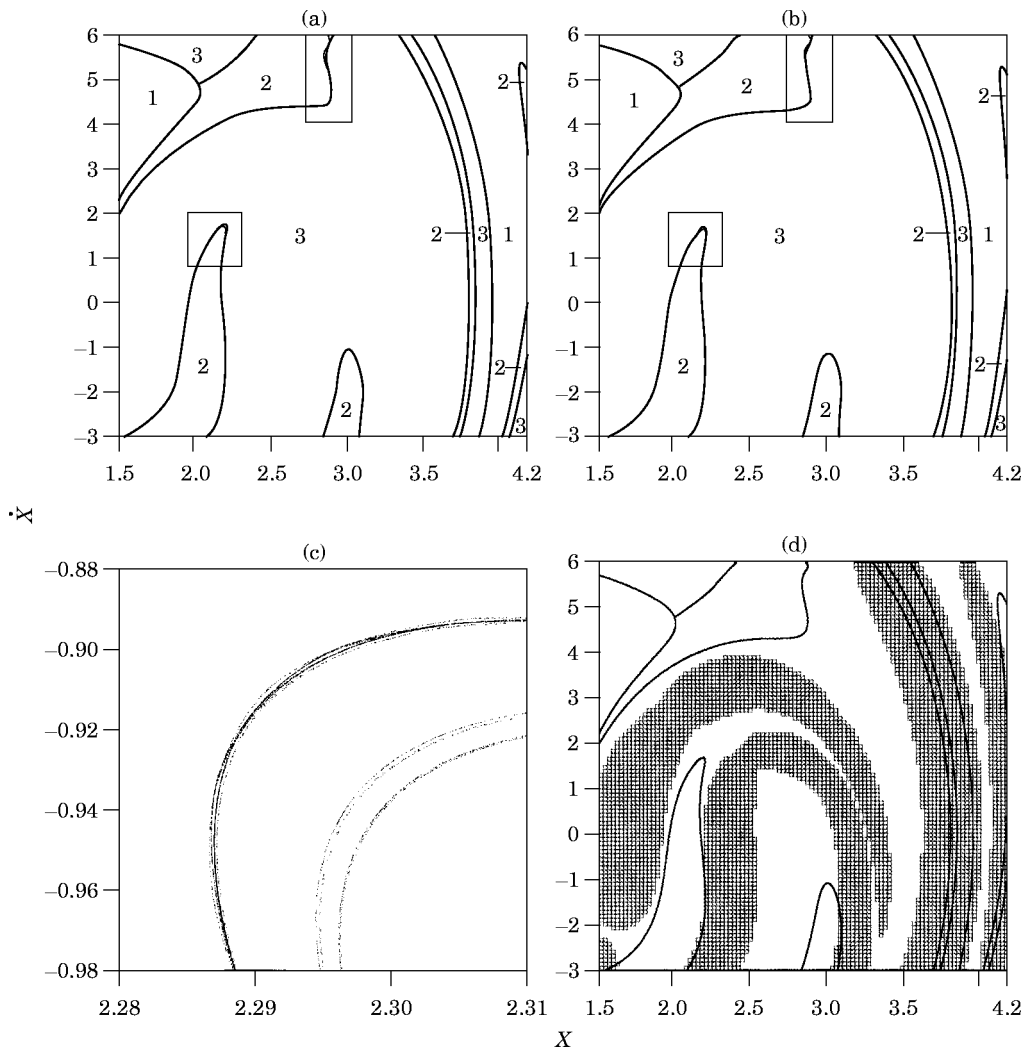


Figure 5. Further analysis of the system given by equation (1), based on interpolated mappings: (a) basin boundaries located by high resolution analysis of ICM; (b) basin boundaries located by high resolution analysis of MICM; (c) the detailed structure of the strange attractor located by the method of refined attracting cells; (d) the region of refined cells located by ARBICM.

attraction. Each refined cell that does not reach a periodic attractor located before 100 periods is considered in the basin of attraction of a strange attractor. If multiple attractors are located in each set of attracting cells, of course, the global analysis using MICM is incorrect. Then, increasing the number of cells or reducing the region of study can improve the accuracy of global analysis. This method is applied to analysis of the system, equation (1), with each attracting cell divided into 9^2 refined cells and $N_p = 10$. The periodic attractors of period three located by various methods are situated at (2.66416, 4.66427), (3.04256, -2.00013) and (2.13566, -0.61915) from global analysis using MICM, (2.66307, 4.67678), (3.04084, -2.00374) and (2.13328, -0.60474) from numerical integration, and (2.66308, 4.67663) (3.04086, -2.00371) and (2.13331, -0.60491) from MICM refined-attracting-cell analysis. The precision of the periodic attractor located is much improved by this method over that from global analysis using MICM. In Figure 5(c)

is shown the structure of the strange attractor in the region of $(2.28, 2.31) \times (-0.98, -0.88)$, which is somewhat distorted since the reference mappings of refined attracting cells can reduce distortion of the attractors located by interpolated mappings to a certain extent only. Note also that high resolution analysis of ICM cannot locate more precise attractors than global analysis using ICM since identical reference mappings are used by the two methods.

We then discuss the precision of analysis using the method of adaptive refinement of bilinear interpolated cell mapping (ARBICM), developed by Tongue [22]. This method uses phase deformation as the criterion for refinement of cells. To study a two-dimensional system, the region of interest is first divided into an array of original cells (O-cells). The four corners of each O-cell are points of integration (POIs), the first mappings of which from numerical integration serve as reference mappings for interpolation, and form a mapped image. In this approach, the ratio of the size of a mapped image to the O-cell size is defined as a quantity s , which judges whether an O-cell is refined. For a system with fractal basin boundaries studied in [22], ARBICM constructs precise reference mappings of refined cells with $s = 10$. This method is computationally more efficient than ICM using uniform cells to yield global analysis with the same order of accuracy. However, to refine cells by this criterion, most basin cells of a strange attractor will be refined because of the sensitivity of initial conditions in the basin of attraction of a strange attractor [14]. Much computational effort is then used to study the basin cells of a strange attractor without improvement of precision of analysis. For example, ARBICM is applied to study the system given by equation (1) with $s = 3$. The 5004 cells (49.1% of the total cells) to be refined are shown by squares in Figure 5(d). These cells do not include the entire basin boundaries, which must be located for efficient further study of basins of attraction. Thus, ARBICM is not suitable for global analysis of systems with strange attractors. By studying a sufficient number of points and introducing the division of uniform cells, IGP can locate the boundary cells that include the entire basin boundaries and have a thickness of one or two cell sizes. However, the large amount of computational effort required becomes restrictive. On the other hand, global analysis using MICM indicates the basin boundaries by boundary cells with a thickness of two or three cell sizes. It is hoped that the location of extra boundary cells can remedy the inaccuracy of the basin boundaries located by interpolated mappings.

A method using exact mappings is further applied to remedy the incompleteness and inaccuracy of the basins of attraction due to the assumption of the sink cell and interpolated mappings. First, the mappings of cells in the basin of attraction of the sink cell are given by numerical integration, until the cells reach the basin cells, to identify their attractors, as previously. Then the basin and boundary cells of attractors are defined again, since the attractors of all cells have been located. Finally, the mappings of points in the boundary cells are given by numerical integration, until these points reach the basin cells, to identify their attractors. Thus, the attractors of all points in the region of interest are located. Moreover, the mappings of points near the basin boundaries given by numerical integration are precise enough to locate the attractors of these points correctly. This further analysis to locate the detailed basin of attraction is therefore complete and precise. This method is applied to detailed global analysis of the systems governed by equations (1–3), with 909^2 points studied. When compared with analysis using IGP, the attractors of all points are located correctly. The basins of attraction of the systems governed by equations (1) and (2) are shown in Figures 6(a) and 6(b). The solid curves denote the basin boundaries located by this method, and the dotted curves show the basin boundaries of the sink cell located by IGP. The complete basins of attraction of systems cannot be located by each of the existing cell mapping method. Due to the assumption of the sink cell, there is still

15% of uncertainty about attractors of points in the region of interest after analysis using cell mapping methods of the system governed by equation (1). In addition, for analysis of the system given by equation (1), the average periods of all points in the boundary cells required to reach the basin cells are only 2.88 periods. Hence this method combines completeness and precision of analysis using IGP and computational efficiency of analyses using cell mapping methods.

The method using exact mappings is also applied to locate exact attractors. First, N_s^n interior-and-boundary points [5] are uniformly sampled within the first registered attracting cell in each set. The mappings of each sampling point are then given by numerical integration within 200 periods, and the two criteria, 10^{-8} and 10^{-5} , are used to locate periodic attractors and their basins of attraction. These mappings are considered to be transient and steady states within the former and latter 100 periods. Then the attracting cells in the same set in which the steady state mappings reside require no further

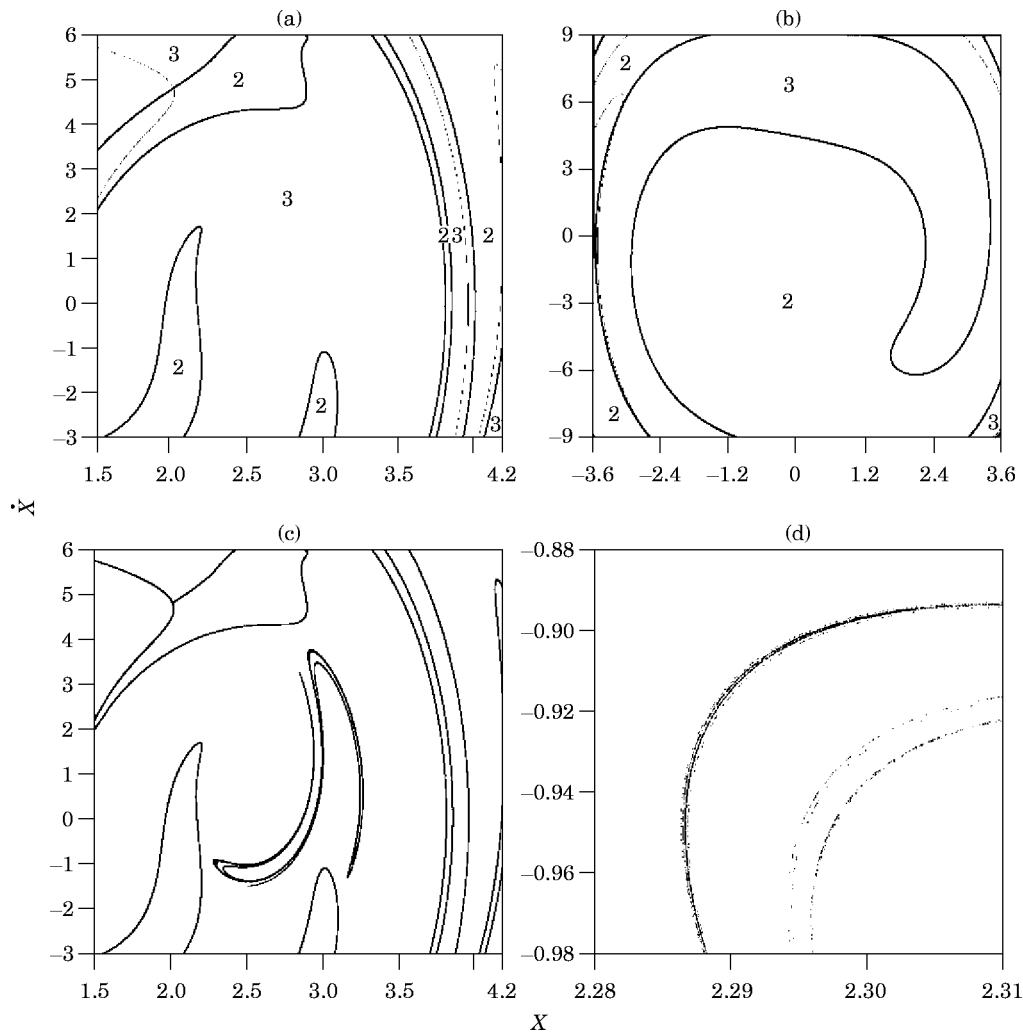


Figure 6. Further analysis based on exact mappings given by numerical integration: (a, b) complete and precise basins of attraction of the systems equations (1) and (2); (c, d) the detailed structures of the strange attractor of the system given by equation (1) in the two regions.

TABLE 2
Computational time required (seconds) for various further analyses

System	Method	Cells	Region of study (%)	Time	Number of points of error
Equation (1)	ICM-HIGH	101 ²	100.0	467	3753
	MICM-HIGH	101 ²	16.3	11	3302
	MICM-RBC	101 ²	16.3	454	51
	MICM-RAC	101 ²	4.5	251	—
	MICM-NIB	101 ²	14.1	1127	0
	MICM-NIA	101 ²	0.47	289	—
	IGP	909 ²	100.0	194 999	0
Equation (2)	MICM-NIB	101 ²	11.6	1078	0
	MICM-NIA	101 ²	0.03	32	—
	IGP	909 ²	100.0	245 539	0
Equation (3)	MICM-NIB	101 ²	19.0	291	0
	MICM-NIA	101 ²	0.03	9	—
	IGP	909 ²	100.0	24 388	0

analysis, since these attracting cells have been correctly located by global analysis using MICM. Other attracting cells are also studied by N_s^n sampling points as above. In addition, if a steady state mapping of a sampling point reaches a basin cell, the basin cell is regarded as an attracting cell in the same set, and is examined as above. If multiple attractors are located by different sampling points of attracting cells in each set, global analysis using MICM is incorrect. Otherwise, the finally located attractors are the same as those located by IGP. This method is applied to analysis of the systems given by equations (1)–(3), with 3^2 interior-and-boundary sampling points within each attracting cell. The attractors located by this method are the same as those located by IGP. In Figures 6(c) and (d) are shown the strange attractors of the system given by equation (1) in the regions of $(1.5, 4.2) \times (-3, 6)$ and $(2.28, 2.31) \times (-0.98, -0.88)$.

The computational times required for various analyses of the systems given by equations (1)–(3) are listed in Table 2. The methods “ICM-HIGH” and “MICM-HIGH” denote high resolution analyses of ICM and MICM; “MICM-RBC” and “MICM-RAC” denote the refined-boundary-cell and refined-attracting-cell methods; and “MICM-NIB” and “MICM-NIA” denote the methods using exact mappings to locate the basins of attraction and attractors. The item “Cells” denotes the number of cells used by global analysis using a cell mapping method. The item “Region of study” shows the ratio of the region studied by a method to the region of interest of a system. To locate detailed basins of attraction, 909² points within the region of interest are studied by each method. The item “Number of points of error” indicates the number of points with incorrectly located attractors when compared with analysis using IGP. The two criteria used to locate periodic attractors and their basins of attraction are 10^{-5} and 10^{-5} for ICM and 10^{-5} and 10^{-4} for IGP. It can be found that high resolution analysis of MICM is far more computationally efficient than high resolution analysis of ICM. This is because only the points in the boundary cells are studied, and all basin cells serve as criteria of attraction of the attractors located. High resolution analysis of MICM is also more precise than high resolution analysis of ICM. Moreover, the computational time required for analysis using the refined-boundary-cell method is of the same order as that required by high resolution analysis of ICM, with the precision of analysis much improved. Note that only IGP and the method using exact mappings can locate exact attractors and complete basins of attraction in the region of

interest. For the three systems, the method using exact mappings locates identical attractors and basins of attraction as IGP with a 100-fold improvement in computational efficiency.

4. CONCLUDING REMARKS

In this paper, MICM was developed to give a more complete and precise global analysis than ICM for deterministic dynamical systems with smooth basin boundaries. Three methods were also developed for further analysis of attractors and basins of attraction: high resolution analysis, refined cell space and exact mappings. For further analysis using each of the three methods, all of the basin cells located by analysis using MICM serve as criteria of attraction for the attractors located; in addition, only the boundary and attracting cells located by analysis using MICM are studied. The method using exact mappings accomplishes a complete and precise global analysis efficiently. Some algorithms and concepts used by GCM are of much help in the development of the proposed methods, since GCM has been well developed.

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