Parameter variation methods for cell mapping

Nonlinear Dynamics **7:** 273–284, 1995.

Parameter Variation Methods for Cell Mapping

J. A. W. VAN DER SPEK, C. A. L. DE HOON, A. DE KRAKER and
D. H. VAN CAMPEN
Department of Mechanical Engineering, Eindhoven University of Technology, P.O. Box 513, 5600 MB Eindhoven, The Netherlands

(Received: 26 July 1993; accepted: 3 January 1994)

Abstract. In the study of nonlinear dynamic systems, the influence of system parameters on the long term behaviour plays an important role. In this paper, parameter variation methods are presented which can be used when investigating a nonlinear dynamic system by means of simple or interpolated cell mapping. In the case of coexisting attractors, the proposed methods determine the evolution of the basin boundaries when a system parameter is varied. Application of the methods to a modified Duffing equation is performed. It is concluded that the proposed methods are very efficient and accurate.

Key words: Cell mapping, continuation, basins of attraction, chaos.

1. Introduction

The equations of motion of a nonlinear dynamic system usually contain one or more system parameters. Mostly, these parameters can assume a value lying in a bounded, but large, interval. A necessary part of the research of a dynamic system is therefore the study of the influence of the system parameter(s) on the long term behaviour. Methods used for this kind of research are called parameter variation methods or *continuation* methods.

Continuation methods are used in combination with periodic solvers, such as the *shooting* method or the *time discretization* method. For a given start-estimation, these solvers yield a periodic solution (if there exists one) of a set of ordinary differential equations. The continuation method determines the evolution of the periodic solution when a system parameter is varied. For more information about continuation methods, see [1,6].

As opposed to the periodic solvers, the method of *cell mapping* is capable of determining all existing attractors and basins of attraction of a nonlinear dynamic system for a fixed value of each system parameter. This method was introduced by Hsu [2,3], who presented the *simple* cell mapping (SCM) and *generalized* cell mapping (GCM) methods. Further research on this area has been done by Tongue [7], who introduced the *interpolated* cell mapping (ICM) method. Cell mapping methods have proved to be solid tools for nonlinear dynamic system investigation and have been applied in many fields of research.

One thing that is still lacking in the established cell mapping methods is a parameter variation method. This method should be capable of determining the evolution of the basin boundaries when a system parameter is varied. Of course, the determination of the basin boundaries for the new parameter value should take less CPU-time than a complete new cell mapping execution. For systems with two or more degrees of freedom, application of cell mapping methods may be very time-consuming. The existence of a continuation method would greatly improve the applicability of cell mapping methods to those systems.

In this paper, methods are presented which predict the basin boundary evolution for a nonlinear dynamic system investigated by means of SCM or ICM. These methods are termed

PVSCM and PVICM respectively. After a regular cell mapping performance, yielding two or more attractors and basins of attraction, the corresponding parameter variation method predicts the basin boundaries and hence the basins of attraction for a varied system parameter value. The necessary CPU-time for one variation step is much smaller than for a new cell mapping execution, as is shown.

In the next sections, the PVSCM and PVICM methods are presented. The concept of parameter variation is explained and corresponding algorithms are given. Application of the methods to a modified Duffing equation is performed. A comparison is made with a regular cell mapping application for the new parameter value. The proposed methods turn out to be very efficient and accurate.

2. PVSCM Method

2.1. Method Explanation

To explain the PVSCM method, we introduce a one degree of freedom nonlinear dynamic system:

$$\begin{aligned} \dot{x}_1 &= x_2 \,, \\ \dot{x}_2 &= f(x_1, x_2, t, \mu) \,. \end{aligned} \tag{1}$$

Here, x_1, x_2 represent the displacement and velocity of the system respectively, t stands for time, and μ is a system parameter. In this paper, only periodically excited systems are considered. Hence, for f we have

$$f(x_1, x_2, t + T, \mu) = f(x_1, x_2, t, \mu) \quad \forall t \geq 0 \,, \tag{2}$$

where $T > 0$ is the excitation period.

The starting-point of the PVSCM method is a regular SCM application to (1) for $\mu = \mu_0$. For this purpose, a bounded region of interest Ω in the state space is chosen and is discretized in cells, numbered $1, \ldots, N_c$ (called *regular* cells). The *sink* cell, which is the complement of Ω in the state space $\mathbb{R}^2$, is identified by index 0. For each regular cell z, the image cell $C(z)$ is determined by means of numerical integration of (1) over T seconds using the cell center point as initial condition. For the sink cell we have $C(0) = 0$ by definition, which means that when the system enters the sink cell, it stays there forever.

Under SCM, all cells are classified as *periodic* or *transient*. A cell z is periodic if $C^m(z) = z$ for some integer $m > 0$. A cell is transient if it is not periodic. Periodic cells or groups of periodic cells represent the long term behaviour of (1); transient cells form the basins of attraction. For each cell $z \in \{0, 1, \ldots, N_c\}$, a group number $Gr(z)$ is determined. $Gr(z)$ denotes to which group z belongs, as a periodic or as a transient cell. By definition, we have $Gr(0) = 1$ for the sink cell.

The determination of a group number for each regular cell z goes as follows. First, each regular cell z is tagged as a *virgin* cell by putting $Gr(z) = 0$. Since the sink cell is a periodic group by definition, we set $N_g = 1$, with N_g the number of periodic groups found by the algorithm. Next, for each cell z a sequence $z, C(z), C^2(z), \ldots$ is constructed. All cells in the sequence receive a temporary group number -1, so they can accordingly be recognized. The sequence is terminated when a cell z^* is found with $Gr(z^*) \neq 0$. When $Gr(z^*) = -1$, z^* already occurred in the sequence which means that a new group has been found given by z^*,

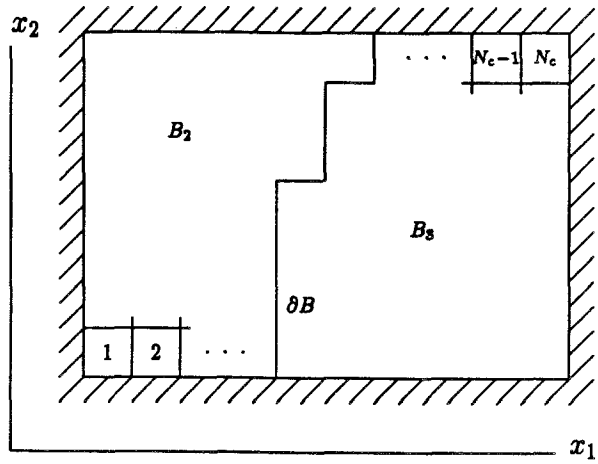

Fig. 1. Partition of region of interest Ω in basins of attraction separated by basin boundary ∂B.

$C(z^*), \ldots, C^{(m-1)}(z^*)$ with m the smallest positive integer for which $C^m(z^*) = z^*$. In this case, N_g is updated and all cells in the sequence receive group number N_g. When $Gr(z^*) > 0$, z^* already occurred in a previous sequence. In this case, all cells in the sequence are transient cells leading to the same group as z^* and therefore receive the same group number $Gr(z^*)$. We refer to [4] for a detailed explanation of the SCM algorithm.

Applying the SCM method to (1), we assume that besides the sink cell two additional periodic groups are found, each representing an attractor. These groups are numbered 2 and 3 according to the above-mentioned procedure. For the sake of simplicity, we assume that each cell in Ω belongs to one of these groups (as a periodic or as a transient cell), so no cell is mapped into the sink cell. Hence, for each regular cell z we have $Gr(z) = 2$ or $Gr(z) = 3$. The region Ω can be divided in two corresponding basins of attraction B_2, B_3, separated by the basin boundary ∂B (see Figure 1). Our goal is to determine the position of the basin boundary ∂B^* for $\mu = \mu^* = \mu_0 + \Delta\mu$ in less CPU-time than is necessary for a regular SCM execution. This may be achieved by only determining the new image cells (i.e., for $\mu = \mu^*$) for a limited number of cells. When no bifurcations occur, the basin boundary wanders through the state space in a continuous way when a system parameter is varied continuously. For $\mu = \mu^*$, the basin boundary has moved over an area ΔB which is bounded by ∂B and ∂B^* (see Figure 2). By iteratively creating an area B which is as small as possible but contains ΔB, a set of cells is obtained of which the new group numbers define the new basin boundary. These cells are referred to as *B-cells*.

Before giving the necessary steps in the PVSCM procedure, we introduce the following definitions:

DEFINITION 1. Two cells z and z' are called *adjoining* if they have at least one cell corner point in common.

In [3], a mathematical definition of *adjoining* is given.

DEFINITION 2. A cell z is called a *boundary cell* if there exists a cell z' which is adjoining to z with $Gr(z) \neq Gr(z')$.

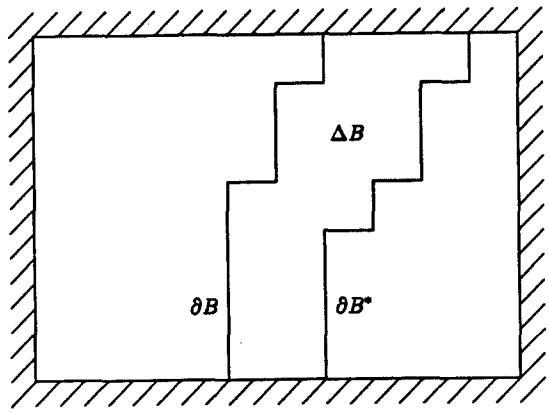

Fig. 2. Definition of ΔB.

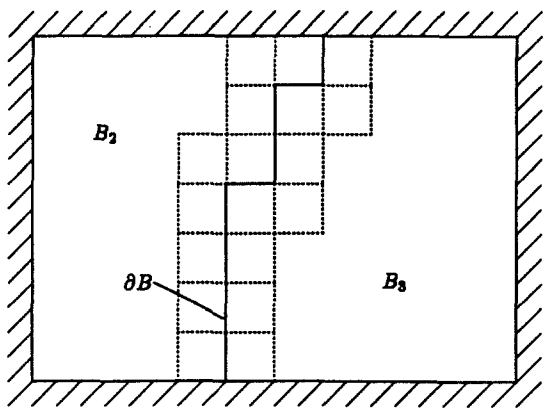

Fig. 3. Definition of boundary cells.

In Figure 3, the boundary cells are shown in Ω for $\mu = \mu_0$. In the PVSCM method, the following steps are taken initially:

1. Determination of the boundary cells for $\mu = \mu_0$. The set of boundary cells is taken as initial estimation for B.
2. Determination of the image cell $C(z)$ for each cell $z \in B$ for $\mu = \mu^*$.
3. Determination of the group number $Gr(z)$ for each cell $z \in B$ for $\mu = \mu^*$.

For the determination of group numbers, a cell sequence is constructed for each B-cell using the new image cells. When a cell sequence leads to a cell z^* outside B, all cells in the sequence receive the same group number as z^*.

The newly determined group numbers produce a new basin boundary $\partial B^{(1)}$, which is bounded by B. At places where $\partial B^{(1)}$ is equal to the boundary of B, B should be expanded. This is done by determining the *new* boundary cells; these are cells which did not belong to B yet but satisfy the definition of a boundary cell, due to the new group numbers of the cells in B. The new boundary cells can then be added to B. In Figure 4, the expansion of B is

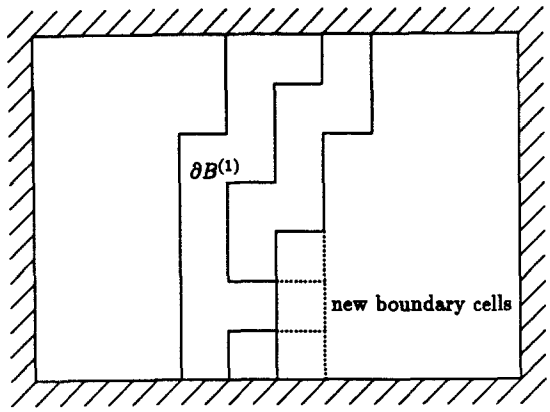

Fig. 4. Expansion of B with new boundary cells.

schematically shown. Steps 4 and 5 in the PVSCM algorithm are hence given by

4. Determination of the new boundary cells.
5. Addition of the new boundary cells to B.

To complete the expansion of B, steps (2–5) are repeated until no new boundary cells are found. In step 2 of course, the image cell needs to be determined only for the *new* B-cells. In step 3 however, it is necessary to determine the new group numbers not only for the new B-cells, but for all B-cells z which eventually map outside B, hence which satisfy $Gr(z) \leq 3$ for the considered example. This is done to restore possible errors. After all, when a new boundary cell $\tilde{z}$ receives a group number $Gr(\tilde{z}; \mu^*) \neq Gr(\tilde{z}; \mu_0)$, all cells $z \in B$ which are mapped onto $\tilde{z}$, need to be given the correct group number $Gr(\tilde{z}; \mu^*)$. This is achieved by re-determining the group number of all B-cells characterized by a group number $g \leq 3$ (cells with $Gr(z) > 3$ have received their group number on the basis of new data, i.e. for $\mu = \mu^*$, so no redetermination of group numbers is necessary for these cells). When no new boundary cells are found, the new basin boundary ∂B^* is defined by the group numbers $Gr(z; \mu^*)$ of all cells $z \in B$.

In the next subsection, a description of the PVSCM-algorithm is given. Here, two remarks need to be made regarding the given procedure: First, it is possible that during the expansion of B a new group is found, e.g., a saddle solution. This does not change anything to the procedure. Continuation of the expansion of B yields all the necessary data to construct the new basin boundaries. Groups found inside B receive group number 4, 5, ... and so on.

Second, the PVSCM method determines the new basin boundaries in a minimal CPU-time. The time-consuming part in SCM is the determination of the image cells, in which integration is involved. Here, only for a limited number of cells – the B-cells – the image cell has been determined. The gain that is being made with respect to a regular SCM performance is obvious.

2.2. PVSCM Algorithm

The PVSCM algorithm makes use of the array of group numbers Gr of a previous SCM calculation. Hence, for each regular cell z the group number $Gr(z)$ is available. Let N_g be

the number of groups found under SCM, then we have $1 \leq Gr(z) \leq N_g$, $z = 1, \ldots, N_c$. Specifically, we have $Gr(0) = 1$. During the PVSCM algorithm, the following arrays and variables are needed:

$C(z)$: image cell of z, $z = 1, \ldots, N_c$,
N_b : number of B-cells,
M : number of *new* B-cells,
$B(i)$: i-th B-cell, $i = 1, \ldots, N_b$,
$Ind(z)$: equals 1 if z is a B-cell, 0 otherwise.

The first step in the PVSCM method is the determination of the boundary cells. When all cells have been checked, M boundary cells have been found and stored in the array B. Hence, initially we have $N_b = M$ and $Ind(B(i)) = 1, i = 1, \ldots, M$.

Steps (2–5), given in the previous subsection, define the general loop of the program. While $M > 0$ holds, the following is repeated:

1. For $i = 1 + N_b - M, \ldots, N_b$ (i.e., for all new B-cells): determine the image cell $C(B(i))$ for $\mu = \mu^*$.
2. For $i = 1, \ldots, N_b$: if $Gr(B(i)) \leq N_g$ then $Gr(B(i)) := 0$.
3. For $i = 1, \ldots, N_b$: if $Gr(B(i)) = 0$ then determine the new group number $Gr(B(i))$.
4. $M := 0$.
5. For $z = 1, \ldots, N_c$: if z is a boundary cell and $Ind(z) = 0$ then
   $M := M + 1$,
   $B(N_b + M) := z$,
   $Ind(z) := 1$.
6. $N_b := N_b + M$.

In the second step of this loop, all B-cells for which a new group number needs to be determined (cells which eventually map outside B and which therefore have group number $g \leq N_g$) are tagged as virgin cells by giving them a group number 0. The search for new boundary cells, which is done in the fifth step of the loop, is quite trivial and can be programmed in many ways.

2.3. Example of Application: Modified Duffing Equation

As an example of application of the PVSCM method we consider the modified Duffing equation:

$$\begin{aligned} \dot{x}_1 &= x_2 \,, \\ \dot{x}_2 &= -dx_2 + x_1 - x_1^3 + 0.3\, \cos(t) \,. \end{aligned} \tag{3}$$

Equation (3) models an Euler support column loaded beyond its buckling point. For $d = 0.15$, a periodic and a chaotic attractor coexist (see [5]). To apply a regular SCM to (3) for this parameter value, we take for Ω: $|x_i| \leq 2.02$, $i = 1, 2$. We discretize Ω in 101×101 cells of size 0.04×0.04. Image cells are determined by means of numerical integration over $T = 2\pi$ seconds.

In Figure 5a, the results are shown of the SCM execution. The periodic attractor is represented by one periodic cell. The chaotic attractor is represented by three periodic groups,

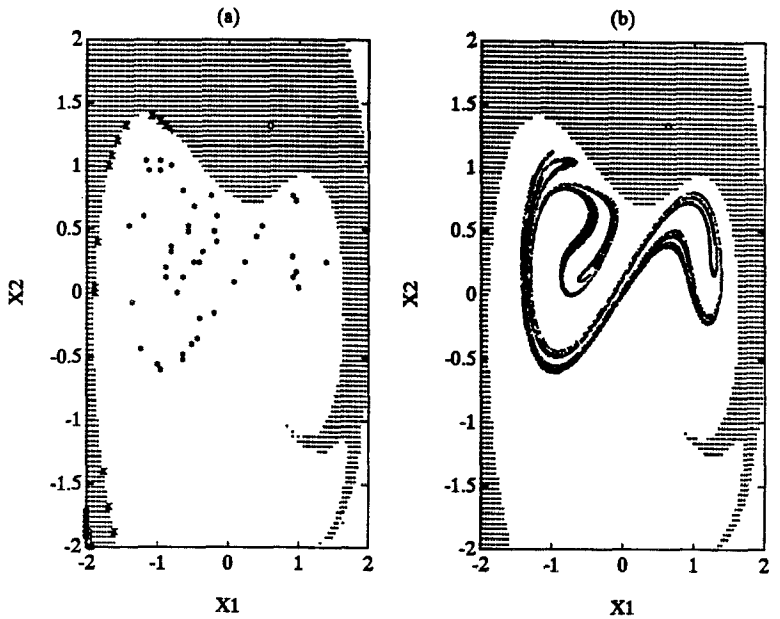

Fig. 5. Attractors and basins of attraction of the modified Duffing equation for $d = 0.15$: (a) SCM results: Periodic attractor (o) and basin of attraction (·); chaotic attractor (∗) and basin of attraction (left blank); saddle solution (+) and transient cells (×); cells which are mapped into the sink cell (o). (b) Exact results: Periodic attractor (o) and basin of attraction (·); chaotic attractor and basin of attraction (left blank).

consisting of 19, 16, and 10 cells respectively. Basins of attraction are given by the corresponding transient cells. Further, a saddle solution is found whose transient cells are lying on the basin boundary. Finally, a small number of cells is found which are mapped into the sink cell. For comparison, the results obtained by regular numerical integration are shown in Figure 5b.

Next, we use the PVSCM algorithm to determine the basins of attraction for $d = 0.17$. For this purpose, it is necessary to renumber the group numbers. In the SCM execution for $d = 0.15$, 6 groups were found. However, 3 of them represent the same chaotic attractor. Hence, only 4 different groups need to be distinguished ($N_g = 4$). After the group numbers have been changed and stored, the PVSCM algorithm may be applied.

The results of the PVSCM performance are shown in Figure 6a. The basins of attraction of both attractors have been determined for $d = 0.17$. The new position of the saddle solution has also been found. In Figure 6b, the domains of attraction are shown obtained by a regular SCM calculation for $d = 0.17$. The results of both methods perfectly match; the PVSCM method is three times as fast however.

2.4. Remarks

Under SCM, a global picture is obtained of attractors and basins of attraction. The attractors however, are always represented by periodic groups which only approximate the exact location of the attractors. To obtain the exact position and form of the attractors, additional research is necessary, especially for a chaotic attractor. In general, a short numerical integration starting from one of the cells which represent the attractor is necessary to get the desired information.

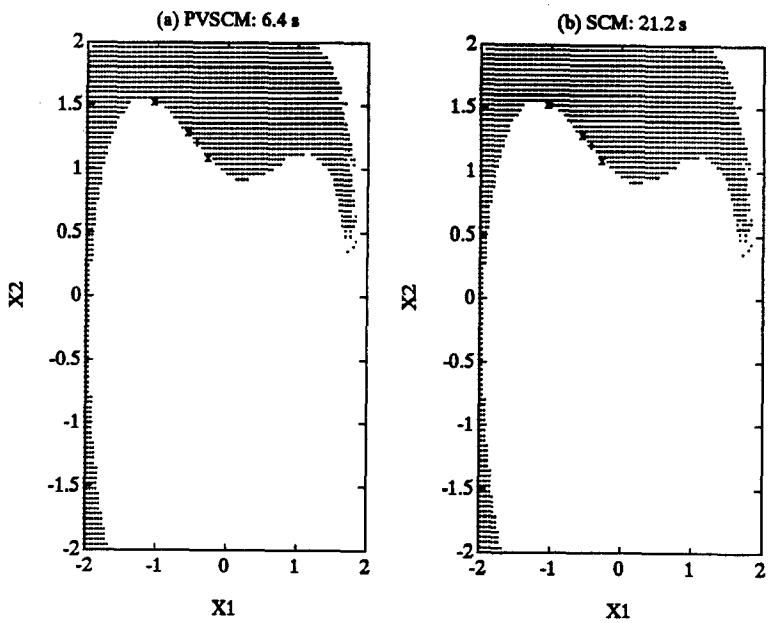

Fig. 6. Basins of attraction of the modified duffing equation for $d = 0.17$: Periodic basin (·); chaotic basin (left blank); saddle solution (+) and transient cells (×).

In this respect, the absence of periodic groups in the results of a PVSCM execution cannot be seen as a shortcoming.

The PVSCM method only produces the basins of attraction for the new parameter value, not the location of the attractors. Only when a solution lies in the region B (e.g., the saddle solution in the previous example), a corresponding group may be found. If desired, the position of a periodic group outside B can be obtained for $\mu = \mu^*$ by creating a cell sequence for one of the cells of this group. In this way, a new periodic group will be found, close to the original one. However, a regular numerical integration starting from the center point of one of the periodic cells will provide the exact position of the attractor in the same order of CPU-time.

The basins of attraction obtained by PVSCM are approximations for those obtained by SCM. By means of adaptively enlarging the set of B-cells, the approximation error is kept as small as possible. Things can go wrong when a B-cell z is mapped onto a cell $\tilde{z} \notin B$ with $Gr(\tilde{z}; \mu^*) \neq Gr(\tilde{z}; \mu_0)$. When $\tilde{z}$ is never going to be part of B, cell z – and possibly more cells in B – will keep a false group number. The chance for this to happen is small, taking into account that the basin boundary changes in a continuous way and that the state of the investigated system moves away from the basin boundary towards the attractor. In the worst case, at least a tendency is obtained of how the basin boundary is changing. Of course, when the parameter variation $\Delta\mu$ is "large", the above-mentioned error-introduction is more likely to happen.

In the example of the modified Duffing equation, we used an extended initial estimation for B. Besides the initial boundary cells, all cells bordering on the sink cell were added to B as well. When a parameter is varied, changes in the basin boundary may occur along the boundary of Ω. To predict this kind of changes as well, the extension of the initial guess for B is necessary. Application of the PVSCM method to (3) for $d = 0.17$ using only the boundary

cells as initial guess for B did not predict the basin boundary changes in the upper left corner of Ω. Apart from that, the results were identical. The necessary CPU-time was 5.5 s.

3. PVICM Method

3.1. Method Explanation

The idea presented in the previous section can be combined with the ICM method in a similar way. Under ICM, cells actually do not play a role. Instead, the region of interest Ω is covered with gridpoints. Each gridpoint is used as initial condition for a numerical integration of the corresponding system over one system period, yielding an image point. By means of additional interpolation between these image points, a sequence of states is constructed for each gridpoint, eventually leading to an attractor. The gridpoint is then added to the basin of attraction corresponding to this attractor. In [7], the ICM method is presented in detail.

By regarding the grid points as cell center points, the parameter variation concept for SCM may be applied to ICM as well. Suppose an ICM execution has been applied to system (1) for $\mu = \mu_0$, yielding two attractors, numbered 2 and 3, and corresponding basins of attraction. For each regular cell z we then have a group number $Gr(z)$, which denotes to which basin z belongs, and an image point $\mathbf{x}(z)$, determined by numerical integration over T seconds. To obtain the basin boundary for $\mu = \mu^* = \mu_0 + \Delta\mu$, again a region B is created which covers all the cells between the old and new basin boundary.

The procedure for the creation of B is the same as under PVSCM, apart from a few (trivial) differences. First, for each new B-cell z the image point $\mathbf{x}(z)$ is determined instead of the image cell $C(z)$. Second, interpolation is used to determine a cell's group number. During interpolation, the new image points should be used when available. Interpolation is stopped when a point is found of which the surrounding grid points, i.e., the grid points used for interpolation, belong to cells which have identical group numbers.

3.2. PVICM Algorithm

In the PVICM algorithm, use is being made of two arrays obtained in the ICM execution for $\mu = \mu_0$. Besides the array of group numbers Gr, a two-dimensional array Ip is available. Here, $Ip(z, i)$ initially contains the i-th coordinate of the image point $\mathbf{x}(z)$ for $\mu = \mu_0$. Whenever for a B-cell z the new image point is determined during the algorithm, Ip is updated. The array Ip contains all necessary data for the interpolation of trajectories. In the algorithm, the same arrays and variables are used as under PVSCM, except for the array $C(z)$ which is not relevant under ICM.

The first step in the PVICM algorithm is the same as under PVSCM, resulting in M boundary cells. Next, the following steps are repeated until $M = 0$:

1. For $i = 1 + N_b - M, \ldots, N_b$: determine the image point $\mathbf{x}(B(i))$ for $\mu = \mu^*$ and store it in Ip.
2. For $i = 1, \ldots, N_b$: if $Gr(B(i)) \leq N_g$ then determine the new group number $Gr(B(i))$.
3. $M := 0$.
4. For $z = 1, \ldots, N_c$: if z is a boundary cell and $Ind(z) = 0$ then
   $M := M + 1$,
   $B(N_b + M) := z$,
   $Ind(z) := 1$.

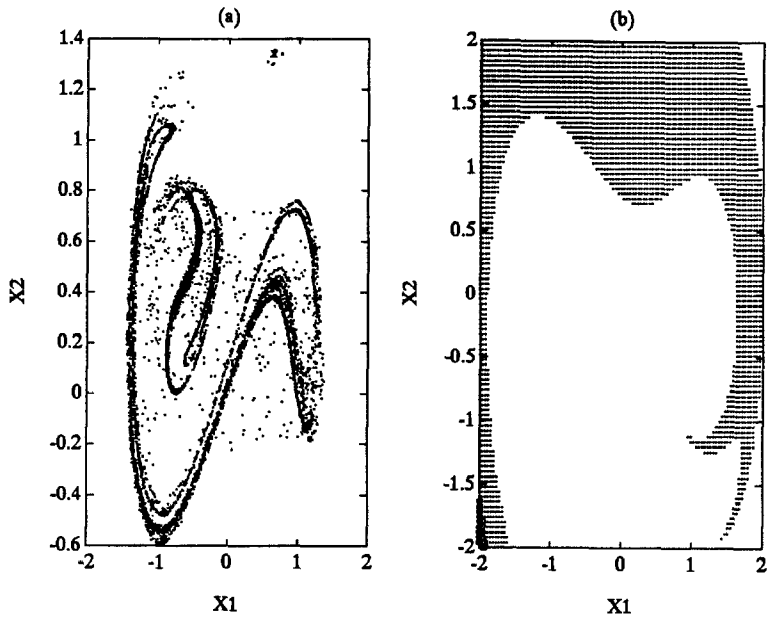

Fig. 7. ICM results for the modified Duffing equation for $d = 0.15$: (a) Periodic (×) and chaotic attractor (·). (b) Basins of attraction of the periodic (·) and the chaotic attractor (left blank); cells which are mapped into the sink cell (o).

5. $N_b := N_b + M$.

The determination of group numbers is realized by interpolation until convergence is obtained, or until a state is reached of which the surrounding grid points belong to cells which have identical group numbers. In the latter case, further interpolation leads to the attractor corresponding to this group number in most cases. By definition, interpolation is stopped and the cell containing the initial trajectory point receives the same group number. When no convergence is obtained within a maximum number of interpolation steps, the trajectory is considered chaotic and the cell containing the initial point receives group number 0.

3.3. Example of Application: Modified Duffing Equation

To illustrate the PVICM method, we consider the modified Duffing equation (3). Figure 7 shows the attractors and basins of attraction obtained by ICM in the same region of interest Ω as under SCM, using the center points of the cells as gridpoints. A trajectory is considered periodic when the distance between two trajectory states is less than 10^{-3}. When no periodicity occurs within 20 interpolation steps, a trajectory is considered chaotic. These criteria yield a periodic solution at (0.637, 1.341) and a chaotic attractor, formed by the terminate points of chaotic trajectories. Due to the periodicity criterium and the recurrent character of the chaotic attractor, 8 additional periodic groups are found on the chaotic attractor. The corresponding basins of attraction, which only consist of very few points, are added to the chaotic attractor's basin of attraction.

After permuting the group numbers, we apply the PVICM method to (3) with $\Delta d = 0.02$. Figure 8a shows the new basins of attraction as well as the newly found saddle solution. Here, also the cells bordering on the sink cell have been included in the initial estimation for B. In

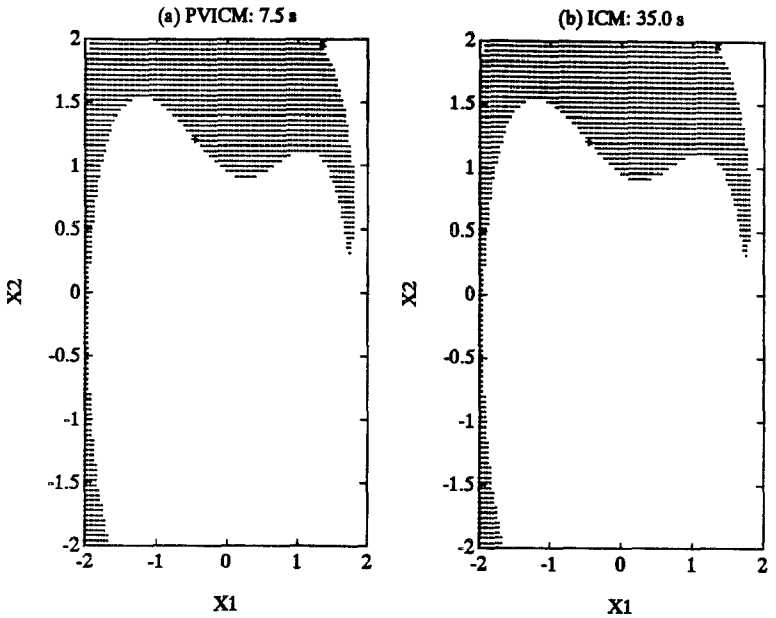

Fig. 8. Basins of attraction of the modified duffing equation for $d = 0.17$: Periodic basin (·); chaotic basin (left blank); saddle solution (+) and transient cell (×).

Figure 8b, the results are shown which are obtained by a regular ICM execution for $d = 0.17$. Again, a very good resemblance in the basins of attraction is achieved. Also the location of the saddle solution is identical for both methods. This time, the CPU-time has been reduced with a factor 5.

Next, we apply the PVICM method to (3) with $\Delta d = 0.03$, which implies a damping variation of 20%. All gridpoints are found to lead to the chaotic attractor for this case. A regular ICM performance for $d = 0.18$ proved the correctness of these results. Hence, the vanishing of the periodic attractor, which occurs somewhere between $d = 0.17$ and $d = 0.18$, can be predicted by means of the PVICM method. Here, the necessary CPU-times for the ICM and PVICM executions are 36.1 s and 15.6 s respectively.

3.4. Remarks

The additional information of ICM with respect to SCM is the location of the chaotic attractor. Unlike under SCM, where the chaotic attractor is represented only by a few periodic groups, the terminate points of chaotic trajectories form a reasonable approximation of the chaotic attractor. This extra information is missing when using the PVICM method. However, the chaotic attractor obtained by regular ICM is still not very accurate when regarding the terminate points near the periodic solution. These points belong to trajectories which needed more than 20 steps to converge to the periodic attractor. Further, part of the chaotic attractor is formed by terminate points which have not converged to this attractor yet, which results in a disorderly picture of the attractor (compared with the picture obtained by regular numerical integration in Figure 5b). Hence, for a correct chaotic attractor, a regular numerical integration is necessary anyway. This means that the lacking of a chaotic attractor for $\mu = \mu^*$ again is not a real shortcoming of the PVICM method.

The chaotic attractor's basin of attraction for $\mu = \mu^*$ obtained by regular ICM consists, besides initial points of chaotic trajectories, also of gridpoints leading to periodic groups on the chaotic attractor. To obtain the correct basin of attraction, all basins of these periodic groups need to be included. Under PVICM however, the correct basins of attraction are obtained without ad-hoc manipulations by the user.

All simulations discussed in this paper were done on a SG INDIGO R4000 32 Mb workstation.

4. Conclusion

A parameter variation (PV) method for cell mapping has been introduced. It has been shown that the method can be applied to both SCM and ICM, in which case it is termed PVSCM and PVICM respectively. The PV methods determine the evolution of the basin boundaries, initially determined by SCM or ICM, when a system parameter is varied. Corresponding algorithms have been presented.

Application of the PVSCM and PVICM methods to a modified Duffing equation has been performed. The obtained results perfectly match with regular cell mapping executions for the varied parameter. The PV methods however are up to five times as fast. The gain in CPU-time when using the PV methods may increase the applicability of cell mapping methods to systems with two or more degrees of freedom.

The presented methods only work when no bifurcations occur during parameter variation. However, the vanishing of attractors will be found in general. In that case, the gain in CPU-time may be smaller than usual. Application to systems with fractal basins of attraction may even produce no gain at all. Due to the followed concept, the number of cells for which a new integration needs to be performed will be much larger.

References

1. Fey, R. H. B., *Steady-State Behaviour of Reduced Dynamic Systems with Local Non-Linearities*, PhD Thesis, Eindhoven University of Technology, 1992.
2. Hsu, C. S., 'A theory of cell-to-cell mapping dynamical systems', *Journal of Applied Mechanics* **47**, 1980, 931–939.
3. Hsu, C. S., *Cell-to-Cell Mapping: A Method of Global Analysis for Nonlinear Systems*, Springer Verlag, New York, Heidelberg, Berlin, Tokyo, 1987.
4. Hsu, C. S. and Guttalu, R. S., 'An unravelling algorithm for global analysis of dynamical systems: An application of cell-to-cell mappings', *Journal of Applied Mechanics* **47**, 1980, 940–948.
5. Kreuzer, E., *Numerische Untersuchung nichtlinearer dynamischer Systeme*, Springer-Verlag, New York, Heidelberg, Berlin, Tokyo, 1987.
6. Seydel, R., 'Tutorial on continuation', *International Journal of Bifurcation and Chaos* **1**, 1991, 3–11.
7. Tongue, B. H., 'On obtaining global nonlinear system characteristics through interpolated cell mapping', *Physica D* **28**, 1987, 401–408.