



Research Paper

Clustered Simple Cell Mapping: An extension to the Simple Cell Mapping method



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ABSTRACT

When a dynamical system has a complex structure of fixed points, periodic cycles or even chaotic attractors, Cell Mapping methods are excellent tools to discover and thoroughly analyse all features in the state space. These methods discretize a region of the state space into cells and examine the dynamics in the cell state space. By determining one or more image cells for each cell, the global behaviour within the region can be quickly determined. In the simplest case – Simple Cell Mapping (SCM) method – only one image corresponds to a cell and usually a rectangular grid of cells is used. In typical applications the grid of cells is refined at specific locations.

This paper, however, introduces a different approach, which is useful to expand the analysed state space region to include all features which properly characterize the global dynamics of the system. Instead of refining the initial cell state space, we start with a small initial state space region, analyse other interesting regions of the state space and incorporate them into a cluster of cell mapping solutions. By this approach, trajectories escaping the original state space region can be followed automatically and additional objects in the state space can be discovered.

To illustrate the benefits of the method, we present the exploration of the phase-space of the *micro-chaos map* – a simple model of digitally controlled systems.

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1. Introduction

Cell Mapping methods (or shortly CM methods) were introduced by C.S. Hsu [1], in order to make the quick and thorough global analysis of nonlinear systems possible. CM methods discretize a region of the state space, thus creating the so called cell state space. For each cell one or more image cell is assigned (to where the dynamics lead from that cell), and by analysing the resulting graph or Markov-chain, periodic orbits, fixed points and their domains of attraction can be found.

The simplest CM method is the Simple Cell Mapping (SCM) and in the simplest case the cell state space is an n -dimensional grid of cells of the same size. The basic idea of the SCM method is that each cell has a single image, which is usually determined using the Centre Point Method [1], namely, a single trajectory from the centre of the *cell domain* is examined. In other words, all states within a cell are *mapped* to a single cell. Due to this property, the method is able to

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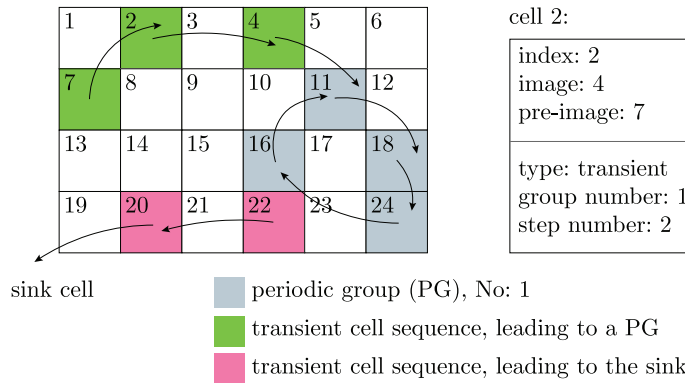


Fig. 1. Explanation of the definitions introduced in Section 1.1.

classify cells either as *periodic* cells (belonging to a periodic group) or *transient* cells (leading to a periodic group). Successful classification of all cells forms the *solution of the SCM*.

There are many variations of the CM methods, usually a relatively fast CM method (for example SCM) is applied to the initial state space region, then further analysis is carried out at certain locations, using more advanced methods (Generalized Cell Mapping, for instance), typically with refined cell state space [2–4]. These methods are excellent if the *interesting region* of the state space is known, but if that is not the case, a method capable of automatically extending the analysed state space region could be more suitable. Our goal is to extend the Simple Cell Mapping with such capability.

To emphasize the relevance of adaptive state space extension, one could recall the following situations:

- The dynamical system has an expectedly complex state space and the enclosing region of state space objects is not known.
- The dynamical system has more than one attractors, and not all of them are found in the initial state space region. Escaping trajectories indicate the possible direction of other attracting structures.
- A lower dimensional state space object, e.g., a basin boundary is being followed.
- Examination of global bifurcations or crises in dynamical systems in cases when the structure and/or the size of state space objects change abruptly during the variation of certain parameters. This situation is typically encountered in piecewise smooth systems.
- Analysing diffusion-like processes, for example intermittent maps [5].

Our approach to solve the problem of state space extension is to find an adjacent region to the initial state space, to where most of the trajectories escape. Afterwards, a separate CM solution is calculated on that region and the two solutions are joined. Upon the joining procedure, new state space objects residing on the boundary of the two cell state spaces are also discovered. This paper introduces this extension, particularly for the Simple Cell Mapping method, because it is the simplest adequate method to discover all objects in the state space [1]. The method of joining separate SCM solutions to a cluster of SCM solutions is referred to as Clustered SCM method. Based on these results, optional later analysis can be carried out using more advanced CM methods [6].

As an example of application, we show the analysis of the so-called *micro-chaos map* [7], where multiple disconnected attractors – possibly consisting of distinguishable communicating repellers are present in the state space. The behaviour of this piecewise smooth system fits into most of the aforementioned situations, as it exhibits a pattern of chaotic attractors and crisis phenomena with the appearance or disappearance of chaotic attractors/repellers [8].

1.1. Definitions and abbreviations

This section describes the basic terms, definitions and properties related to the Simple Cell Mapping, which are used throughout the paper. Also some auxiliary subroutines are presented, which are necessary for the implementation of the method (see Fig. 1).

- *Cell state space* (CSS): the bounded and discretized state space region, which is continuously covered by arbitrary *cell domains*. In the simplest case n -dimensional rectangular cuboids of the same size can be used to discretize an n -dimensional state space.
- *Cell domain*: bounded domain of the state space, part of the *cell state space*. In the simplest case it can be represented by a centre point in the state space and lengths along each dimension.
- *Cell*: object having its unique *index* referencing to a *cell domain* and various properties (e.g. *image*, *pre-image*).
- *Cell index* (or shortly *index*): cell property; a unique identifier.
- *Image*: property of a cell, one or more reference to other cells. The dynamics from the *cell domain* corresponding to the cell lead to the *cell domain(s)* indexed by the *image(s)*.

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