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Irreducible elementary cellular automata found

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ABSTRACT

Many multi-scale systems can be greatly simplified by using successive coarse-graining (CG) for approximation of microscopic degrees of freedom. As shown by Israeli and Goldenfeld in seminal papers [1,2], the local CG procedure can be developed also for elementary cellular automata (ECA) which represent a simplistic modeling metaphor. This allows for extracting the large-scale behavior of the original systems without accounting for small-scale detail and studying predictability of emergent phenomena in complex systems. However, due to the high computational complexity of the brute-force CG algorithm used in [1,2], the results obtained are very fragmentary. They do not allow to draw viable conclusions about reducibility of ECA for larger grain sizes than $N=4$ (i.e. for coarser resolution of coarse-graining). In this paper we present a novel CG algorithm of substantially lower computational load. Thereby, much more cellular automata can be decided in terms of their reducibility and mutual transitions. We find out that the number of "hard" – irreducible – ECA, which have coarse-grained representations, decreases with increasing the "grain" size of the approximation procedure and for $N=7$ converges to a stable set of 4 irreducible inequivalent ECA: {30, 45, 106, 154}. According to Wuensche's taxonomy of ECA this is the complete set of strong chain-rules representing maximally chaotic automata. Simultaneously, it is also the complete set of strong surjective automata, i.e. highly irreversible automata. We show that our algorithm can be used both as a valuable tool for theoretical investigations on cellular automata taxonomy and as a useful metaphor of coarse-graining procedures employed to more realistic modeling paradigms such as the particle method.

1. Introduction

The current challenges in studying biological systems for which macroscopic scales (e.g. the tissue scale) are tightly coupled with microscopic processes (molecular or cellular level), involve developing of new modeling paradigms. The non-linear interactions across many spatio-temporal scales make modeling biological systems both very demanding computationally and unreliable in the scope of classical modeling paradigms (e.g. [3–5]).

Preferably, we are looking for a unified computational framework, which could be matched to the following spatio-temporal scales of interest throughout the process of successive coarse-graining of finer scales. The coarse-graining (CG) can be understood as a numerical equivalent of some renormalization procedures used from many years in physics for simplification of formal mathematical models (e.g. [6]). In terms of computational modeling it can be defined as an approximation process, which limits the number of microscopic degrees of freedom (DOF) and the frequency of their motion starting from the smallest to the largest scales of interest. The primary challenge is to develop a CG model that is significantly easier to simulate but that reproduces the same (or similar) physical behavior as an underlying microscopic model. This would allow for extracting the large-scale behavior of the original systems without accounting for small-scale detail and studying predictability of emergent phenomena in complex systems.

Signal decomposition and signal multiresolution are the good metaphors of the notions of coarse-graining and multiscaling (e.g. [7]). Every signal can be decomposed onto its approximations and details on successive resolution levels by using a set of basis functions with compact support (such as wavelets, RBFs,[1] etc.). Finally, the signal can be represented as the sum of the approximation on a given resolution level and all the details from finer scales. By cutting off the least important details, i.e. all of them having the weights below a certain threshold, the signal can be reconstructed by using

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[1] RBF – radial basis function.

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the coarsest approximation and only a fraction of the most important details. This rises the following question. Does a similar scheme exist in the context of multiscale systems decomposition?

To find the analogies between signal and multiscale systems decomposition let us consider elementary 1-D cellular automata (ECA) as the most simplistic model of computations. In the scope of this conceptual framework we can try to answer the following questions. Can be the ECA systems decomposed? Does exist a general and efficient coarse-graining procedure for cellular automata?

In this paper we stick to the concept of coarse-graining, which has been introduced to 1-D cellular automata by Israeli and Goldenfeld [1,2]. Thus, in this context, the paper is an extension of the idea presented in [1,2]. First, we briefly present the idea. Then we demonstrate the CG algorithm of much lower computational complexity than the original one [1–3]. Then we show that it allows for coarse graining much broader class of automata on a machine that could not cope with the same task employing the brute-force algorithm from [2]. Consequently, we can estimate the number of CA's with CG ability for grain sizes $N>2$. Finally, in the conclusions, we sketch the analogy between coarse-graining of cellular automata and more realistic modeling paradigm, namely, the particle method.

2. Coarse-graining of cellular automata

According to Israeli and Goldenfeld [1,2] and employing the same notation, let us define the original cellular automata CA as $A=(a(t),\ \Sigma_A,\ f_A)$ and its coarse-grained equivalent $B=(b(T),\ \Sigma_B,\ f_B)$. The states of A and B are labeled by finite alphabets Σ_A and Σ_B of sizes $|\Sigma_A|$ and $|\Sigma_B|$, respectively. The update rules, defined as $f_i:\{\Sigma_i\}^{\Theta}\to\Sigma_i$, where Θ stands for the neighborhood size (i.e. $\Theta=3$ for 1-D basic CA) and $i\in\{A,B\}$, consist of a complete number $R_i=|\Sigma_i|^{|\Sigma_i|^{\Theta}}$ of CA rules and govern the evolution of lattices of CA states $a(t)$ and $b(T)$ in discrete times t and $T=N\cdot t$, respectively. The projection function $P:\ \Sigma_A^N\to\Sigma_B$ is used to map the block of N cells from A (i.e. A^N grain *supercell*) into a single cell of B. This projection has to satisfy the following CG condition [1,2]:

$$P\cdot\underbrace{f_A\cdot\cdots\cdot f_A}_{N}\cdot a=f_B\cdot P\cdot a \tag{1}$$

The expression $f_A\cdot(\cdots)$ means, that we apply the update rules f_A of automata A to every cell in the lattice $a(t)$, while $P\cdot(\cdots)$ denotes the CG procedure. Eq. (1) says, that by running N times the cellular automata A and then coarse-graining it by using $P(.)$, we obtain the same configuration as applying $P(.)$ at first (i.e. coarse-graining of A to B), and then running automata B only once. Eq. (1) has to be satisfied for any starting configurations $a(0)$ of A. Israeli and Goldenfeld [1,2] developed a brute-force procedure for finding coarse-grained configuration of a given automata A, which can be outlined as follows.

Let us define a supercell automata:

$$A_N=(a^N(t),\ \Sigma_A^N, f_{A^N})$$

which operates over blocks of N cells from $a(t)$ lattice. For 1-D automata with neighborhood of size $\Theta=3$ the local function f_{A^N} is then $f_{A^N}:\{\Sigma^N\}^3\to\Sigma^N$. We can compute easily the value of f_{A^N} for some $x=(x_1\,;x_2\,;x_3)$ where $x_i\in\{\Sigma^N\}$ and $i=1,2,3$. This could be done by converting x into $3N$-element lattice of automata A, and by running A exactly N times:

$$y=\underbrace{f_A\cdot\cdots\cdot f_A}_{N}\cdot x$$

Now we can choose the alphabet of coarse-grained automata B, which fits into the alphabet of A_N, i.e.

$$\Sigma_B\subseteq\Sigma_{A^N}$$

Otherwise, for $\Sigma_B\equiv\Sigma_{A^N}$ mapping function $P(.)$ is injective. There are no benefits from coarse-graining in that setup as we do not reduce the size of the new automatas' alphabet.

By employing all these definitions, we can rewrite Eq. (1) as follows:

$$f_B[P(x_1),P(x_2),P(x_3)]=P(f_{A^N}[x_1,x_2,x_3])$$

We need to keep in mind, that $P(.)$ is not injective, and thus it is possible that $(P(x'_1);P(x'_2);P(x'_3))=(P(x_1);P(x_2);P(x_3))$ for different triples of N-element blocks, i.e. $(x'_1;x'_2;x'_3)\neq(x_1;x_2;x_3)$. In that case for those triples we have:

$$f_B[P(x_1),P(x_2),P(x_3)]=f_B[P(x'_1),P(x'_2),P(x'_3)]$$

Hence, in general:

$$\forall(x,x'\mid P(x_i)=P(x'_i)):P(f_{A^N}[x_1,x_2,x_3])=P(f_{A^N}[x'_1,x'_2,x'_3]) \tag{2}$$

which defines the correct CG projection $P(.)$. The CG process eliminates degrees of freedom of local processes without loosing the global features of CA evolution. For example, as shown in Fig. 1a and b, the rule 165 is the coarse-grained version of the rule 90. In [2], the authors present the full diagram of elementary rules that can be coarse-grained into other elementary rules within grain size $N\leq 4$. It is worth to mention that the cellular automata of complexity from class IV (such as the rule 110) can be coarse-grained only to trivial rules, i.e. 0 and 255.

The mapping function $P(.)$ is responsible for information loss. Only when $\Sigma_B\equiv\Sigma_{A^N}$ no information is being lost, since $P(.)$ is injective. For such the alphabet Σ_B, the coarse-graining of A is trivial and it always exists. Therefore, it is reasonable to consider alphabets Σ_B that are much smaller than Σ_{A^N}. For example, as shown in Fig. 1c, by increasing the alphabet Σ_A (i.e. assuming that $\Sigma_A\subset\Sigma_B\subset\Sigma_{A^N}$) the finer scale information can be extracted. Summarizing, the main conclusions from Israeli and Goldenfeld CG approach [1] are as follows:

1. By applying this CG procedure to the most of ECA, it is possible to obtain their approximations.
2. Many coarse-grained CA can be predictable or trivial (0, 255 rules).
3. Finer, physically important DOF, can be incorporated to the CG model by increasing the alphabet $|\Sigma_B|>|\Sigma_A|$ and extending the rule set.

In the following section we present a new algorithm which enables us to extend the scope of applicability of Israeli and Goldenfeld CG procedure on greater alphabets and supercell sizes. This would allow to formulate much stronger conclusions about ECAs reducibility than those presented in [1,2].

3. Fast coarse-graining algorithm

The simple brute-force algorithm for finding projection $P(.)$ described in [2] is very computationally demanding. We need to consider all possible cellular automata for being likely the result of coarse-graining of A. For each CA we verify all mapping functions $P(.)$ and, finally, for each mapping $P(.)$ we have to process all possible starting configurations for Nth block version of CA. For a CA with neighborhood of size Θ, alphabet Σ and block size N, the computational complexity of this method is as follows:

$$O(|\Sigma|^{|\Sigma|^N}+|\Sigma|^{|\Sigma|^{\Theta}}+|\Sigma|^{N\Theta})$$