# On generative morphological diversity of elementary cellular automata

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## Structured abstract

### Purpose

Studies in complexity of cellular automata do usually deal with measures taken on integral dynamics or statistical measures of space-time configurations. No one every tried to analyze a generative power of cellular-automaton machines. We aim to fill the gap and develop a basis for future studies in generative complexity of large-scale spatially extended systems.

### Methodology and approach

Let all but one cells be in alike stat in initial configuration of a one-dimensional cellular automaton. A generative morphological diversity of the cellular automaton is a number of different three by three cell blocks occurred in the automaton's space-time configuration.

### Findings

We build a hierarchy of generative diversity of one-dimensional cellular automata with binary cell-states and ternary neighborhoods, discuss necessary conditions for a cell-state transition rule to be on top of the hierarchy, and study stability of the hierarchy to initial conditions.

### Research implications

The method developed will be used – in conjunction with other complexity measures – to built a complete complexity maps of one- and two-dimensional

cellular automata, and to select and breed local transition functions with highest degree of generative morphological complexity.

### Originality/value

The hierarchy built presents first ever approach to formally characterize generative potential of cellular automata.
*K*eywords: cellular automata, morphological diversity, elementary rules

## 1  Introduction

Morphological diversity — the variety of local patterns emerging in development of a spatially-extended system – is an underlying concept in analysis of natural systems and design of technical systems. The diversity's value is particularly pronounced in modern studies of biological populations adaptability and evolution, identification of spatially-extended systems and physical constructibility.

With regards to population developments, it is widely accepted that a diversity is a vehicle of evolution of biological [5, 8, 6] and socio-cultural population [14], and a key factor determining progress in socio-economical systems [24, 19]. Diversity of computational processes is an essential feature of adaptable and optimal cooperative computing systems mimicking biological populations [22, 23, 21].

Identification of spatially-extended system is the second application domain of morphological diversity. Identification of a discrete system, e.g. automaton array, is a reconstruction of local transition rules from a given series of global transformations [1]. Typically, an identification algorithm scans each pair of global configurations of a given system, extract a list of different neighborhood states present in one configuration and corresponding states of cells in subsequent configuration. Completeness of identification of a system, measured in a number of local transitions extracted, depends on morphological diversity of the system. In the framework of identification the generative diversity – a morphological diversity of a system evolving from a singleton state — characterizes response of the system to a local stimulation, or perturbation. The closest analogy would be a physiological experiment when we electrically stimulate living cells or tissues and record their response to stimulation. The richer response the more features of the cells or tissues we uncover.

Construction of physical objects in discrete spaces is the third application domain for morphological diversity, particularly in the framework of cellular-automaton based design. Cellular automata are emerging computational tools of designing structure parts of building architectures [9], conglomerates of buildings [7] and urban developments [4]. By constructing a hierarchy of morphological diversity of a discrete system modeling some structure one enables selection of local transition rules with reach behavior to be used in structural designs.

The paper presents first ever attempt to exhaustive study of morphological complexity. We have chosen elementary cellular automata — one-dimensional

arrays of cells, each cell takes two states and updates its states depending on states of its two closes neighbors — as most primitive but behaviorally rich models of discrete systems. Results presented in the paper based on previous studies in cellular-automaton complexity [25, 26] and classification and parameterization of one-dimensional cellular automata [10, 11, 12, 20].

The paper is structured as follows. In Sect. 2 we recall definitions of elementary cellular automata and introduce generative morphological diversity. A hierarchy of diversity is built and its sensitivity to certain initial conditions is analyzed in Sect. 3. Prospectives of further research are outlined in Sect. 4.

## 2   Basics

An elementary cellular automaton (ECA) is a one-dimensional array of cells, which take states 0 and 1 and each cell $x$ updates its state $x_i^t$ depending on states of its two neighbors $x_{i-1}^t$ and $x_{i+1}^t$ by function $f : \{0,1\}^3 \to \{0,1\}$. All cells update their states at the same time and by the same function. There are 256 possible functions $f$ which for brevity can encoded by digital numbers $0 \ldots 255$ by taking output table of each function as binary encoding of a digital number. For example, the cell-state transition table

| $x_{i-1}^t$ | $x_i^t$ | $x_{i+1}^t$ | $x_i^{t+1}$ |
|:---:|:---:|:---:|:---:|
| 0 | 0 | 0 | 0 |
| 0 | 0 | 1 | 1 |
| 0 | 1 | 0 | 1 |
| 0 | 1 | 1 | 1 |
| 1 | 0 | 0 | 1 |
| 1 | 0 | 1 | 1 |
| 1 | 1 | 0 | 1 |
| 1 | 1 | 1 | 0 |

can be represented by a sequence of bits (01111110) which in turn is a binary representation of number 126. The encoding was popularized in [25].

Let ECA of $n$ cells evolved for $\tau$ steps then one can represent space-time configuration of the automaton by matrix $\mathbf{M}=(m_{ij})_{1\leq i\leq n, 1\leq j\leq \tau}$ such that $m_{ij} = x_i^j$. A morphological diversity $\mu$ is a number of different $3 \times 3$ site blocks

| $m_{i-1j-1}$ | $m_{ij-1}$ | $m_{i+1j-1}$ |
|:---:|:---:|:---:|
| $m_{i-1j}$ | $m_{ij}$ | $m_{i+1j}$ |
| $m_{i-1j+1}$ | $m_{ij+1}$ | $m_{i+1j+1}$ |

of cell-states found in $\mathbf{M}$. For example, blocks extracted from the space-time configuration of Rule 126 ECA are shown in Fig. 1.

We have chosen $3 \times 3$ cell blocks to characterize morphology of space-time configuration because a minimal block must include a cell neighborhood (three cells), include at least two subsequent local configurations (to characterize identifiability) and sides corresponding to time and space must be have the same

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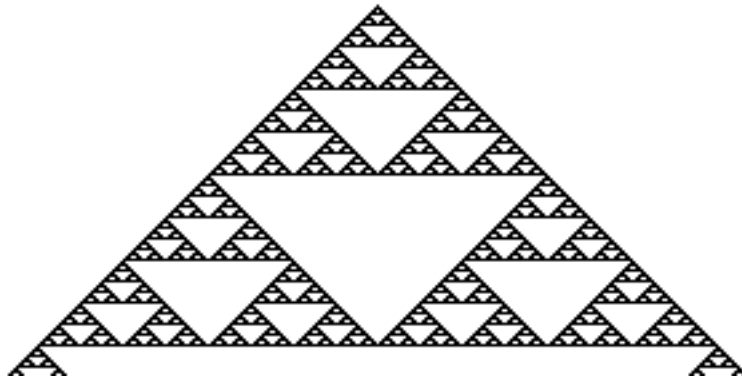
(a)

| 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 1 |
| 0 0 0 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 1 | 0 0 1 | 1 0 0 | 1 0 0 | 1 0 1 | 0 1 1 |
| 0 0 0 | 0 0 1 | 1 0 0 | 1 0 1 | 0 1 1 | 1 1 1 | 1 1 0 | 1 1 1 | 1 1 1 | 1 1 0 |

| 0 0 1 | 0 0 1 | 0 1 1 | 0 1 1 | 0 1 1 | 1 0 0 | 1 0 0 | 1 0 0 | 1 0 1 | 1 1 0 |
| 0 1 1 | 1 1 1 | 1 1 0 | 1 1 1 | 1 1 1 | 1 1 0 | 1 1 0 | 1 1 1 | 1 1 1 | 0 1 1 |
| 1 1 1 | 0 0 0 | 1 1 1 | 0 0 0 | 1 0 0 | 0 1 1 | 1 1 1 | 0 0 0 | 0 0 0 | 1 1 1 |

| 1 1 0 | 1 1 0 | 1 1 1 | 1 1 1 | 1 1 1 | 1 1 1 | 1 1 1 | 1 1 1 | 1 1 1 | 1 1 1 |
| 1 1 1 | 1 1 1 | 0 0 0 | 0 0 0 | 0 0 0 | 0 0 1 | 0 0 1 | 1 0 0 | 1 0 0 | 1 0 1 |
| 0 0 0 | 0 0 1 | 0 0 0 | 0 0 1 | 1 0 0 | 0 1 1 | 1 1 1 | 1 1 0 | 1 1 1 | 1 1 1 |

(b)

Figure 1: Space-time configuration of Rule 126 ECA developing form a single 1-state cell (a) and $3 \times 3$ blocks (b) occurred in the space-time configuration. In the configuration (a) cells in state 1 are shown by black rectangles, cells in state 0 are blank; time arrow points downward.

number of cells. We calculate morphological diversity using blocks of neighborhood states taken at three subsequent time steps. This reflects the fact that physical constructions are built in time intervals and that their structure, as a norm, could not be reversed. Another advantage of choosing $3 \times 3$ blocks to calculating diversity is that it can be used to characterize formation of $d$-dimensional structures by $(d-1)$-dimensional systems.

We calculate $\mu$ for a singleton configurations: at the beginning of evolution only one cell takes state 1 and others state 0. We allow automaton to evolve for $\tau$ steps and extract list $\mathcal{L}$ of $3 \times 3$ blocks from its space-time configuration $\mathbf{M}$. Experimentally we found that for most rules list $\mathcal{L}$ stabilizes over at most hundred time steps, which is indicator of $\tau$ choice.

Due to symmetries the elementary transition rules can be grouped in the classes with equivalent behavior [11, 12, 13]. We analyze morphological diversity for one rule, with minimal decimal value, from each equivalence class. The $\mu$-hierarchy is an ordering of the representative rules by values of $\mu$ calculated from space-time configurations generated by the rules.

# 3   Hierarchy of generative morphological diversity

The morphological diversity hierarchy, $\mu$-hierarchy, of the equivalence classes is shown in Fig. 2. When comparing the hierarchy with behavioral classification [20] we see that top third of the hierarchy is occupied by rules, which are commonly classified as chaotic. Bottom third of the hierarchy includes rules with two-cycle, fixed point and null behavior. Rules with periodic behavior lie closer to the top of $\mu$-hierarchy.

Domination of rules classified as chaotic is due to the number of different $3 \times 3$ blocks generated, which is indeed will be higher for truly random cell-state transitions. In the examples of space-time configurations generated by rules with $\mu \geq 30$, shown in Fig. 3, we see that Rule 30 and 45 exhibits varieties of traveling defects, localizations. The mobile localization collide one with another and produce other traveling localizations in the result of collisions. Generators of mobile localizations, aka glider guns, are also observed in the space-time configurations generated by Rules 30 and 45 (Fig. 3ab). Spatial dynamics of interacting localizations is rather asymmetrical, thus wider range of $3 \times 3$ blocks emerge in the space-time dynamics. Other rules with $\mu \geq 30$ (but Rule 110) produce patterns with reflection symmetry, mirror line is a time arrow crossing origin of the space-time pattern, cell assigned the state '1' in the initial configuration.

Is it possible to predict morphological diversity of the rules using only cell-state transition table? So far we do not see any reliable techniques of such prediction. We compare the diversity $\mu$ with two most know 'internal' parameters — Langton's $\lambda$ [10] and Wuensche's $Z$ [26, 27] (Fig. 4). We found that top three highest-diversity rules have $\lambda$ ratio equals 0.5, and top two rules in

| $\mu$ | Classes | chaotic | complex | periodic | two-cycle | fixed point | null |
|---|---|---|---|---|---|---|---|
| 64 | 30, 45 | ● | | | | | |
| 53 | 150 | ● | | | | | |
| 51 | 105 | ● | | | | | |
| 38 | 110 | | ● | | | | |
| 31 | 73 | ● | | | | | |
| 30 | 126, 161 | ● | | | | | |
| 27 | 41 | | | ● | | | |
| 25 | 22 | ● | | | | | |
| 24 | 62 | | | ● | | | |
| 22 | 60, 94 | ● | | ● | | | |
| 21 | 18, 26, 90, 154 | ● | | ● | | | |
| 20 | 57 | | | | | ● | |
| 19 | 9 | | | | ● | | |
| 18 | 25 | | | | ● | | |
| 17 | 54 | | ● | | | | |
| 16 | 77 | | | | | ● | |
| 15 | 37 | | | | ● | | |
| 14 | 11, 13, 43 | | | | ● | ● | |
| 13 | 78 | | | | | ● | |
| 12 | 15, 28, 156 | | | | ● | | |
| 11 | 3, 5, 6, 35, 38, 134 | | | | ● | | |
| 10 | 1, 27, 29, 33 | | | | ● | | |
| 9 | 50, 58, 178 | | | | ● | ● | |
| 8 | 51 | | | | ● | | |
| 7 | 14, 46, 142 | | | | ● | ● | |
| 6 | 2, 10, 24, 34, 42, 56, 74, 106, 130, 138, 152, 162, 170, 184 | ● | | | ● | ● | |
| 5 | 7, 19 | | | | ● | | |
| 4 | 4, 12, 36, 44, 76, 108, 132, 140, 164, 172, 204 | | | | ● | ● | |
| 2 | 23 | | | | ● | | |
| 1 | 0, 8, 32, 40, 72, 104, 128, 136, 160, 168, 200, 232 | | | | | ● | ● |

Figure 2: Morphological diversity $\mu$-hierarchy of equivalence classes [11, 12, 13] (only one representative rule is shown for each class) versus behavioral classification of the classes [20].

(a) Rule 30

(b) Rule 45

(c) Rule 150

(d) Rule 105

(e) Rule 110

(f) Rule 73
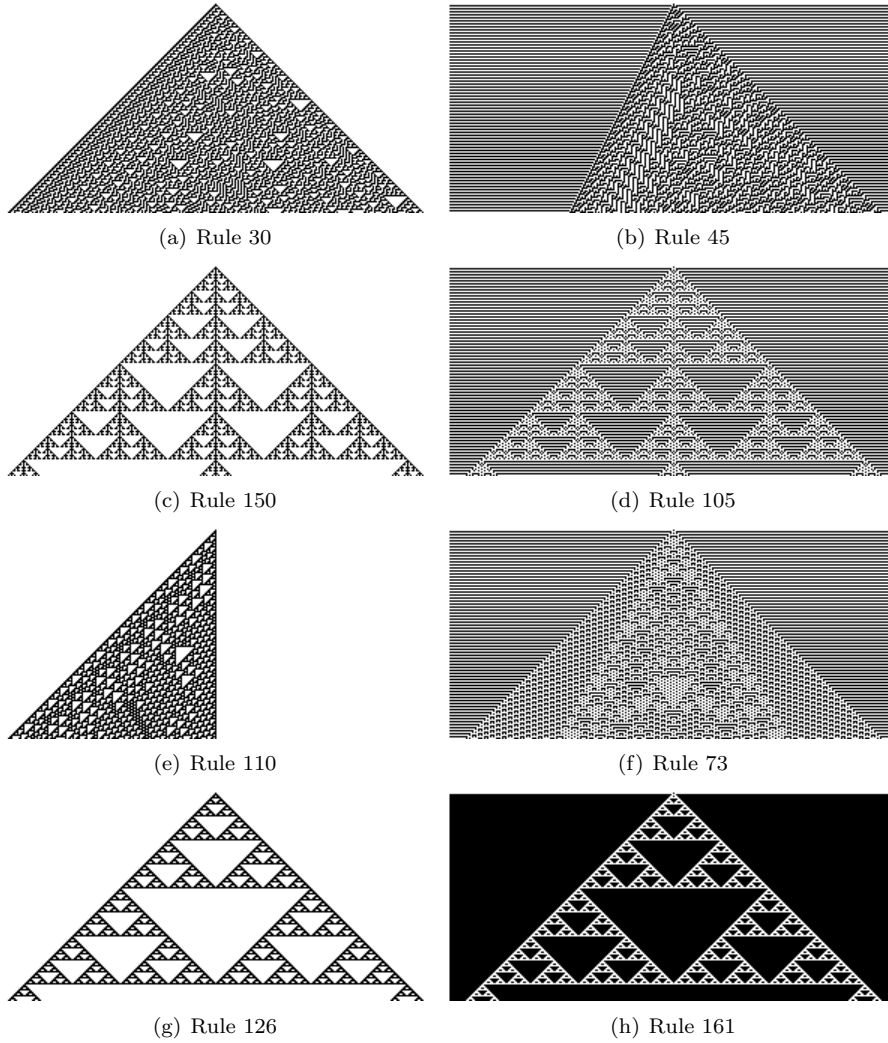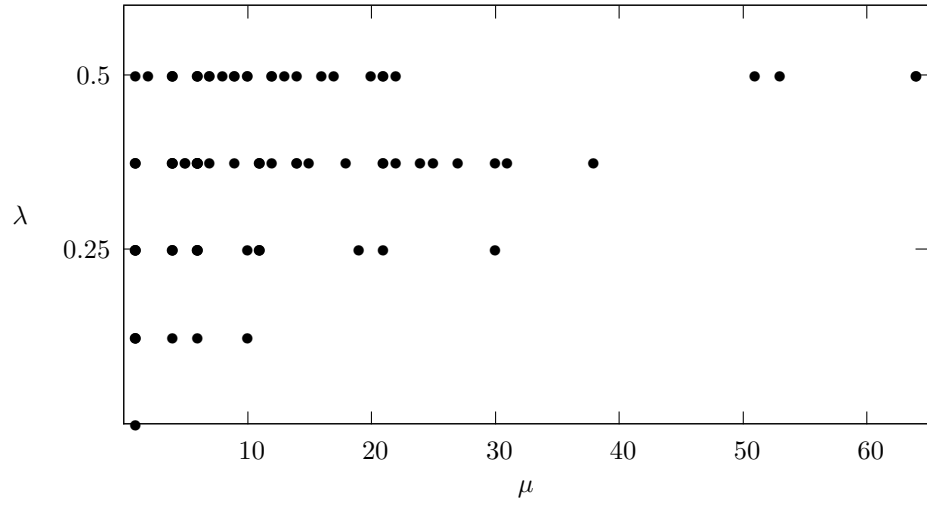
(g) Rule 126

(h) Rule 161

Figure 3: Exemplary space-time configurations of rule classes with $\mu \geq 30$. Initial condition is (1)-start, time arrow points downward, cells in state '0' are blank, cells in state '1' are black.

Figure 4: Morphological diversity $\mu$ versus Lagton's $\lambda$ (a) and Wuensche's $Z$ (b) parameters.

$\mu$-hierarchy have $Z$ value 1. These can indicate that equal ratio of cell-states in the outputs of cell-state transition table of an ECA rule is a necessary but not sufficient condition for the rule to exhibit highest morphological diversity. A positive outcome of the finding is that we can significantly reduce a search space when looking for a high-diversity rules in CA with large neighborhoods or great number of states.

We have built $\mu$-hierarchy of morphological diversity based on space-time configurations developed from the only initial configuration, where all cells but one take state '0'. Is the $\mu$-hierarchy stable under changing initial conditions? To answer we consider four initial configurations $\mathcal{I} = \{0\ldots010\ldots0, 0\ldots0110\ldots0, 0\ldots01110\ldots0, 0\ldots01010\ldots0\}$. We will refer to the elements of $\mathcal{I}$ as (1)-, (11)-, (111)- and (101)-start, respectively. Based on the $\mu$-hierarchy versus initial conditions plot is shown in Fig. 5 we make the following observations.

Equivalence classes **30**, **45** and **110** are not affected by variances in initial configurations from $\mathcal{I}$, the diversity of rules of these classes always fixed to 64.

Morphological diversity of classes **105** and **150** depends on the choice of initial configuration from $\mathcal{I}$. The rules are at the top of $\mu$-hierarchy in the conditions of (11)-start, but slide down to 2nd and 3rd place in the hierarchy for (1)- and (101)-starts.

There are also rules which disappear from the top of $\mu$-hierarchy when initial conditions are changed. Thus rules of class **73** climb up the hierarchy for (11)-start, slide down the bottom for (111)-start, and disappear from the list of rules with $\mu \geq 30$ for (101)-start. These movements of class **73** in $\mu$-hierarchy are due to stationary, or still, cluster of '1'-state in the space-time configuration developed for (11)-start (Fig. 6a), and briefly expanding domain of '1'-states for (111)-start (Fig. 6b).

And finally we should indicate equivalence classes, which demonstrate higher morphological diversity, $\mu \geq 30$, only for certain initial conditions. These are classes **90**, **26**, **60** for (111)-start, and classes **22** and **126** for (101)-start. Classes **41** and **106** appear only for the initial conditions of (11)- and (111)-start. See space-time configurations generated by representative rules of the classes in Fig. 7.

## 4    Discussion

We constructed a hierarchy of generative morphological diversity for equivalence rule classes of elementary cellular automata. We found that rules with chaotic behavior are at the top of hierarchy, followed by rules with periodic behavior and complex rules. Two-cycle and fixed point rules are at the bottom of the hierarchy. Chaotic rule classes **30** and **45** and complex rule **110** are insensitive to initial conditions while other high-diversity rules may slide down or climb up the hierarchy when initial conditions are changed. We did not find simple criteria to select rules with high morphological diversity without generating space-time configurations. However we confirmed that equal ratio of cell-states in outputs of cell-state transition table of a rule is a necessary condition for the

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| $\mu$ | (1)-start | (11)-start | (111)-start | (101)-start |
|---|---|---|---|---|
| 67 | | 105 | | |
| 66 | | 150 | | |
| 65 | | | | |
| 64 | 30, 45 | 30, 45 | 30, 45 | 30, 45 |
| 63 | | | | |
| 62 | | | | |
| 61 | | | | |
| 60 | | | | |
| 59 | | | | |
| 58 | | | | 150 |
| 57 | | | | 105 |
| 56 | | | | |
| 55 | | | | |
| 54 | | 106 | 106 | |
| 53 | 150 | | 150 | |
| 52 | | | | |
| 51 | 105 | | 105 | |
| 50 | | | | |
| 49 | | | | |
| 48 | | | | |
| 47 | | | | |
| 46 | | | | |
| 45 | | | | |
| 44 | | | | |
| 43 | | | | |
| 42 | | | 41 | |
| 41 | | | | |
| 40 | | | | |
| 39 | | 73 | | |
| 38 | 110 | 110 | 110 | 110 |
| 37 | | | | |
| 36 | | | | 126 |
| 35 | | | 90 | |
| 34 | | 41 | | |
| 33 | | | | 22 |
| 32 | | | 26, 60 | |
| 31 | 73 | | | |
| 30 | | | 73 | |

Figure 5: Hierarchy of morphological diversity $\mu$ for various initial conditions $\mathcal{I}$. Only equivalence rule classes with $\mu \geq 30$ are shown.

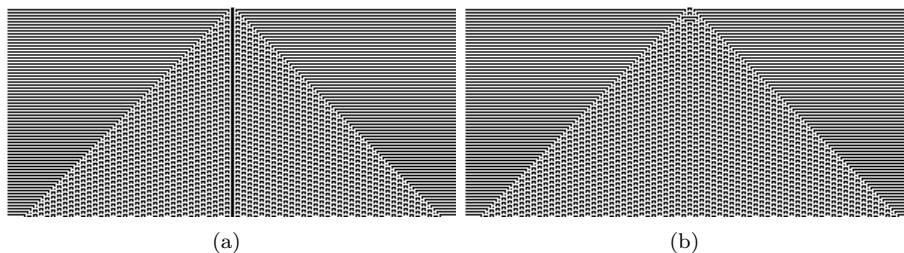<div align="center">(a)                  (b)</div>

Figure 6: Exemplary space-time configurations of rule 73 for (11)-start (a), (111)-start (b) . Time arrow points downward, cells in state '0' are blank, cells in state '1' are black.

rule to be on top of morphological diversity hierarchy.

Further studies will concern with building hierarchies of morphological diversity of discrete models of biological populations and establishing links between morphological diversity and localization dynamics in spatially extended discrete systems.

We have already obtained first results in this directions while analyzing primitive automaton models of two-species populations [3]. We found that the basic types of inter-species interactions can be arranged in the following complexity hierarchy [3]:

$$\text{commensalism, amensalism} \prec \text{competition} \prec \text{parasitism} \prec \text{mutualism.}$$

which indicates that evolution of populations favors mutualistic interactions due to their complexity of local interactions between species.

Search for spatially extended non-linear systems with rich localization dynamics will discover novel substrates for implementation of collision-based computing devices [2]. In a collision-based computer quanta of information, e.g. values of Boolean variables, are encoded to states of traveling localizations, e.g. gliders in cellular automata, solitons in optical media, wave-fragments in reaction-diffusion chemical media, defects in molecular arrays. When two or more traveling localizations collide they change their states thus updating values of the variables they represent. The computation is implemented at the sites of the collision.

Commonly only complex cellular-automata rules, e.g. rule rule 54 [15] and rule 110 [17], were considered as capable for universal computation. However recently we demonstrated that even so-called chaotic rules, e.g. Rule 30, exhibit very rich dynamics of traveling and stationary localizations which can be discovered by applying certain filtration procedures [16, 18]. This may indicate to high computational potential of the chaotic cellular automaton rules.

We can speculate that generative morphological diversity is determined, and proportional to, richness of localization dynamics, therefore the morphological diversity can be employed to select, or breed, non-linear systems capable for sophisticated collision-based computing [2]. This hypothesis will be verified in
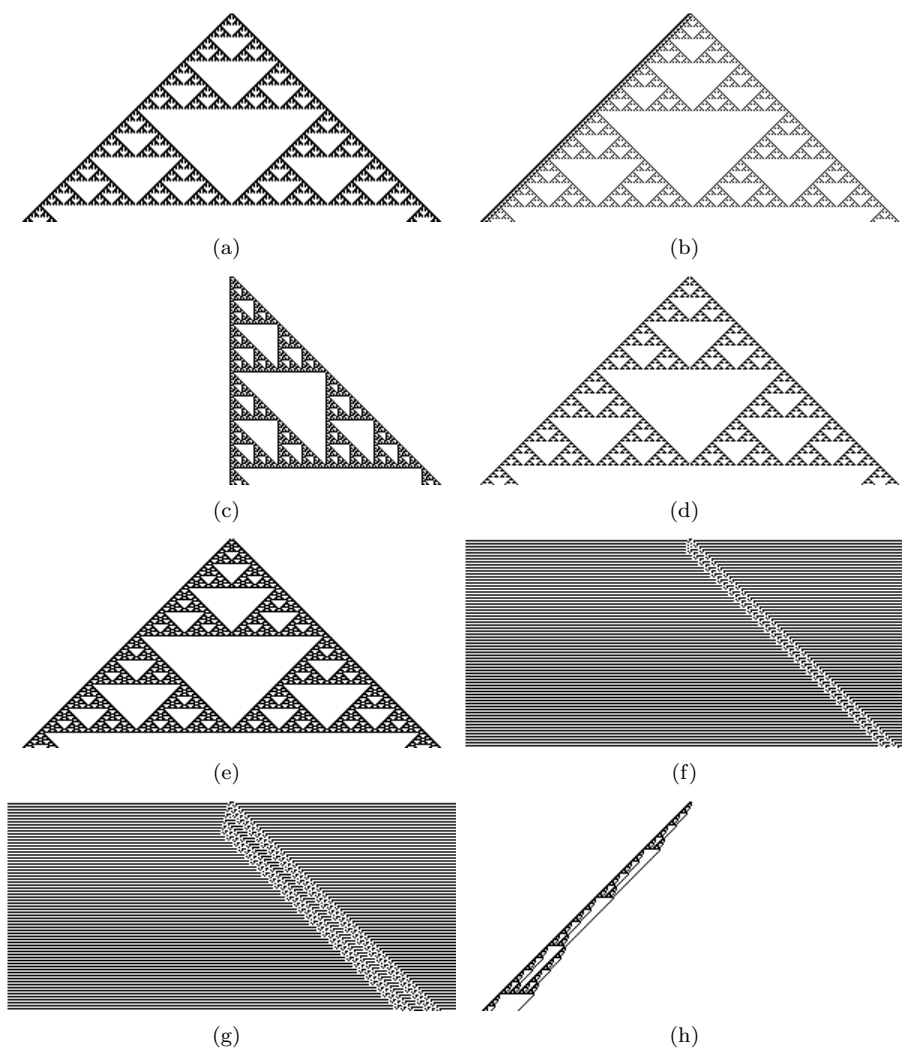
<div align="center">11</div>

Figure 7: Exemplary space-time configurations of (a) Rule 90, (111)-start, (b) Rule 26, (111)-start, (c) Rule 60, (111)-start, (d) Rule 22, (101)-start, (e) Rule 126, (101)-start, (f) Rule 41, (11)-start, (g) Rule 41, (111)-start, (h) Rule 106, (11)-start. Time arrow points downward, cells in state '0' are blank, cells in state '1' are black.

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our further studies.

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