CA-NEAT: Evolved Compositional Pattern Producing Networks for Cellular Automata Morphogenesis and Replication

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***Abstract*—Cellular Automata (CA) are a remarkable example of morphogenetic system, where cells grow and self-organise through local interactions. CA have been used as abstractions of biological development and artificial life. Such systems have been able to show properties that are often desirable but difficult to achieve in engineered systems, e.g. morphogenesis and replication of regular patterns without any form of centralised coordination. However, cellular systems are hard to program (i.e. evolve) and control, especially when the number of cell states and neighbourhood increase.**

In this paper, we propose a new principle of morphogenesis based on Compositional Pattern Producing Networks (CPPNs), an abstraction of development that has been able to produce complex structural motifs without local interactions. CPPNs are used as Cellular Automata genotypes and evolved with a NeuroEvolution of Augmenting Topologies (NEAT) algorithm. This allows complexification of genomes throughout evolution with phenotypes emerging from self-organisation through development based on local interactions. In this paper, the problems of 2D pattern morphogenesis and replication are investigated. Results show that CA-NEAT is an appropriate means of approaching cellular systems engineering, especially for future applications where natural levels of complexity are targeted. We argue that CA-NEAT could provide a valuable mapping for morphogenetic systems, beyond cellular automata systems, where development through local interactions is desired.

***Index Terms*—Cellular Automata, Compositional Pattern Producing Network (CPPN), NeuroEvolution of Augmenting Topologies (NEAT), EvoDevo, Artificial Life.**

1. Introduction

Complex self-architecturing systems are difficult to program, i.e. by top-down engineering. Kowaliw and Banzhaf [1], [2] argue that the bottom-up methodology of artificial development is an appropriate means of approaching complex systems engineering. However, achieving some sort of self-architecturing properties, e.g. morphogenesis or self-replication, is not trivial. One way of ”programming” such developmental systems is through artificial evolution, i.e. an evolutionary and developmental approach (EvoDevo) [3]. Searching for a solution for an artificial EvoDevo system that targets levels of complexity found in nature can be intractable, e.g. a cellular automata system with hundreds of cellular states and large neighbourhoods or a deep neural network with millions of nodes and weights. An appropriate mapping which scales well and at the same time allows solutions to be evolved incrementally, starting with a solution encoded into a small genome that is gradually complexified by adding new degrees of freedom, is desired. However, exploring a high-dimensional space in search for a solution can take prohibitively long time, regardless of the encoding [4].

In this work a cellular system is used as test bed of morphogenetic engineering. A traditional CA table-based encoding is replaced by a *Compositional Pattern Producing Networks* (CPPNs) mapping, a developmental encoding often used in systems without local interactions. In our work CPPN is used as developmental encoding based on local interactions, i.e. a true morphogenetic cellular system. The cellular automata CPPNs are evolved through a *NeuroEvolution of Augmenting Topologies* (NEAT) algorithm, a method that evolves increasingly complex networks. The approach is termed CA-NEAT. All cells in the systems are uniform, i.e. they share the same genome network. Two benchmark problems are investigated: 2D morphogenesis and replication of structures of increasing complexities.

The paper is organised as follows: Section 2 gives background information on CA, CPPNs and NEAT, together with a motivation for using them together in a morphogenetic engineering system. Section 3 describes the investigated problems and the experimental setup. Section 4 presents the results of the experiments, which are further discussed in Section 5. Finally, Section 6 describes some possible directions for future work and Section 7 concludes the paper. Appendix A contains some graphical visualisations of the solutions found in the outlined experiments.

2. Background and Motivation

2.1. Cellular Automata

Cellular Automata (CA) were first studied in the 1940s by von Neumann and Ulam [5]. CA were inspired by biological organisms, and introduced as models that could emulate some of these organisms' interesting and remarkable properties, such as multi-cellular development (e.g. embryogenesis), reproduction (clonal or sexual) and robustness (e.g. self-repair).

CA have been extensively studied, in particular within the field of *artificial life* [6]. Michael J. Flynn has speculated that CA and cellular computing might be the path forward [7] for novel bio-inspired computational machines. Matthew Cook proved that a CA of a certain type, e.g. Rule 110, can be Turing complete [8].

A CA consists of a grid of very simple units called cells. A cell can be in one out of a finite set of states. Sipper [9] described the three core principles of the cellular computing paradigm:

- **Simplicity**: a cell is simple and can do very little by itself.
- **Vast Parallelism**: the number of cells is very large, much larger than the number of processors in a conventional parallel computer.
- **Locality**: all interactions between cells take place on a purely local basis. No cell knows or controls the entire system.

The cells in a CA use the information available from their neighbours and a set of rules to transition from one state to the next, i.e. CA transition function. Depending on the starting state of the whole system and the transition function, it is possible to observe interesting emergent or self-organising behaviour over time and space, e.g. ordered, periodic, chaotic patterns. These interesting CA often enter an *attractor* [10], [11]. If a sequence of states repeats periodically it is referred to as *cyclic attractor*, and if the CA stabilises into a permanent state it is called a *point attractor*.

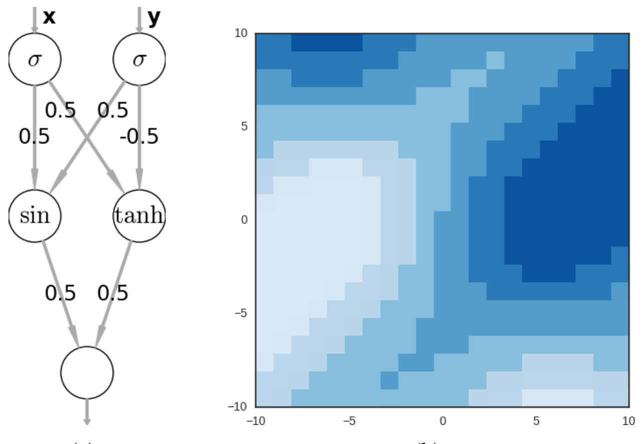
2.1.1. Transition Functions. Langton [6] formally describes finite CA as consisting of a finite set of cell states Σ of size $K = |\Sigma|$, a finite input alphabet α, and a transition function Δ. Each cell has a N-sized neighbourhood. The number of possible neighbourhoods can be expressed by equation (1).

$$|\alpha| = |\Sigma^N| = K^N \tag{1}$$

The transition function for a CA must thus encode a mapping of $|\alpha|$ different inputs to one of K states. The number of possible unique transition functions is thus $K^{(K^N)}$.

Traditionally Δ has been encoded as a complete mapping $\Delta : \Sigma^N \rightarrow \Sigma$, which can be implemented as a lookup table. When working with non-trivial CA where both K and N can be relatively large numbers, it becomes a problem to store the mapping Δ in an efficient way, and the space of possible Δ becomes too large to be explored by exhaustive enumeration.

Elementary CA transition functions have been studied extensively, and it has been reported that most rules lead to ”uninteresting” behaviour, either falling into an ”order” which is either static or repeating periodically, or into chaos, where all useful information is quickly lost in noise. It has been speculated that it is in the critical border region between these behaviours where interesting computations can occur [6]. In order to find these ”interesting” Δ, smart heuristic searches are often applied [12], e.g. evolutionary computation.



(a) (b)

Figure 1: An example composition of the sigmoid, sinusoid and hyperbolic tangent functions. The discrete coordinates of (b) are first normalised to $[-1.0, 1.0]$ and then mapped to various output values through the CPPN (a).

2.2. CPPNs

Artificial Neural Networks (ANNs) [13, Chapter 1] have been used in many different applications related to artificial life and intelligence, such as robotics or machine learning. An ANN is a directed graph structure, with vertices (referred to as neurons) and edges (referred to as connections). This is inspired by neuroscience, with the brain consisting of neurons and synapse connections. ANNs are useful because they consists of many discrete parts that can be individually or collectively tuned by some adaptive process, and are easily expanded. The *universal approximation theorem* [14] states that relatively simple ANNs can approximate a wide variety of functions, and the field of deep learning [15] shows that a large complex structure with enough tuning can perform very complex tasks, such as image classification [16] or natural language processing [17]. A *Compositional Pattern Producing Network* (CPPN), which was introduced by Stanley in 2007 [18], is a special type of ANN that is employed as an *artificial development encoding*. Like an ANN, a CPPN consists of a set of nodes with activation functions, weights and biases, as well as weighted connections between nodes. Likewise, external values are input to the first layer, then undergo transformation by weights and activation functions before being output by the final layer.

In contrast to ANNs, which are usually structured with neurons of the same activation functions arranged in layers, the CPPN has few such restrictions on topology and layer-wise heterogeneity and often employs a variety of different activation functions. Different activation functions are included to capture specific patterns seen in natural development, such as a Gaussian function to create symmetric patterns, or sine functions to create repeating patterns.

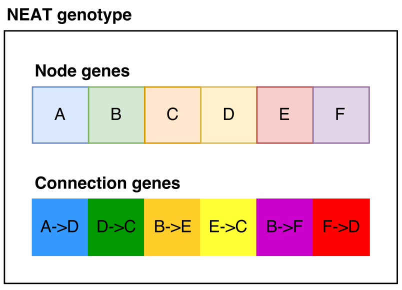
Additionally, CPPNs are normally applied across a broader range of possible inputs than ANNs. For example, Figure 1 shows a CPPN and its output when mapped over a 2D Cartesian grid. The particular composition of functions in the CPPN produces a particular pattern, hence the name. A CPPN is able to produce a pattern without multiple steps of development, in contrast to a CA, where local interactions and time is required. CPPNs have been used both to produce patterns for the sake of the patterns, e.g. as evolutionary art [19], [20], three-dimensional forms [21], musical accompaniments [22], or artificial flowers [23], but also to create the neural connectivity patterns of larger ANNs for agent [24], [25], [26], [27] and robot control tasks [28], [29], [30].

2.3. Artificial Evolution and Development

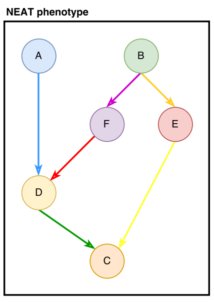
The bio-inspired design methods of *artificial evolution* and *artificial development* take principles from the natural processes of evolution [31], exploration and adaption of populations to environmental conditions, and development [32], the processes enabling a multicellular organism to emerge by growth and differentiation from a single cell. Artificial development and artificial evolution take inspiration from biology's EvoDevo process in order to explore and handle large and complex solution spaces.

Algorithms for artificial evolution, e.g. Genetic Algorithms (GAs) [33] or Genetic Programming [34], are based on populations of candidate solutions (*genotypes*), starting with a random generated initial population, each candidate is evaluated and assigned a *fitness*. A selection process picks individuals from the population that get to reproduce. This selection process is often stochastic, with a bias towards picking the individuals with the highest fitness, but some chance of picking a less fit individuals. Individuals that are selected for reproduction are paired up. Genotypes of the pair are combined in some fashion to create a new genotype. Random mutations are applied in order to produce new features not present in either parent. Repeating this generational algorithm the search space, i.e. the space of all solutions the genotypes can represent, is explored and exploited toward novel genotypes that encode good solution to the problem at hand.

Artificial development is an *indirect mapping* process. In contrast, in a *direct mapping* the genotype encodes the entire information of each candidate solution i.e. *phenotype* [29]. Such indirect mappings can be inspired by biological development where an initial unit, a cell, holds the complete building plan (DNA) for an organism. It is important to note that this plan is generative, it describes how to build the system, not what the system will look like. The indirect mapping process maps genetic information in the genotype to a phenotype that expresses structure behaviour and function [3]. In a system including a developmental mapping, the role of the genome is radically changed, from a system where the genome is considered a description to a system where the genome may be viewed as information on how to build the system. The "build" process can be based on self-organisation governed by rules given in the genotype, e.g. gene regulation [35]. As such the phenotype is an emerging structure. Therefore, the genome size may not reflect the size or complexity of the phenotype and opens for systems that can generate very large-scale repetitive structures [36], or even structure of arbitrary size [37]. Further, a developmental mapping is not a process that is "turned off" when the finalised adult stage is reached. The process is working on the organism/artefact throughout its lifetime. In [38], Banzhaf and Miller discuss the "challenge of complexity" in evolving systems and argue that Nature solved such challenge by "inventing" developmental processes.



(a) Genotype



(b) Phenotype

Figure 2: An example NEAT genotype and corresponding phenotype. This example only shows the topology that the genotype encodes, leaving out the weights and activation functions.

2.3.1. NEAT.

NeuroEvolution of Augmenting Topologies (NEAT) is a genetic algorithm variant introduced by Stanley and Miikkulainen in 2002 [39], designed specifically to evolve ANNs. Because CPPNs are special variants of ANNs, they can also be evolved with the NEAT algorithm [18]. NEAT has been applied successful to a variety of complex control tasks [40], [41].

A NEAT genome consists of genes that encode nodes and connections between them. Figure 2 shows an example genotype to phenotype mapping. NEAT starts with an initial population of very simple networks, typically with just the input and output nodes and connections between them. Over generations, more nodes and vertices are added or disabled, activation functions are changed, and weights are adjusted. The process of gradually expanding the genome is called *complexification*, and reflects how life on earth is believed to have started with simple organisms and gradually evolved into more complex creatures [42], [43].

The genes that make up a NEAT genome are marked with an *innovation number* so that they may be recognised as the same gene in different individuals. As new features are added to the genomes, the individuals making up the population become gradually less similar. The degree of similarity is measured through a measure called the *compatibility distance*. When the distance between individuals pass a certain threshold, they are segregated into separate species. This process is called *speciation*. Pair selection for reproduction happens within species. Typically the species that have the most fit individuals will produce more children, while the less fit species will produce fewer (but not 0) children.

When a new species appears with a new feature, the feature will not be tuned and likely affect the fitness of the individuals negatively. NEAT protects new species for a certain amount of time, allowing them time to adjust before being evaluated and, if performing poorly, being eliminated to make more room for the more fit species.

One notable variation of NEAT is called *HyperNEAT*

[44]. In this process, NEAT is used to evolve CPPNs whose output determine the topology of ANNs. The indirect HyperNEAT encoding allows larger networks to be evolved with complex connectivity patterns. Additionally, because HyperNEAT can learn from the geometry of the task, it is possible to increase the number of ANN inputs and outputs without further training [45], [46]. If the evolved CPPN creates a useful network connectivity pattern at a small scale, it often also produces a useful output at a larger scale.

2.4. Motivation

NeuroEvolution of Augmenting Topologies has been shown to evolve CPPNs that produce patterns with repetitions, repetition with variation, symmetries, and different kinds of regularities, without using temporal development and local interactions. However, in natural processes of development such as embryogenesis, local interactions and developmental time are key requirements. Biological morphogenetic systems are the result of a continuous computation, i.e. development, where intermediate phenotypes emerge along the developmental path, and these intermediate phenotypes influence the decoding and regulation of the genotype for the next phenotypic stage. Development is a combination of interactions between genotype and phenotypes, and with the environment. As such, natural development can be considered a dynamical systems where the phenotype changes continuously due to growth of new cells and adaptation to external perturbations, i.e. environment. Morphogenetic processes may be considered as Dynamical Systems with Dynamical Structures $(DS)^2$ [47]. In such $(DS)^2$ systems, state transition functions and the set of state variables can change over time (caused by morphogenetic processes). In this paper, we argue that CPPN is an appropriate means for developmental systems based on local interactions, which provides a mapping for the next phenotypic stage for each component of the cellular system. Such mapping uses only local information, i.e. the state of each cell and its neighbours. NEAT provides a practical evolutionary strategy for CPPN complexification.

2.5. Other Related Work

Wolper and Abraham [48] used evolved CPPNs to find seed patterns for Conway's Game of Life [49]. Both CPPN-NEAT (objective search) and novelty search [50] were investigated. However, CPPNs were not used as developmental encodings. Many different kinds of CA encodings have been previously investigated. These include *conditionally matching rules* [51], [52], [53] where conditions have to be satisfied to determine the next state of a cell, *instruction-based development* [54], [55] where transition functions are replaced by a program, *self-modifying cartesian genetic programming* [56] where a variation of genetic programming is used, and *variable length gene regulatory networks* [57]. Nichele and Tufte [58] investigated an instruction based encoding where genomes could complexify during evolution. In [59] traditional CA transition functions are evolved through complexification. Nichele et al. [60] also proposed an instruction-based development with instructions that could self-modify the genome program during evolution. Cheney and Lipson [61] investigated the evolution of 3D CA soft-robot morphologies through CPPNs. However, in this last work CPPNs make use of topological information instead of a developmental approach, as often done with CA.

3. Methodology and Experimental Setup

In order to conduct the experiments described in the following sections, a custom Python framework was developed to implement CA-NEAT. The experiments presented target problems and patterns of different complexities, allowing for direct comparison of results with the literature [58].

Briefly described, the system consists of an evolutionary loop based on the NEAT algorithm. Each individual NEAT genotype is developed into a CPPN genotype, which is used as the transition function for a CA system. The performance of the developed phenotype for the CA problem at hand is used as fitness measure.

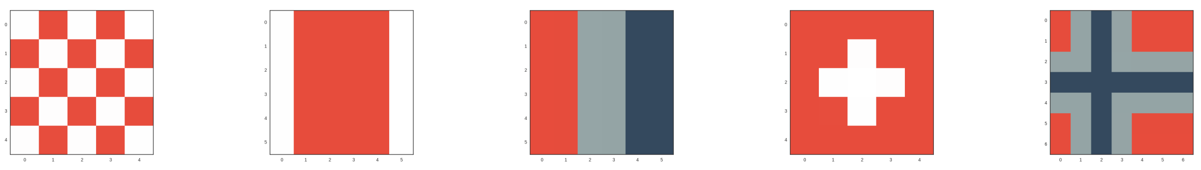
3.1. Problems Under Investigation

Morphogenesis and replication are two distinct yet fundamental processes in biological systems, and their complexity is not fully understood yet. For example, Venter and colleagues [62] have chemically synthesized a minimal bacterial genome that includes only the genes essential for sustaining life, e.g. metabolism and growth. However, out of the total 473 genes, 149 have unknown function. Self-replication in machines was first studied by von Neumann [63] using a 29 states 2D cellular automaton and has been a central problem in artificial life since then. von Neumann was interested in the general question "What kind of logical organization is sufficient for an automaton to be able to reproduce itself?". In both biological and artificial cellular systems, the cell is an autonomous unit that serve as construct and constructor of the emerging organism. By being able to transfer biological properties of replication and growth in artificial systems, artificial morphogenetic systems could move towards frontiers that are not reachable by current methodologies.

For the investigation in this paper, the problems of 2D replication and morphogenesis are chosen, as to be able to compare results with those in the literature [58]. The five "flag" patterns shown in Figure 3 were investigated. These patterns represent a wide variation of properties such as number of states and symmetries.

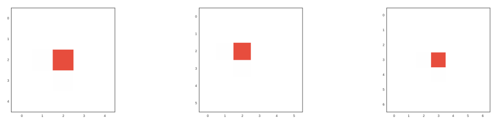
Each experiment consists of 100 independent runs. All experiments have a population size of 200 individuals and elitism degree of 1. Each generation-population is segregated into species by NEAT, with selection and reproduction happening within these groups. *Sigma scaled selection* [64] is used to select pairs for reproduction.

During development of the system, a variation of different configurations was tested for different problems. However, for the results included herein, a choice was made to use the same CPPN-NEAT configuration, and as close to the same CA configuration as possible for all problems. This makes it easier to make comparison between experiments, but also means that the settings chosen may favour some experiments over others. The optimisation of CPPN-NEAT parameters is outside the scope of this paper.



(a) 5x5 ”Mosaic” 2 states (b) 6x6 ”Border” 2 states (c) 6x6 ”Tricolor” 4 states (d) 5x5 ”Swiss” 2 states (e) 7x7 ”Nordic” 4 states

Figure 3: Patterns being investigated. Each color represents a different cell state, white represents the quiescent state.



(a) 5x5 (b) 6x6 (c) 7x7

Figure 4: Seed patterns for morphogenesis. For the 6x6 patterns there is no central cell, so the seed is not symmetric.

3.1.1. Morphogenesis. The morphogenesis problem is defined as the development of a complex pattern from a simple ”seed” pattern. The biological analogy and inspiration is *embryonic development*, with the seed pattern also referred to as *zygote*. Figure 4 shows the seed patterns used in these experiments.

The fitness evaluation for a morphogenesis phenotype consists of the following steps:

1) Develop seed pattern for 30 iterations
2) For each stage
    a) Compare cell by cell with target pattern
    b) Calculate ratio of correct out of total cells
3) Pick max of values from step 2
4) Use function (2) with value from step 3 as x

$$f(x) = x * \frac{e^{5*x}}{e^5} \tag{2}$$

Function (2) is used to reduce the contribution to the score from quiescent cells, while ensuring that $f(1.0) = 1.0$. For instance, with the ”Mosaic” pattern shown in Figure 3 (a) a completely quiescent pattern would have a ratio of 0.52. With the correction the fitness in this case is reduced to 0.05, which is much more appropriate for a ”lifeless” CA.

Because every iteration of the CA is counted equally and separately, the fitness evaluation does not care if the CA becomes stable, enters a cycle, or neither within the 30 allotted iterations.

3.1.2. Replication. The replication problem start with one instance of some pattern in a larger grid, and over time develop into a state where multiple copies of the pattern exists in the grid, which may then replicate again. The biological analogy of this is cell division and asexual (clonal) reproduction. For the replication problem the seed pattern is thus one copy of the target pattern in a larger grid.

The fitness evaluation for a replication phenotype is as follows:

1) Develop seed pattern for 30 iterations
2) For each stage
    a) For each region of target pattern size
        i) Compare cell by cell with target pattern
        ii) Calculate ratio of correct out of total cells
    b) Pick max 3 values from (a)
    c) Multiply any non-1.0 value by a penalty factor of 0.9
    d) Calculate mean of three values
3) Pick max value from stage (2)

In this case the number of replicas sought is three. There is no further contribution to the score if there are more than three perfect replicas. Once again a penalty is applied, this time to penalise the contribution from any imperfect replica pattern.

Compared to the evaluation of morphogenesis of the same pattern, the replication evaluation is much more computationally expensive. Therefore it will always take longer to collect results for a replication problem than the same-pattern morphogenesis problem. However, both morphogenesis and replication are properties that are present in biological systems and are highly desided in artificial morphogenetic systems.

3.2. Cellular Model

For both the aforementioned problems, a 2-dimensional CA model was used. For the morphogenesis problem the grid is of fixed size with toroidal border conditions. For the replication problem the grid is automatically expanding to accommodate growth in any direction. In theory this means an infinite grid, but since the CA may only iterate 30 times, there is a practical limit to how large it may grow. In both problems, the von Neumann neighbourhood (Figure 5) is used.

3.3. CPPN-NEAT

The nodes of the evolved CPPNs can have any of the activation functions listed in Table 1.

In each run of each experiment, an initial population of 200 genomes is generated. These have an input layer with one node per member of the CA neighbourhood, and an output layer with one node per possible cell state. The

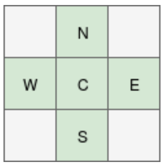


Figure 5: The von Neumann neighbourhood includes the four cardinal directions as well as the centre.

TABLE 1: Possible activation functions

Type	Equation
Sigmoid	$f(x) = \frac{1}{1+e^{-x}}$
Hyperbolic tangent	$f(x) = tanh(x)$
Sinusoid	$f(x) = sin(x)$
Gaussian	$f(x) = ae^{-\frac{(x-b)^2}{2c^2}}$ a, b, and c are constants
Rectified linear unit	$f(x) = max(0, x)$
Identity	$f(x) = x$
Clamped	$f(x) = \begin{cases} 0 & x \leq 0 \\ x & 0 < x < 1 \\ 1 & x \geq 1 \end{cases}$
Inverse	$f(x) = \frac{1}{x}$
Logarithmic	$f(x) = log(x)$
Exponential	$f(x) = e^x$
Absolute value	$f(x) = \lvert x \rvert$
Hat	$f(x) = \begin{cases} 1 - \lvert x \rvert & \lvert x \rvert < 1 \\ 0 & otherwise \end{cases}$
Square	$f(x) = x^2$
Cube	$f(x) = x^3$

input layer neurons have a sigmoid activation function which is never changed. When the initial population is created, the number of connections for each individual is randomly initialised to be between 50% and 100% of being fully connected. Figure 6 illustrates this. As the evolutionary algorithm iterates on the population, new individuals come into existence that have hidden nodes and different connections and activation functions.

The inputs to the CPPNs are the values of the neighbourhood, but normalised to the range $[-1.0, 1.0)$ to accommodate the sigmoid input layer. Table 2 shows an example of this normalisation. The output of the CPPN is a set of values, one per possible CA state. The final step of the transition function finds the highest of these values, and outputs the state that correspond to that output node.

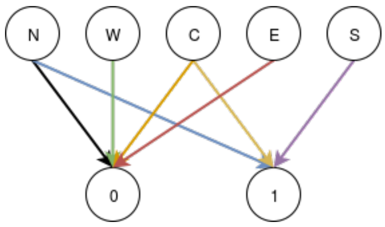


Figure 6: Example first-generation CPPN with 7 out of 10 possible connections.

TABLE 2: Example normalised states

State	Normalised value
A	-1.0
B	-0.5
C	0.0
D	0.5

There is also a *quiescent rule* hardcoded into the transition function. One of the CA cell states is considered to be the *quiescent* or *dead* state. If all the values in the input neighbourhood are quiescent, the output is always quiescent.

The speciation rule in NEAT puts the individuals of the population into separate species. Sometimes a mutated child will be so dissimilar from its parents that it will be placed in a new species. The parameter called the *stagnation limit* determines how soon a new species may be eliminated if not performing well. This value is set to 15 generations in these experiments.

3.4. Implementation

The system developed consists of a combination of self-made and library code. The CA subsystem was built from scratch to fit the available CPPN-NEAT implementations. It supports 1D and 2D topologies with various border conditions. For each problem there is a problem-specific fitness function which receives a genotype as input from the NEAT subsystem, develops the transition function and iterates the CA before evaluating the performance and returning a fitness value to the NEAT system.

The NEAT portion of the system is mostly based on the library `neat-python`[1]. Data structures for genomes and networks as well as various functions have been used without modifications. The main evolutionary loop was re-implemented with modifications. This was done for multiple reasons, including to take advantage of parallelism using `Celery`[2] and to store the results in a database using `SQLAlchemy`[3]. Other software dependencies include `matplotlib`[4] and `seaborn`[5] for visualisation, and `dill`[6] for data and code serialisation. The complete framework software for CA-NEAT is available on Github[7].

4. Results

In this section, results for morphogenesis and replication of different structures are given. Each experiment consists of 100 independent runs using the same configuration, with different initial populations (randomly initialised). Each run continues the evolutionary loop until an optimal solution has been found or it is stopped when the maximum number of generations has been reached. Because of the difference in number of generations required, some experiments finish quickly, while others are executed for hundreds of generations until stopped.

Some of the optimal solutions found were visually inspected to check the correctness of the evaluation algorithms. Appendix A contains some example solutions for various problems, selected to display a variation of behaviours. Such figures provide valuable insight on the inherent difficulty of the targeted problems.

1. https://github.com/CodeReclaimers/neat-python/
2. http://celeryproject.org/
3. http://sqlalchemy.org/
4. http://matplotlib.org/
5. http://seaborn.pydata.org/
6. https://github.com/uqfoundation/dill
7. https://github.com/mathiasose/CA-NEAT

TABLE 3: Summary of results. The metrics shown are the success rate and the mean number of generations until a solution is found, with standard deviation also shown. In the case of 100% success rate, the number of generations column shows how many generations it took until the final solution was found. In the case of less than 100% success rate, the column shows how many generations were run until the experiment was stopped.

Problem	Success rate %	Mean generations	σ generations	Generations until stop
Mosaic morphogenesis	100	1.2	0.4	2
Border morphogenesis	1	270	0	509
Tricolor morphogenesis	100	56.5	228.8	2189
Swiss morphogenesis	76	147.7	158.9	600
Mosaic replication	100	4.2	10.6	99
Swiss replication	100	7.7	5	20
Tricolor replication	55	55.8	52.6	200
Nordic replication	0	-	-	200

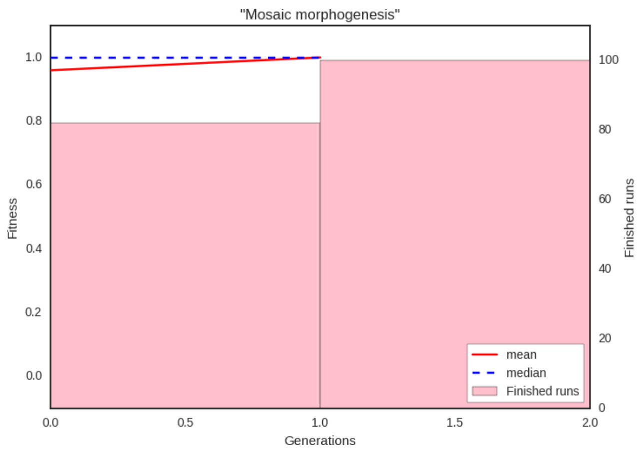


Figure 7: Mosaic pattern morphogenesis, all generations.

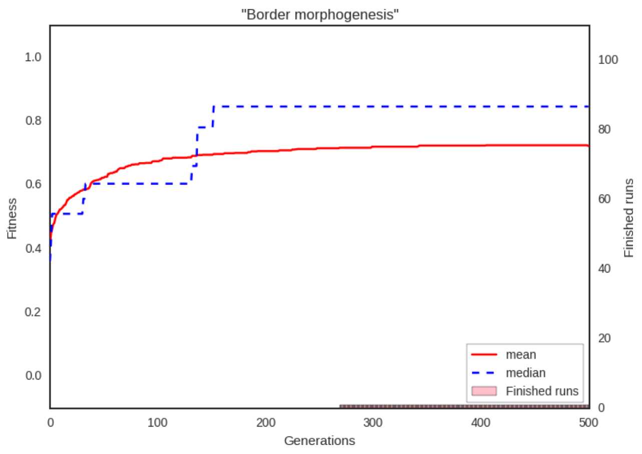


Figure 8: Border pattern morphogenesis, 500 first generations. The value where the median stabilises represents the fitness for a solution with one wrong cell.

Table 3 depicts the obtained results. It is particularly important to highlight the evolution over time (generations), not just the final result achieved at the end of the experiment. There are multiple metrics that can be used to visualise such data. In the figures shown in this section, three metrics have been used:

1) The **mean** of the **highest fitness** for each generation of each run.
2) The **median** of the **highest fitness** for each generation of each run.
3) The **cumulative** number of **runs that have finished** (success rate).

The choice of the *highest* value (out of 200 individuals) as representative of a whole generation, combined with the fact that the populations have elitism, means that the values shown in the graphs will only increase over time, never decrease.

Some of the figures show all generations of the experiment, until every single run has succeeded. Others are cut short, either because the experiment was stopped or to exclude statistically insignificant outlier values that makes the figure less clear. In these cases, this is clearly mentioned in text.

4.1. Morphogenesis

Figure 7 shows the results of the ”Mosaic” morphogenesis. In this particular case there existed an optimal solution among the initial population in 80% of the runs. The remaining runs succeeded after one reproduction cycle.

Figure 8 shows the results from the ”Border” morphogenesis. This has a very different evolutionary process compared to the ”Mosaic” morphogenesis. In this case no optimal solution is found for a fairly long time. The populations find local maxima solutions which have only one incorrect cell, but struggle to find the global maxima that gives the 100% correct patterns. At ca. 150 generations the median value is equal to the fitness given to a solution with one incorrect cell. After 270 generations one of the populations is successful, but after 500 generations no other population has succeeded, and the experiment is terminated.

Figure 9 shows the results from the ”Swiss” morphogenesis. From both the mean line and the success histogram we can see that there is an initially rapid increase that gradually diminishes. By 150 generations 50 of the runs have succeeded, but by 300 generations only 11 more have finished, and by 600 generations the number of successful runs is 76. At this point the experiment is terminated.

Figure 10 shows the results of the ”Tricolor” morphogenesis. There is a large number of runs that complete in the first 15 generations, after which the rate of completion slows down. At 25 generations 80 runs have completed, but by 100 generations only 13 more have finished. This experiment was allowed to run to completion, but results after the first 100 generations are omitted from the figure. The last runs succeeded at generations 117, 149, 177, 302, 534, 607 and 2189.

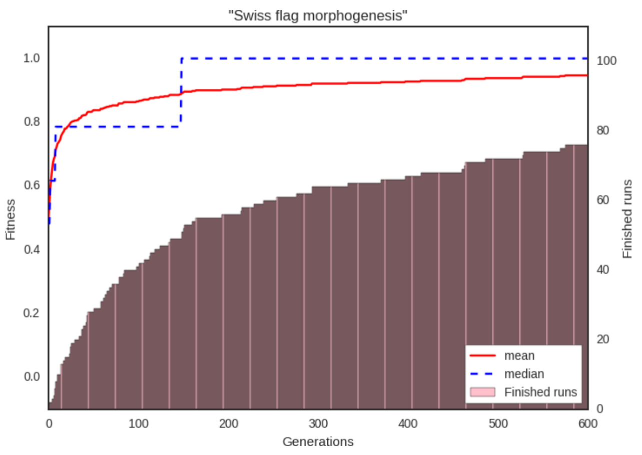


Figure 9: Swiss flag pattern morphogenesis, 600 first generations.

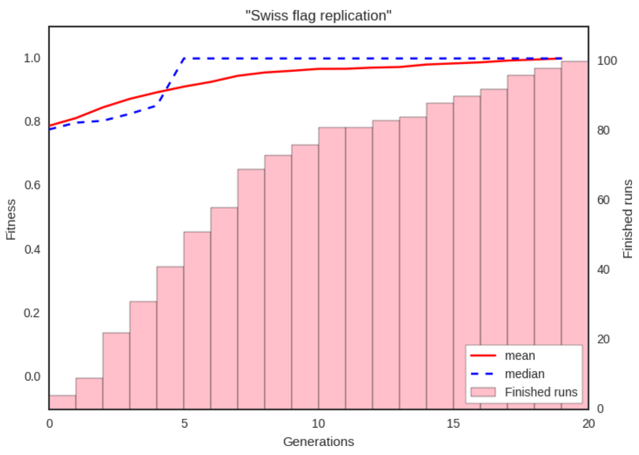


Figure 12: Swiss flag pattern replication, all generations.

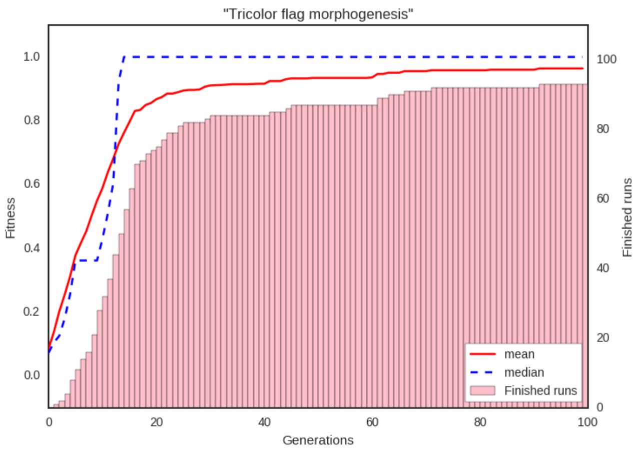


Figure 10: Tricolor flag pattern morphogenesis, 100 first generations.

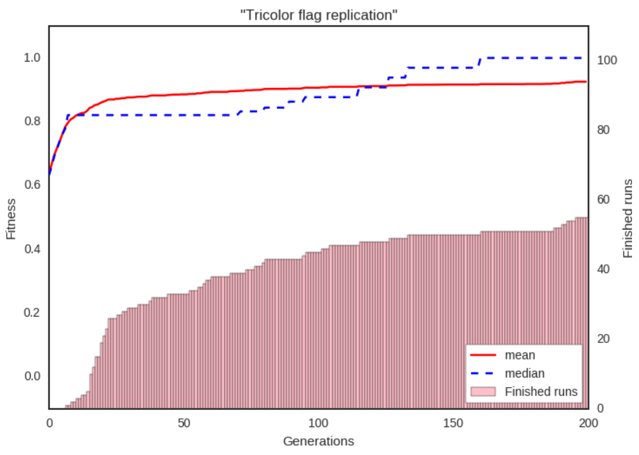


Figure 13: Tricolor flag pattern replication, 200 first generations.

4.2. Replication

Figure 11 shows the results of the ”Mosaic” replication. By 25 generations 98 runs have completed. The last two finished at 38 and 99 generations.

Figure 12 shows the results of the ”Swiss” replication. Again we see the number of successful runs increase quickly at first, before slowing down. In five generations, 50 of the runs have completed, but the last 50 succeed over the next 15 generations.

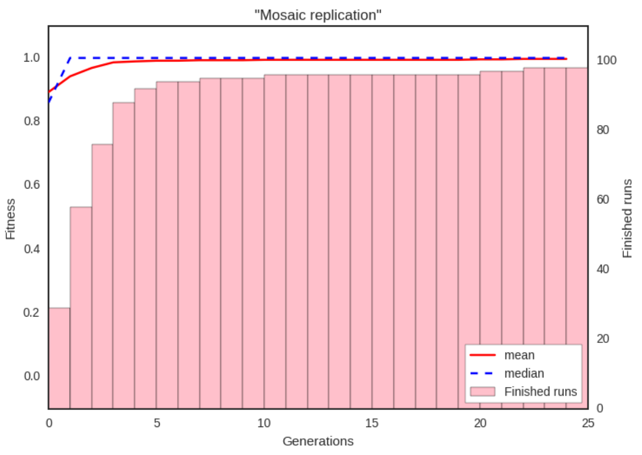


Figure 11: Mosaic pattern replication, 25 first generations.

Figure 13 show the results of the ”Tricolor” replication. In this case the first results started appearing after five generations. Like other cases there is a quick rise in finished runs early on, which drops off gradually. By 100 generations, 45 runs have succeeded, and by 200 generations there are 55 finished runs, at which point the experiment is ended.

Figure 14 shows the results of the ”Nordic” replication. The populations quite quickly reach local maxima at 0.7, but are not able to find their way out of there to the global maximum. The experiment was run up to 200 generations without any further change.

4.3. Size of Genomes

In addition to the number of completed runs, another interesting result is the sizes of the genotypes of optimal solutions. NEAT genotypes consists of a fixed number of input and output nodes $N + K$, 0 or more hidden nodes, and some number of connections between nodes. When evaluating NEAT genotypes, it is interesting to consider these numbers both separately and combined.

Table 4 shows measures of the optimal genotype sizes for each experiment. Since some runs finish with a generation where there is more than one optimal solution present,

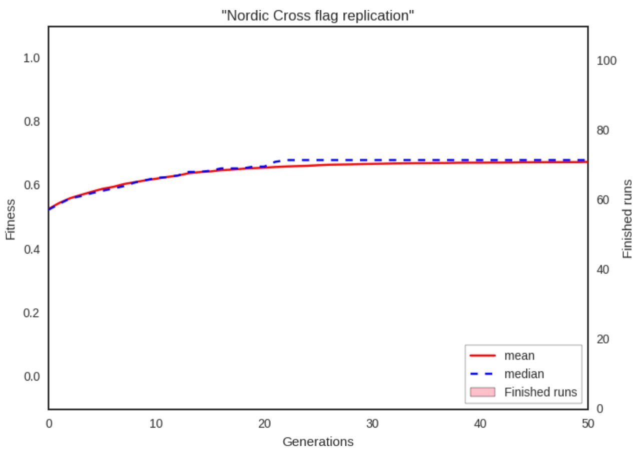


Figure 14: Nordic cross pattern replication, 50 first generations. Further generations up to 200 did not have any significant change in the mean or median lines.

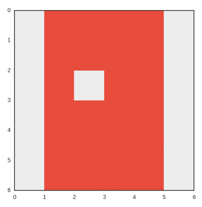


Figure 15: ”Border” pattern with only one wrong cell. CA-NEAT manages to find a pattern like this for the majority of the runs by 150 generations, but struggles to find the 100% correct pattern.

the number of optimal genotypes may be higher than the number of finished runs.

5. Discussion

In some cases we observe that there is at least one optimal solution among the individuals generated as part of initial populations, e.g. ”Mosaic” morphogenesis and ”Mosaic” replication. This means that there exists a simple solution consisting of only the input and output layers with connections. In all cases where there exists many solutions early, we can also notice a pattern in the cumulative number of completed runs that follows a cumulative chi-squared distribution [65], with a rapid rise that gradually diminishes. The most extreme of these cases is the ”Mosaic” morphogenesis where 80 runs complete in the initial generation and the last 20 in the second generation. This result can be explained by the symmetry and repetitiveness in the target pattern, and CPPN has been shown particularly successful when targeting morphologies with such properties. However, CPPNs usually exploit topological information to achieve symmetry and regularity. In the work herein, the same result is achieved without any available topological information, and only through developmental processes based on local interactions, i.e. a self-organising morphogenetic behaviour. For more complex patterns, more generations are obviously required in order to evolve and complexify the networks in the initial population.

It is somewhat surprising which problems are easily solved and which ones are not. We can observe that the ”Swiss” replication is much easier than the ”Swiss” morphogenesis. This is in line with results in [55], [60], when instruction-based development or conditionally-matching rules are used. However, the ”Tricolor” morphogenesis is easier than the replication of the same pattern, as it is often the case when CA transition functions are used (obviously with worst results). The fact that the ”Border” morphogenesis is more difficult than the ”Tricolor” morphogenesis might seem not intuitive, since the ”Border” pattern has both fewer colours (states) and one more symmetry. Figure 15 shows an example of the imperfect patterns produced by CA-NEAT for the ”Border” morphogenesis. One plausible explanation is that the symmetry is deceptive and leads to a local maxima, while the ”Tricolor” experiment avoids this, since symmetry in solutions will not give better scores in such case. Novelty search [50] might be explored for deceptive tasks. This is further discussed in the Future Work section.

CA-NEAT does quite well for three out of four replication problems, but does not succeed at the ”Nordic” replication. This problem was expected to be difficult, since the pattern is rather complex (shifted symmetries). However, instruction-based encoding in [58] found solutions for this task. One possible solution for this problem would be to exploit CPPN ability to produce such patterns when topological information is available to the evolved networks. This is discussed further in the Future Work section.

As mentioned earlier, optimisation of NEAT parameters was outside the scope of this experimentation. As such, populations were initialised without hidden nodes. Alternatives could be to initialise the population with one or more hidden nodes, a larger CA neighbourhood, and an increased NEAT mutation rate to encourage innovation. This is also discussed further in the Future Work section.

5.1. Comparison with Literature

The patterns and structures investigated herein are widely used benchmarks in the literature [66], [67]. For example, in [58] similar problems are investigated with an instruction-based encoding, as well as a table-based encoding for comparison.

When comparing results, it is important to consider the differences in the experimental setups. In particular, the populations in NEAT have to be much larger to allow speciation. This gives CA-NEAT an advantage in cases such as the ”Mosaic” morphogenesis where a large initial population is likely to contain an optimal solution. Conversely, it means it takes longer for each generation of CA-NEAT, so results that require development over generations may be found *faster* with smaller populations. In [58] all populations ran up to 10000 generations before being terminated.

5.1.1. Morphogenesis. For the ”Mosaic” morphogenesis, table based evolution has a success rate of 58% and instruction-based 98%. With CA-NEAT this rate was 100%. The table-based and instruction-based evolutions took on average 1336 and 1257 generations respectively, while the NEAT search had found all solutions in two

TABLE 4: Sizes of genomes of optimal solutions. Genomes consist of node genes and connection genes, which may be counted considered separately or combined. Each genome has a fixed number $N + K$ input and output nodes, plus some number (possibly 0) of hidden nodes. When considering genome size, only the hidden nodes are counted.

		Min	Max	Mean	Median	Mode(s)	σ
Mosaic morphogenesis (241 results)	Hidden nodes	0	1	0.1	0	0 (213 occurrences)	0.3
	Connections	4	11	7.1	7	6 (53 occurrences)	1.5
	Both	4	12	7.2	7	6 (49 occurrences)	1.6
Border morphogenesis (1 result)	Hidden nodes	7	7	7	7	7 (1 occurrence)	0
	Connections	16	16	16	16	16 (1 occurrence)	0
	Both	23	23	23	23	23 (1 occurrence)	0
Tricolor morphogenesis (119 results)	Hidden nodes	0	14	2	2	1 (31 occurrences)	2.1
	Connections	6	32	15.1	15	16 (20 occurrences)	4.3
	Both	6	46	17.1	17	13, 14, 18 (11 occurrences)	6
Swiss morphogenesis (61 results)	Hidden nodes	0	13	2.9	2	2 (19 occurrences)	3.1
	Connections	5	22	10.2	9.5	9, 10 (13 occurrences)	3.7
	Both	6	32	13.1	11	11 (12 occurrences)	6.5
Mosaic replication (136 results)	Hidden nodes	0	10	0.6	0	0 (81 occurrences)	1.2
	Connections	4	21	7.6	7	7 (41 occurrences)	2
	Both	4	31	8.2	8	7 (33 occurrences)	3
Swiss replication (114 results)	Hidden nodes	0	3	0.5	0	0 (63 occurrences)	0.7
	Connections	7	14	9.5	9	9 (32 occurrences)	1.5
	Both	7	16	10	10	9 (28 occurrences)	2
Tricolor replication (47 results)	Hidden nodes	0	20	4.8	4	2 (14 occurrences)	4.2
	Connections	8	41	14.7	14	8 (7 occurrences)	5.7
	Both	8	61	19.5	17	17 (5 occurrences)	9.5

generations. This is mostly explained by the large NEAT population and relatively simple target pattern.

For the ”Swiss” morphogenesis, table-based evolution had a success rate of 23% and instruction-based 100%. The average generations until solution was 2668 for table-based and 285 for instruction-based. CA-NEAT results seems comparable to the instruction-based results, with a 76% success rate by generation 600, and an average generations of 147.7 so far, in the same order of magnitude as the instruction-based result.

There is a stark contrast between the results of the ”Border” morphogenesis, where table-based evolution has a 69% success rate and instruction-based 98%. CA-NEAT has a 1% success rate at 500 generations.

For the ”Tricolor” morphogenesis, table-based evolution has a 19% success rate and instruction-based evolution has a 46% success rate. CA-NEAT improves both of these with a large margin, with a success rate of 92% at 100 generations, 99% at 607 generations and finally 100% at 2189 generations. CA-NEAT has an average number of generations at 56.5, compared to 5002 for table-based and 6424 for instruction-based.

5.1.2. Replication. For the ”Mosaic” replication, table-based evolution has a success rate of 85% and instruction-based 100%. CA-NEAT also has a 100% success rate and average generations of 4.2, compared to 39.7 for instruction-based encoding, a significantly better result.

For the ”Swiss” replication, table-based evolution has a success rate of 1% and instruction-based a 100% rate. CA-NEAT has a 100% success rate too, with 7.7 average generations, compared to the 41.8 of the instruction-based evolution, also a significant difference.

For the ”Tricolor” replication, table-based evolution has a success rate of 8%, and instruction based a 100% rate. CA-NEAT has a 45% success rate at 100 generations, and an average generations of 34.6 at that point. Compared to the instruction-based average of 41.8 generations after all runs, the performance of CA-NEAT seems lower in this case.

5.2. Size and Topology of CPPN Phenotypes

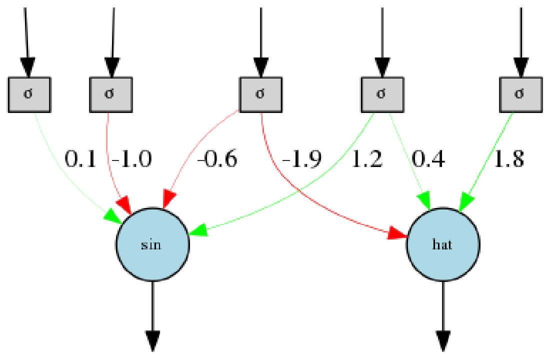
In all the experiments where multiple solutions were found, there existed at least one solution with no hidden nodes. This indicates that a CPPN-based encoding *can* be efficient at those particular problems. However, it has not been determined whether these small CPPNs encode solutions that are fast at morphogenesis, fast at replicating, or how many replicas they produce, nor how many steps of CA development they require.

Some of the found CPPNs were visually inspected to try to understand their topologies. Figure 16 shows two of these visualisations. In solutions with many hidden nodes, the structure seems disorderly to a human, and it is difficult to understand the relationship between input and output based on topology alone.

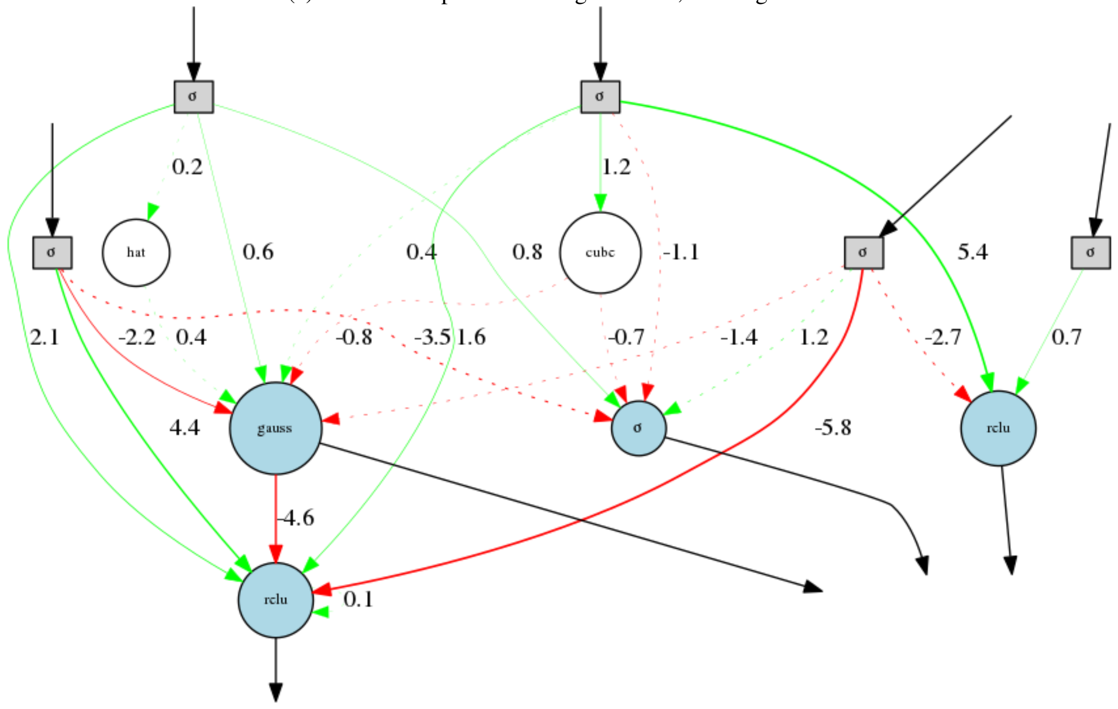
In solutions with hidden nodes, it is often possible to see some nodes that are not connected to the output nodes. These are a kind of *vestigial structure* [68]. In a final solution these could be pruned away to reduce the genome size without changing CA behaviour. During evolution these should probably be left in place, as they could be reconnected by mutations and possibly produce positive effects.

6. Future Work

There are many aspects of the CA-NEAT model that have not yet been tested or analysed. In the remainder



(a) "Mosaic" replication along one axis, like Figure A.14.



(b) "Tricolor" morphogenesis that reaches a point attractor equal to the target pattern. The two hidden nodes are not connected to output nodes and are thus "vestigial". See Figure A.10 for the CA development of this phenotype.

Figure 16: Examples of found CPPN encodings. Dashed lines represent disabled connections. The visualisation library optimises the figures to have few crossing connections, and does not care about presenting nodes as structured layers.

of this sections, possible directions for future work are analysed and discussed.

6.1. Other Morphogenetic Engineering Problems

The framework developed for this project is quite generic and can handle a variety of problems already. Code that is specific to a problem is contained in the fitness function for that particular problem. In order to test a new class of problems, it would be enough to use a new fitness evaluation function.

The experiments presented in this paper concern development and replication of 2D patterns, as proof of concept that CA-NEAT is a promising avenue for morphogenetic engineering and self-assembly of complex structures and morphologies through local interactions. Morphogenetic systems can be considered very powerful and decentralised computing machines, where computation and memory are totally distributed and the actual computation is a result of self-organisation and emergence. There are many other morphogenetic computational problems that could be explored, e.g. the majority problem [69], the firing squad synchronisation problem [70], or mathematical and algorithmic problems such as square calculation [71]. Another variation of replication problem, known as *replicating loops* [72], as well as morphogenesis in 3D space [73] are target problems for future research.

6.2. Fitness Evaluation Variations

Over time NEAT will keep expanding genomes, increasing the number of nodes and connections of the CPPN topology. When comparing two CPPNs that produce the same CA rules, it is the less complex CPPN that is most desirable, due to its lower memory footprint and running time. The fitness evaluation function could be amended to reward smaller genomes, encouraging this.

Another aspect that could be considered for certain problems, such as morphogenesis, is that of attractors. For the morphogenesis problem, the arguably best result is to find the shortest possible attractor that contains the target state, preferably a point attractor. One option could be to introduce a penalising factor inversely proportional to the length of the cycle. In a replication problem, one might consider the emergence of a new copy of the original pattern as the repeating of a cycle, and thus reward a quicker replication in such case.

6.3. Variations of Cellular Model

The CA-NEAT experiments herein have shown different degrees of success. However, the NEAT parameters have not been optimised and the same settings have been used for all the experiments. An exploration of various parameters and relative performance is desired in future research, as to be able to pinpoint suitable setting for such morphogenetic engineering systems.

An interesting idea for further work is to allow evolution to optimise the neighbourhood definition. The neighbourhood radius could be expanded easily with CPPN, as it would simply be an addition of new input nodes. This would create much more diversity in the initial population, and possibly create genotypes that are more complex for harder problems. Figure 17 proposes one implementation of larger neighbourhoods, where there are many input nodes available, but only the closest ones are connected in the initial population. When mutating new genotypes, new inputs could be re-connected, and over time evolution would determine if such innovation was beneficial and worth to be retained.

It would be also trivial to include environmental information in the form of one or more additional CPPN input nodes. For example, each cell could know something about the physics of the CA world. e.g. its position (coordinates or distance from the origin coordinate), or chemicals in the environment. The addition of an abstraction layer on top of the CA layer (e.g. chemicals layer) has been shown beneficial for cellular systems. In [74], a French flag organism was shown to possess beneficial properties for morphogenetic systems, such as self-repair and self-regulation, as a result of local interactions with neighbouring cells as well as with the environment (chemicals). Biological cells have different means of receiving positional information [75]. Topological information has been shown to be a key contributor to CPPN-based solutions, even without local interactions. It is therefore reasonable to imagine that CA-NEAT would also benefit by including positional information as available input to the CPPN, in the form of coordinates or gravity (direction). We envision that complex solution will be easily achieved with CA-NEAT through development based on local interactions with the addition of topological information.

6.4. Novelty Search

In [48] it was shown that novelty search in combination with NEAT produced some interesting results where objective search did not. Considering that the objective-based search did not entirely succeed at finding solutions to some of the deceptive problems in this paper, novelty search could provide a different strategy of exploring the solution space without getting trapped in local maxima. In particular, one challenge is giving fitness scores to intermediate non-optimal solutions in such a way as to reward the solutions that will eventually lead to optimal solutions and avoid rewarding ”dead ends”. Novelty search [50] attempts to solve the problem by disregarding the objective score and instead rewarding phenotypes that exhibit previously unseen behaviour.

7. Conclusion

In this paper we presented a novel method for self-organisation of morphogenetic cellular systems based on development through Compositional Pattern Producing Networks. CPPNs are used as developmental mappings that take advantage of local interactions. CPPNs have been evolved with the NeuroEvolution of Augmenting Topologies algorithm and Cellular Automata have been used as the experimental platform. One of the main issues of morphogenetic engineering systems, and Cellular Automata in particular, is the difficulty of programmability and control when the number of components, their types (or states) and their local interaction neighbourhoods become larger (towards systems at complexity levels found in nature). CPPNs provide an appropriate mapping that scales well in all these cases, e.g. linear increase of input CPPN nodes when the neighbourhood is increased as opposed to CA transition functions that would grow exponentially, or linear increase of CPPN output nodes when the number of states is increased as opposed to CA transition functions that would grow exponentially. The CA-NEAT morphogenetic framework has been tested on two different problems, the development of structures from a seed and the replication of structures of increasing complexities. The presented results have shown promise in most of the experiments, considering that NEAT parameters were not optimised as it was outside the scope of this study. We suggest that the natural way forward is to incorporate topological/positional information in CA-NEAT, as CPPNs have been proven successful even with development without local interactions. We argue that CA-NEAT could provide a valuable EvoDevo approach to self-organising decentralised control and programmability of morphogenetic systems.

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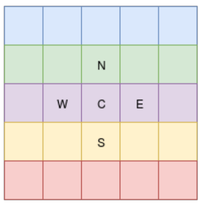

(a)

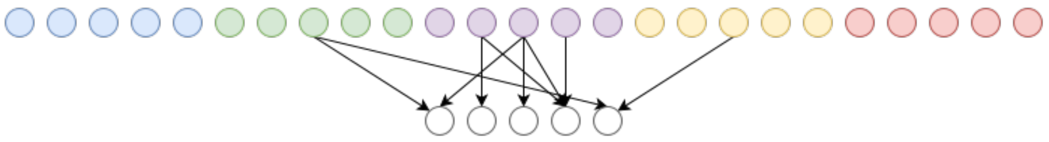
(b)

Figure 17: An example CPPN with a large available input neighbourhood, but only the Von Neumann sub-neighbourhood connected to the output layer.

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Appendix A.
Sample Solutions

This appendix contains some visualisations of hand-picked example solutions that were found.

In morphogenesis cases where a previous state is revisited (a cycle is found), the number above the last state shown indicates which previous state it is equal to.

For the morphogenesis examples up to 30 states are shown, including states after the target pattern is seen. For replication examples, the visualisations stop after an optimal (3 copies) solution is seen.

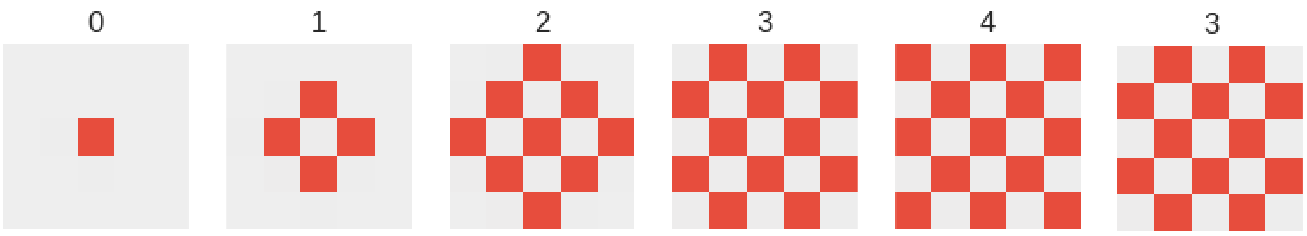

Figure A.1: A solution to the ”Mosaic” morphogenesis where the CA finds a two-step cycle that includes the target pattern.

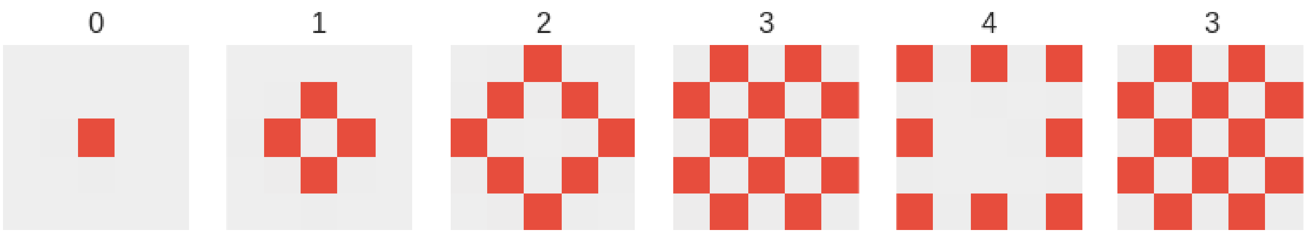

Figure A.2: Another two-state cycle that includes the target state.

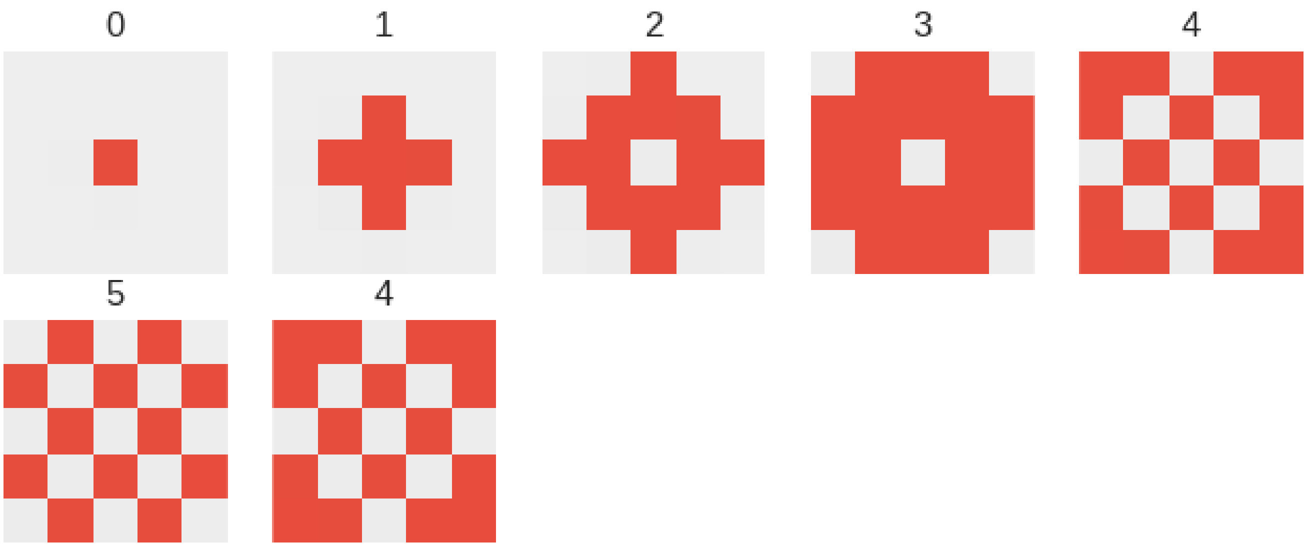

Figure A.3: Another two-state cycle that includes the target state.

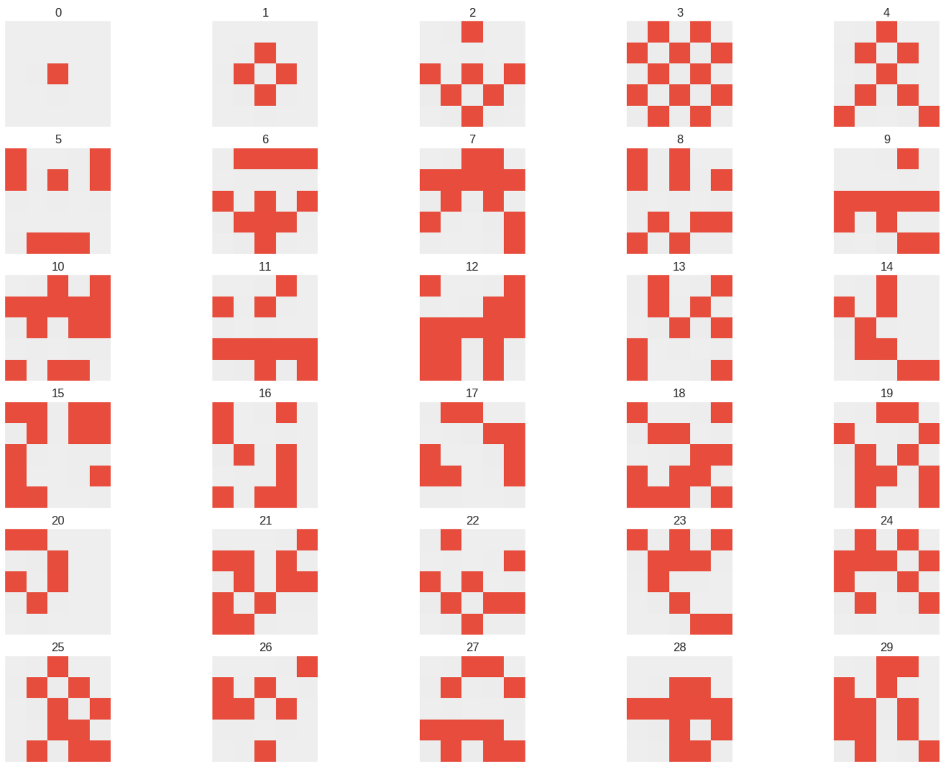

Figure A.4: A solution where the target pattern can be seen early, but when the CA continues it becomes chaotic.

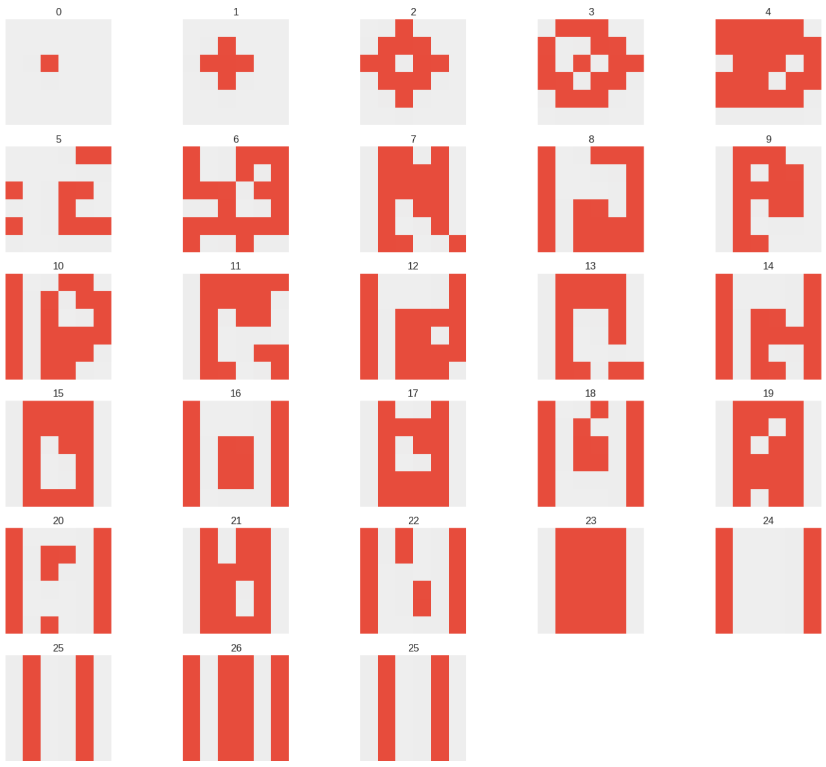

Figure A.5: The only solution that was found for the ”Border” morphogenesis. After finding the target state in iteration 23, the CA goes in to a two-step cycle which does not include the target state.

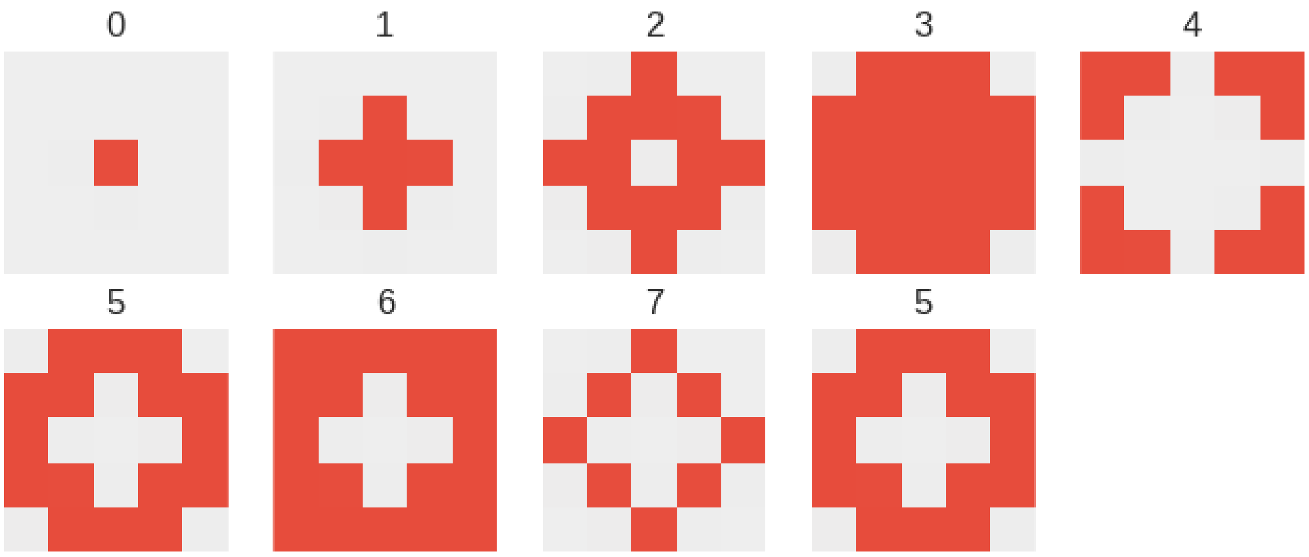

Figure A.6: A solution to the ”Swiss” morphogenesis where the CA goes in to a three-state cycle that contains the target pattern.

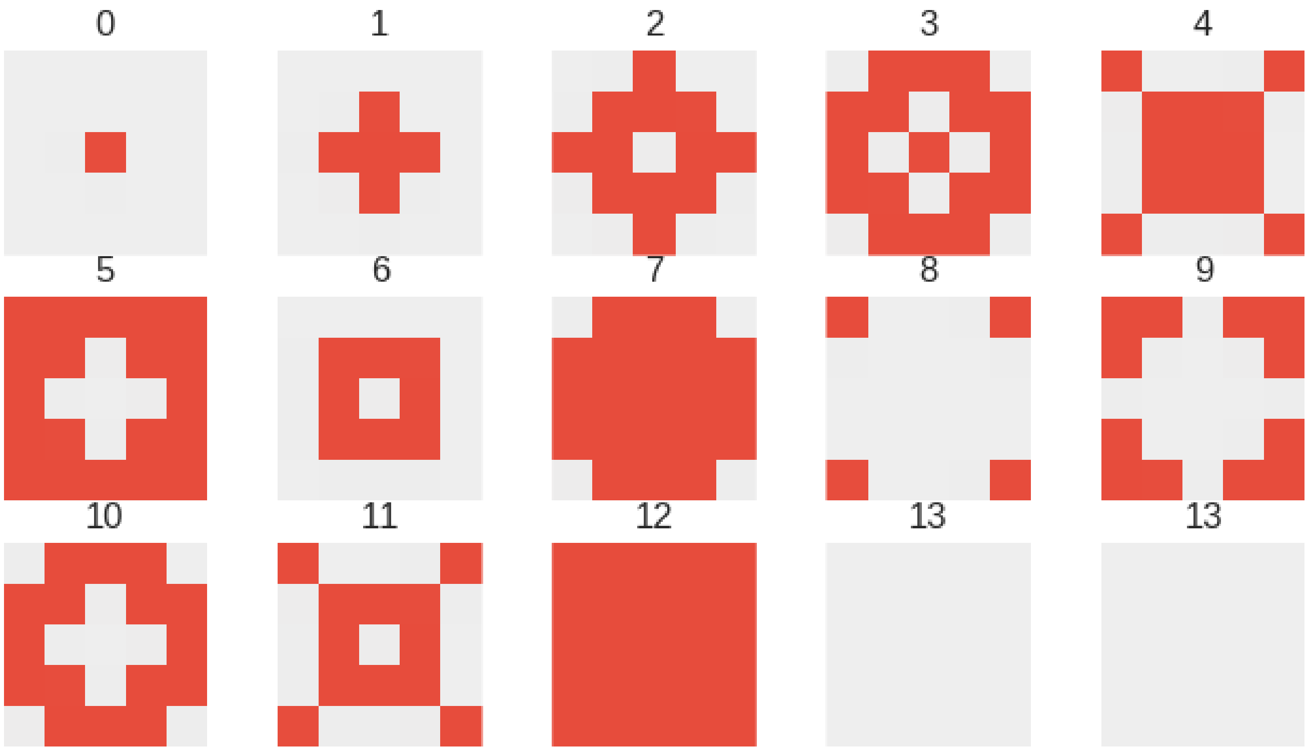

Figure A.7: Another solution, where after visiting the target state the CA eventually annihilates itself completely.

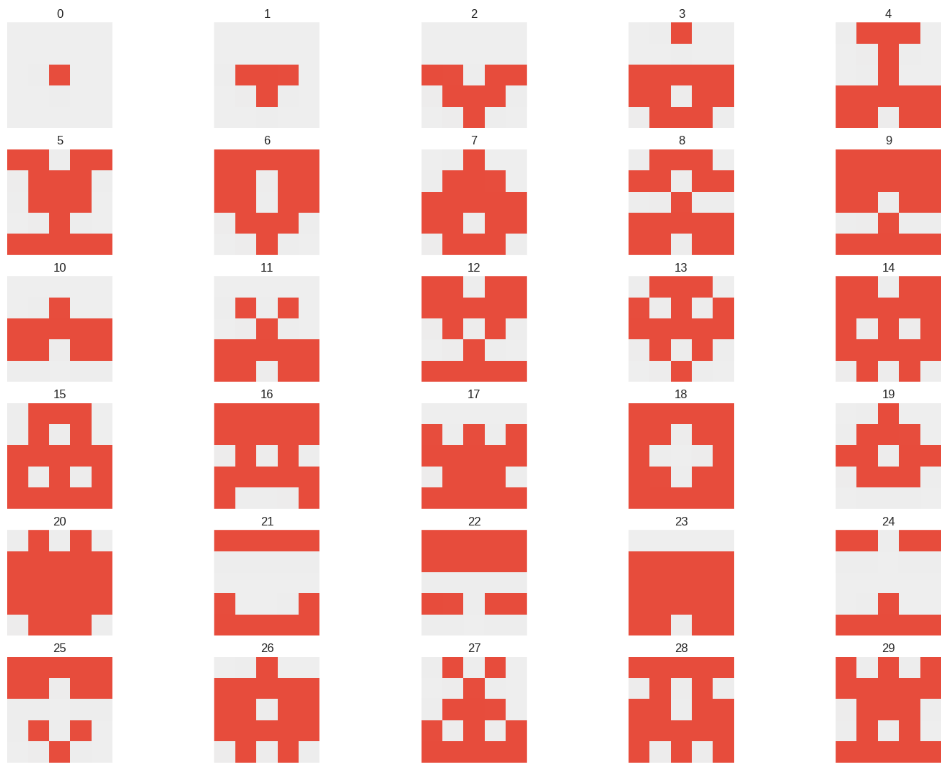

Figure A.8: A solution where the CA develops with one of two possible symmetries, but still finds the solution that has two symmetries.

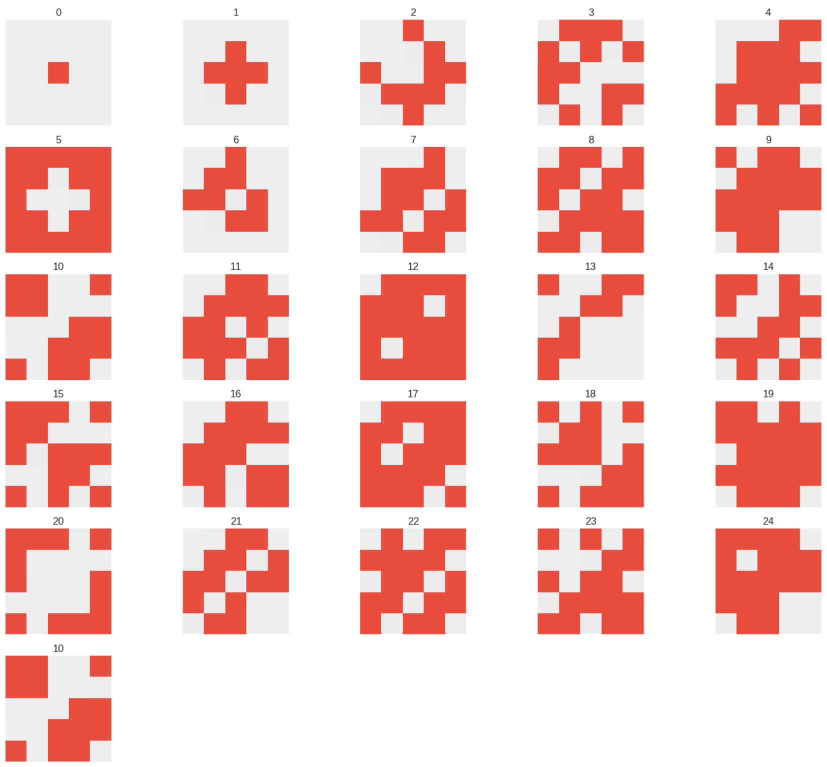

Figure A.9: A solution that quickly finds the target pattern, but then keeps developing and finds a longer cycle that does not include the target pattern.

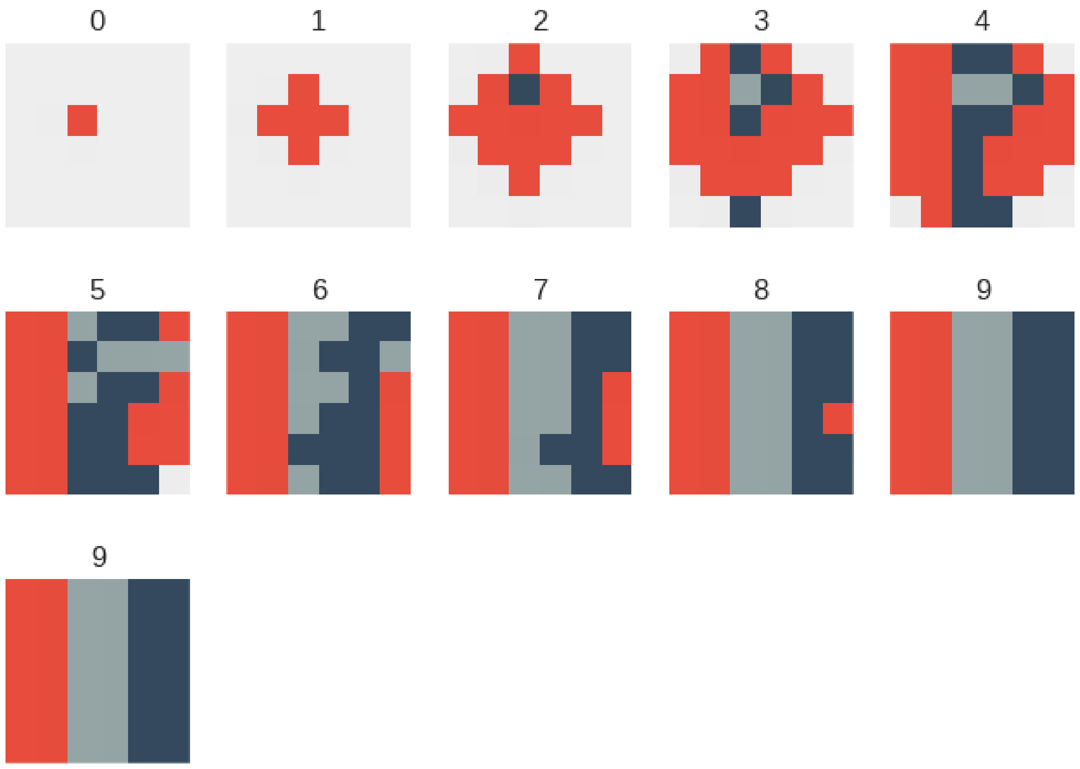

Figure A.10: A solution to the ”Tricolor” morphogenesis that finds a point attractor equal to the target pattern.

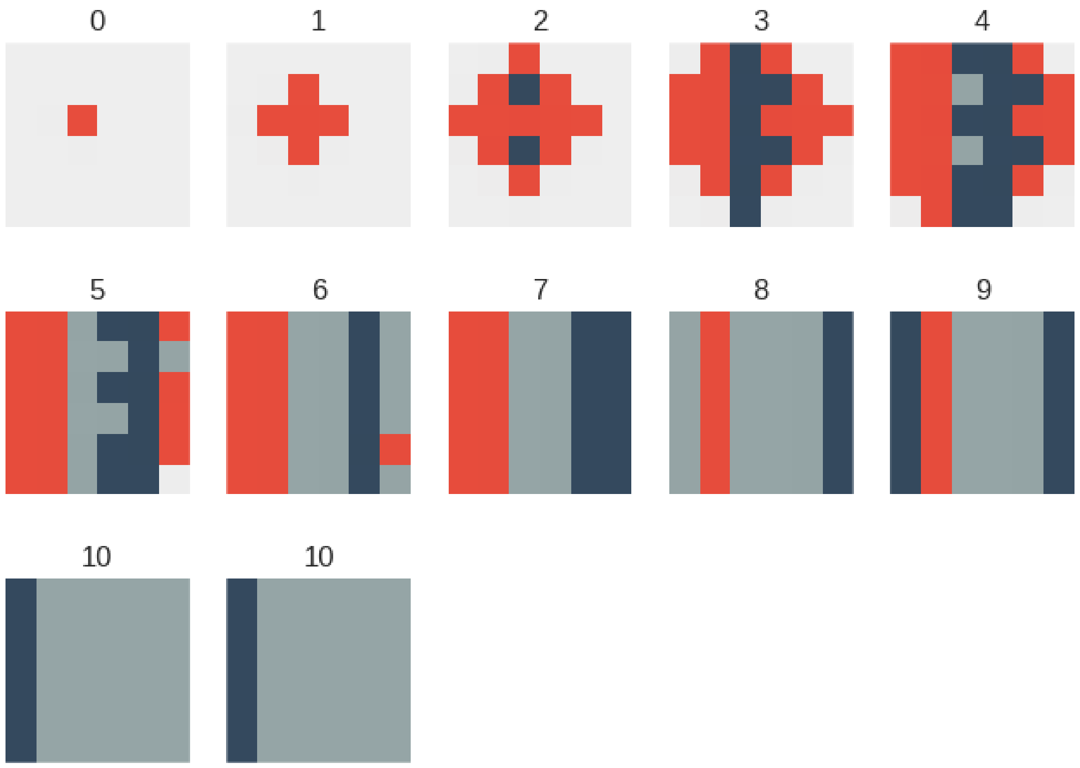

Figure A.11: Another solution which visits the target pattern, but stabilises in a point attractor not equal to the target.

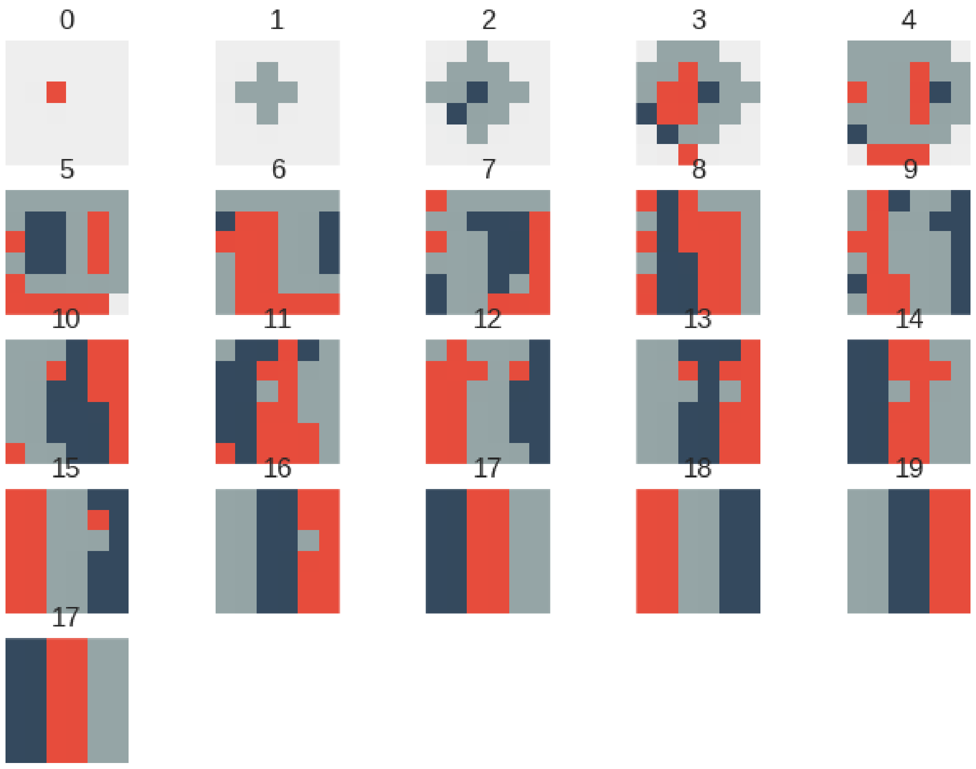

Figure A.12: A solution which stabilises into a ”Tricolor” pattern and then cycles through different permutation of the colours.

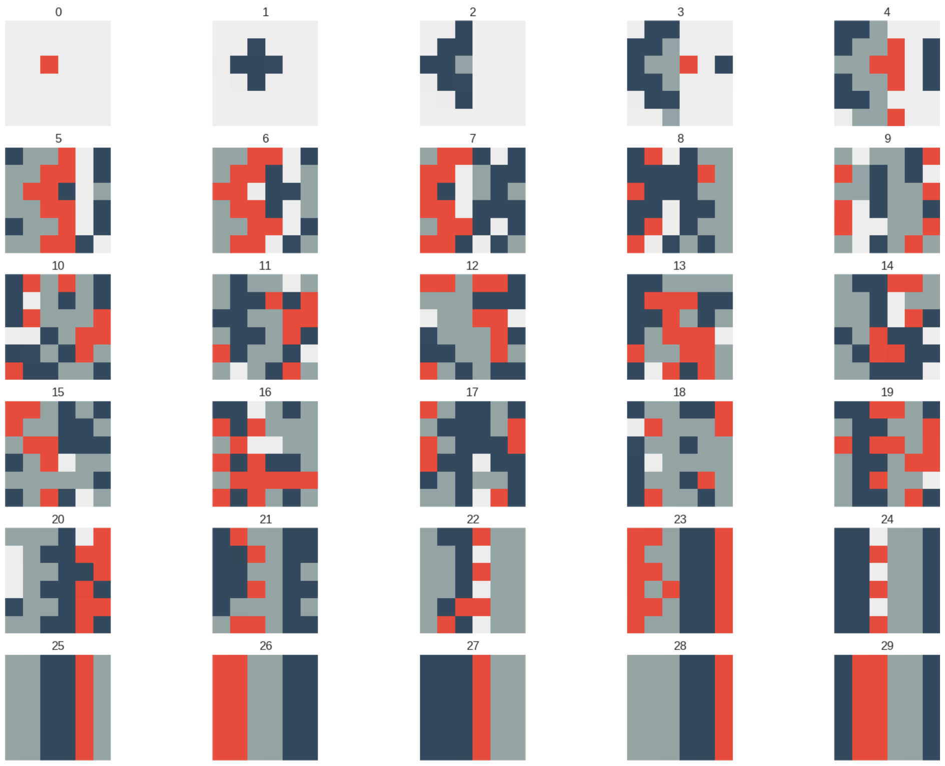

Figure A.13: A solution that looks very chaotic for a very long time, but eventually manages to recover and create patterns with vertical lines.

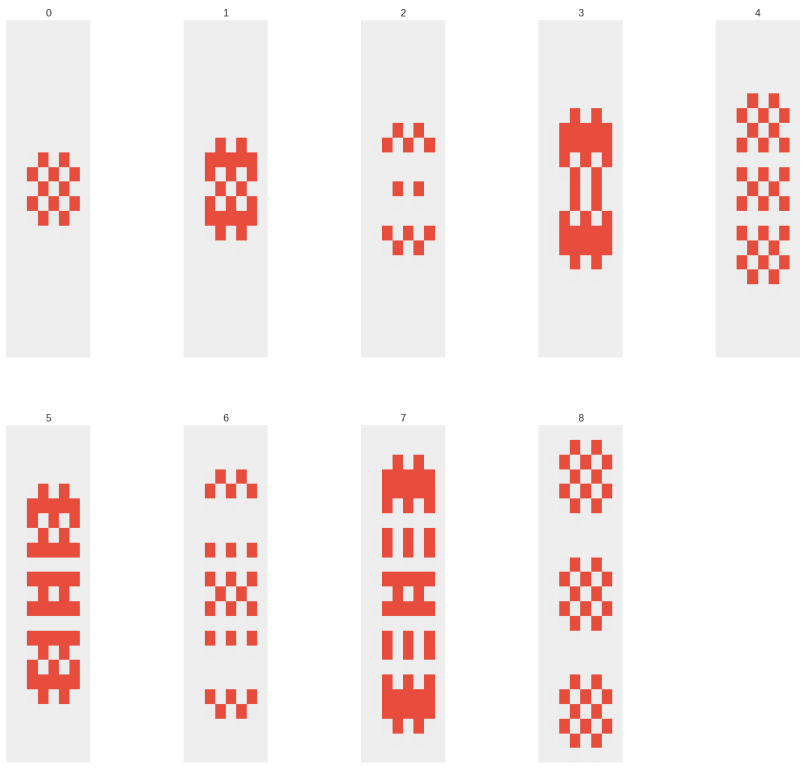

Figure A.14: A solution to the ”Mosaic” replication, where expansion happens only along one axis.

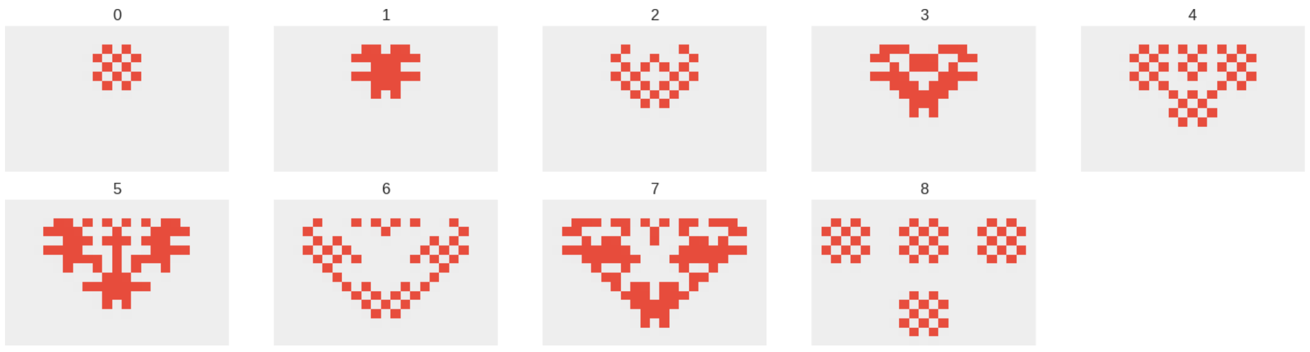

Figure A.15: Another solution, where replication is done in three directions while retaining the original.

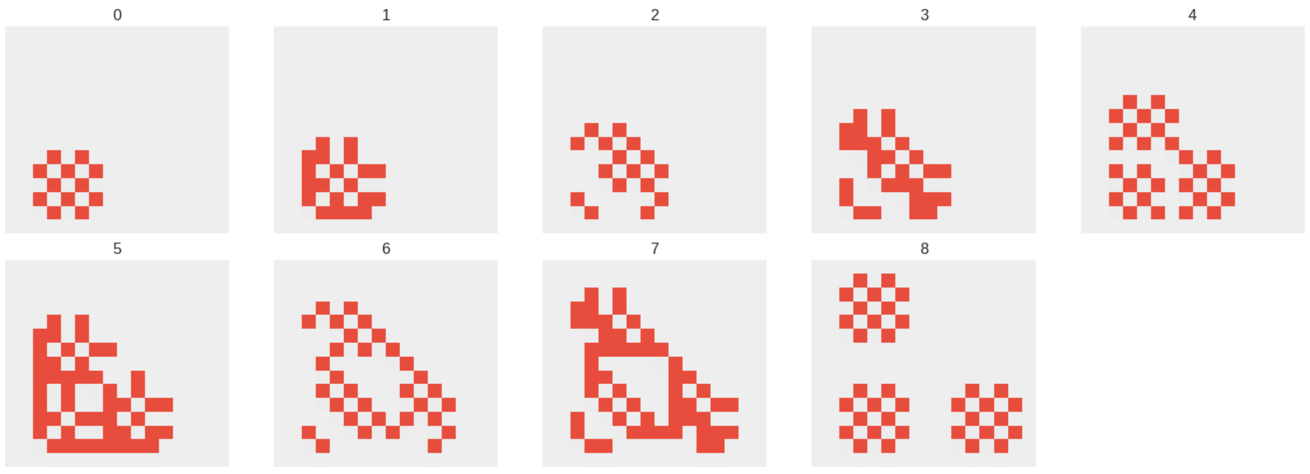

Figure A.16

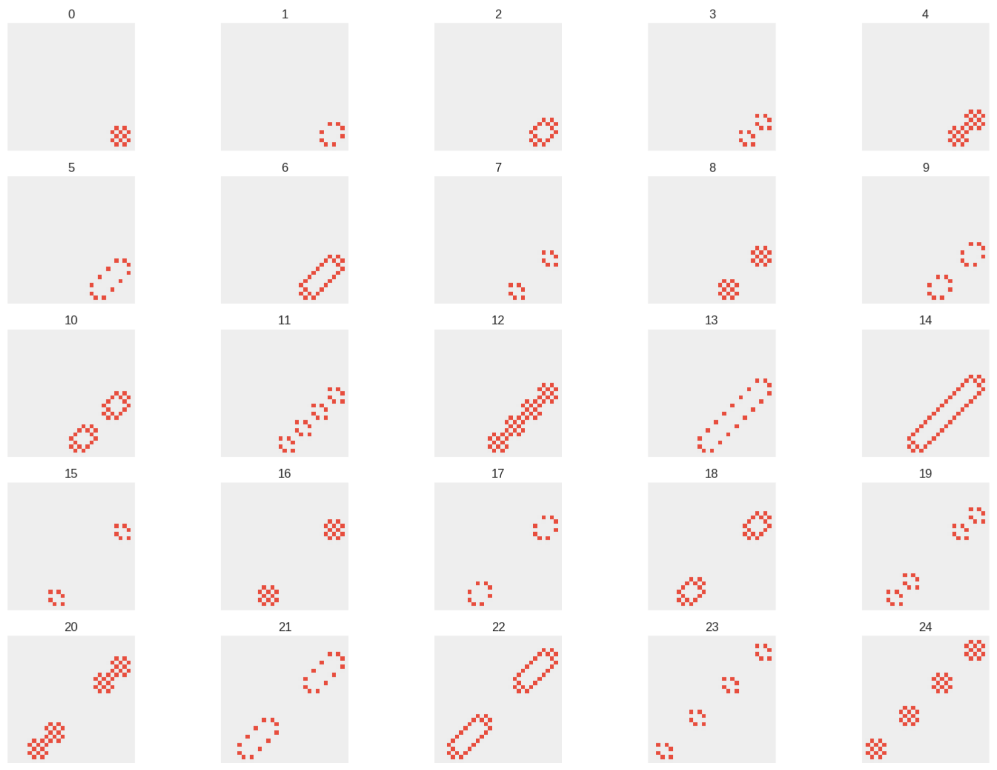

Figure A.17: An example of multiple stages of replication. First the original replicates into two copies. Then each copy tries to replicate, but they interfere with each other and instead return to one copy each, but at a greater distance. Then they each succeed in replicating, producing four copies total.

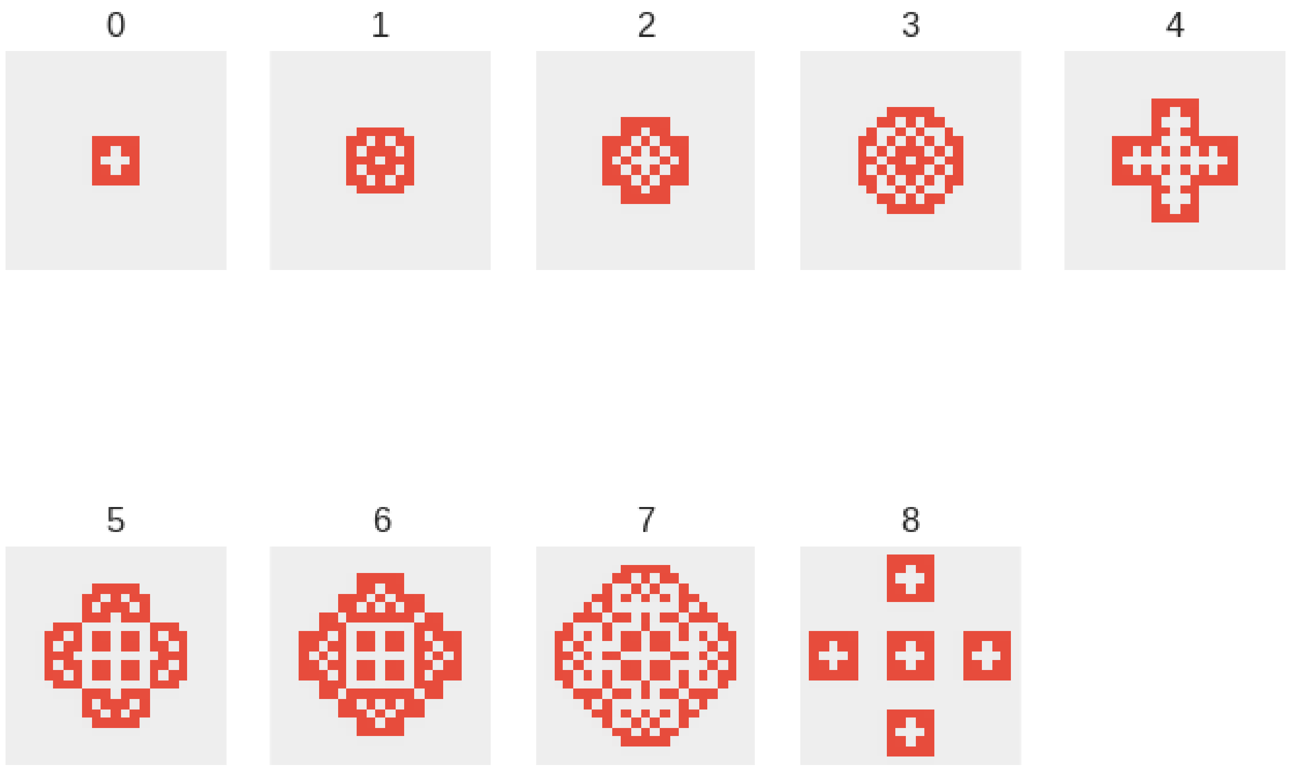

Figure A.18: A solution to the ”Swiss” replication that expands symmetrically along both axes.

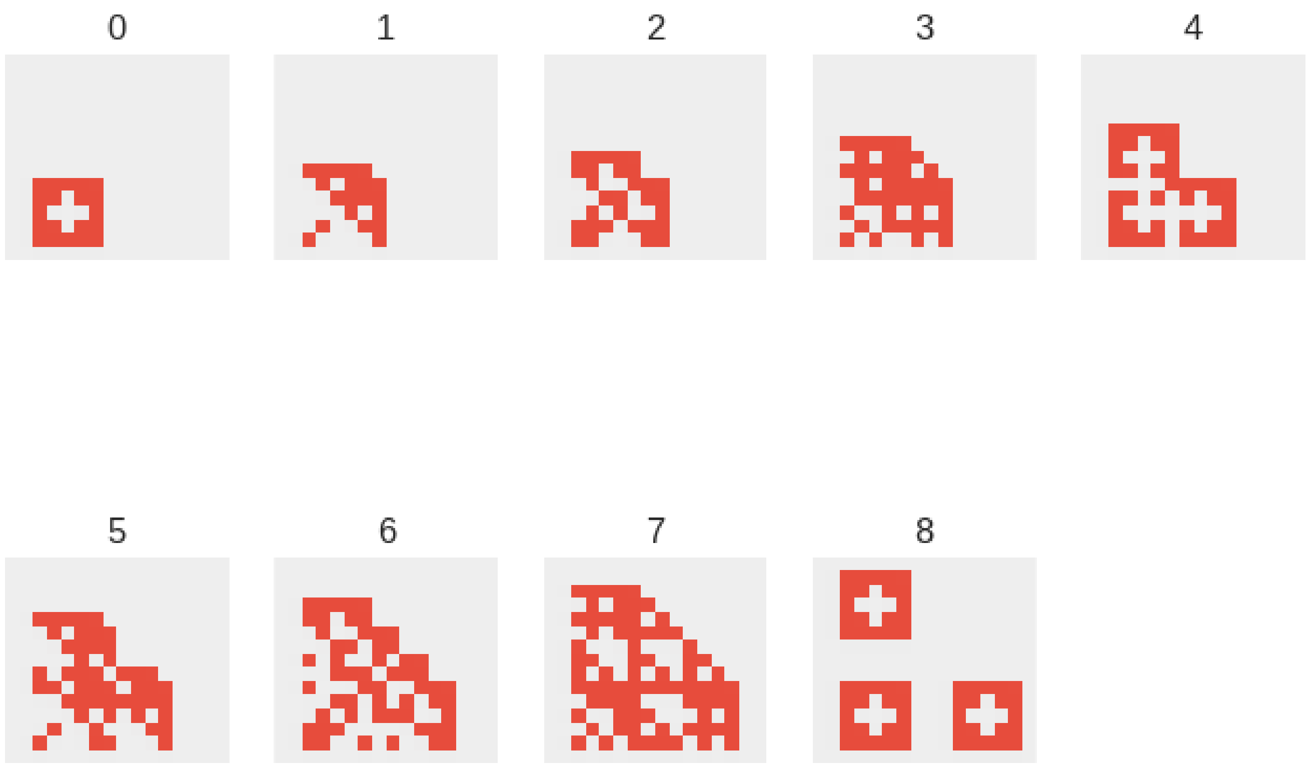

Figure A.19: A solution which expands in two orthogonal directions.

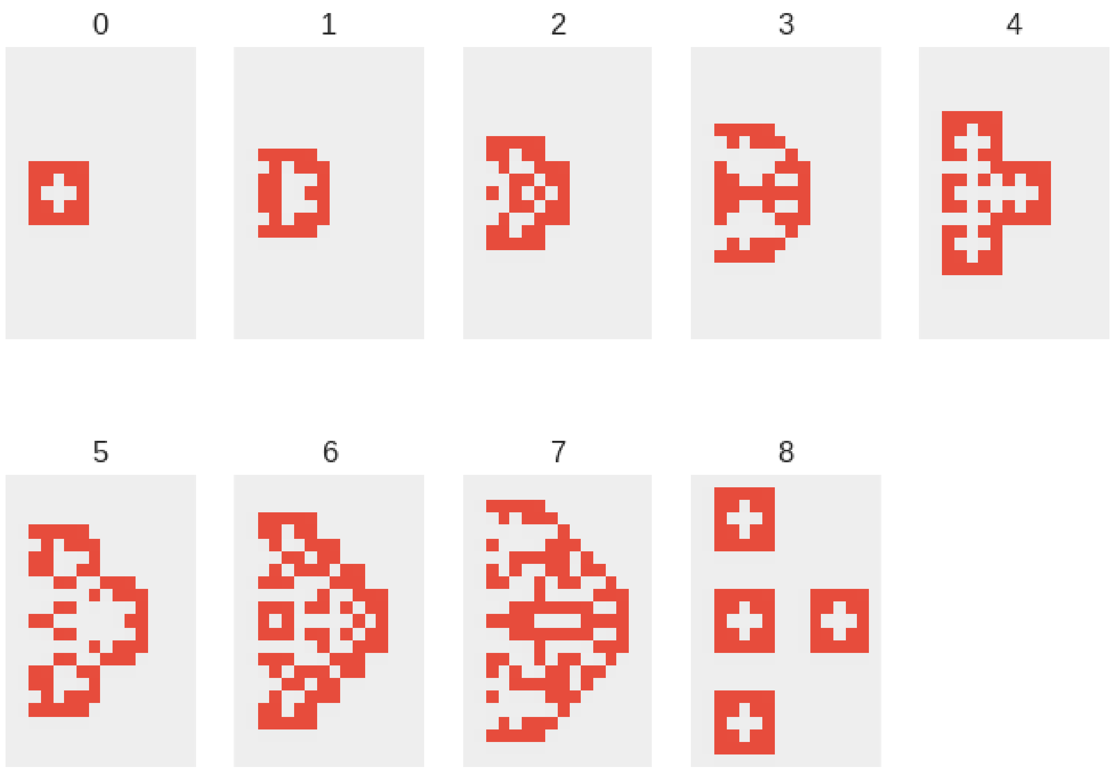

Figure A.20: A solution which is like that of Figure A.18, except the CA ”forgot” one direction.

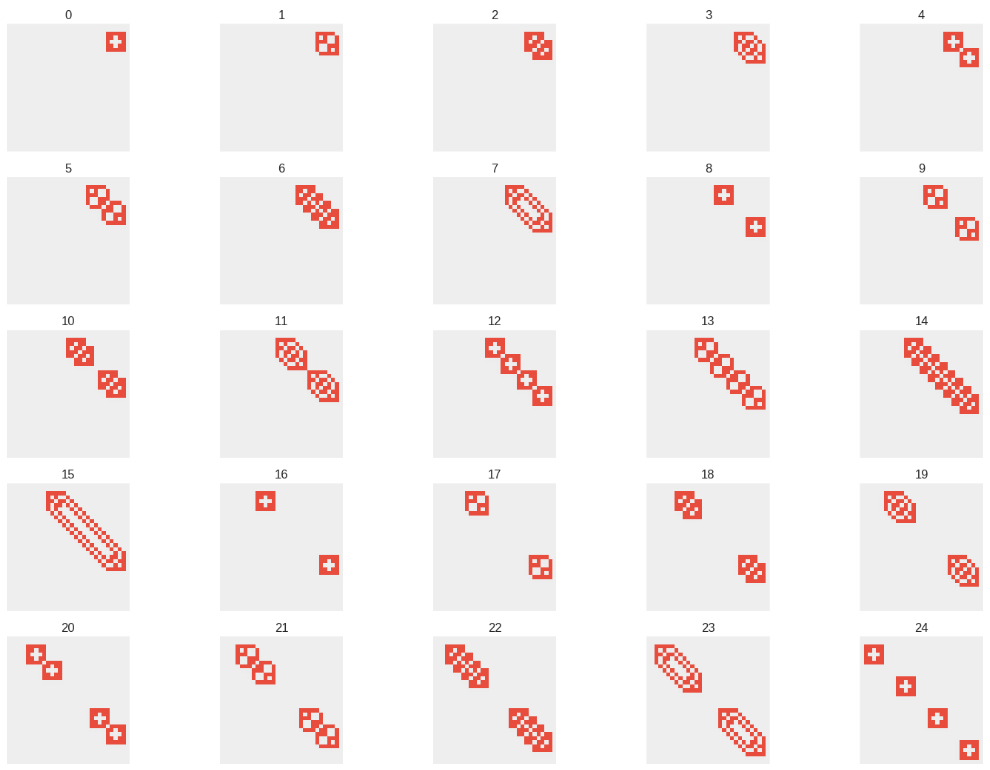

Figure A.21: A solution that has the same behaviour as that of the ”Mosaic” replication in Figure A.17.

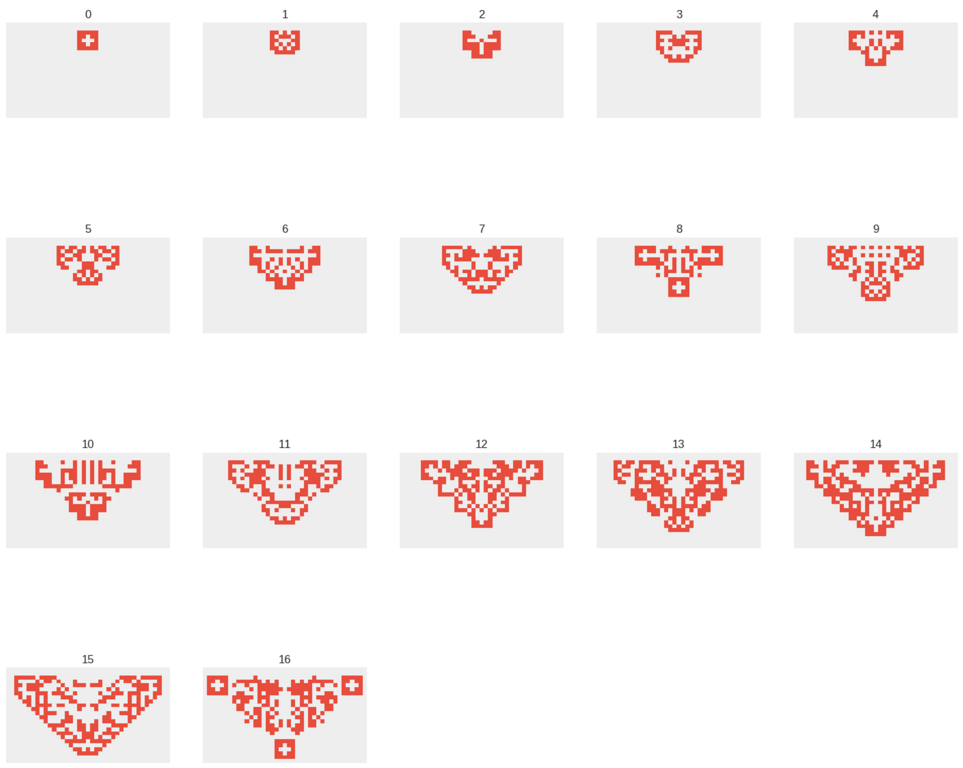

Figure A.22: A solution which illustrates that the fitness function doesn’t care about noisy ”background” patterns as long as it finds at least three perfect replicas.

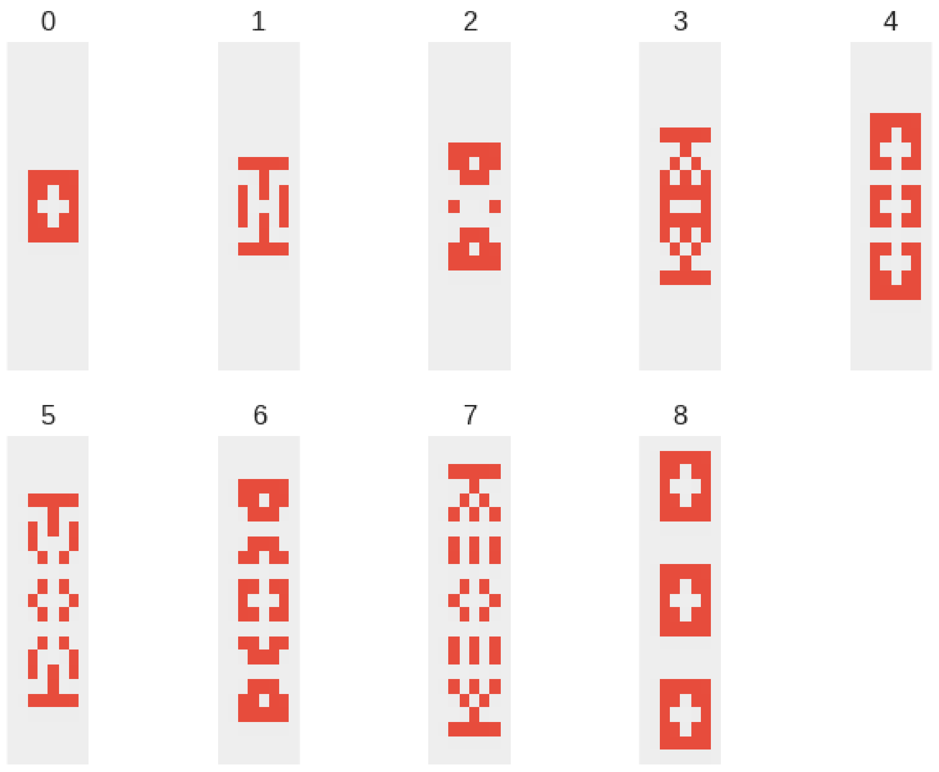

Figure A.23: A solution which expands only along one axis.

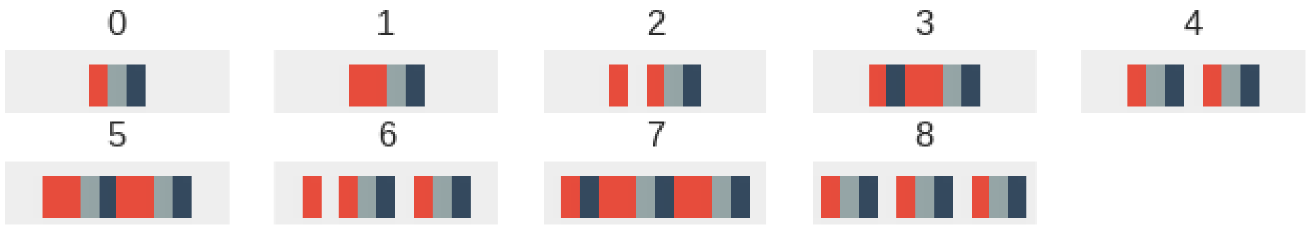

Figure A.24: A solution to the ”Tricolor” replication. All the found solutions expanded only along the horizontal axis.

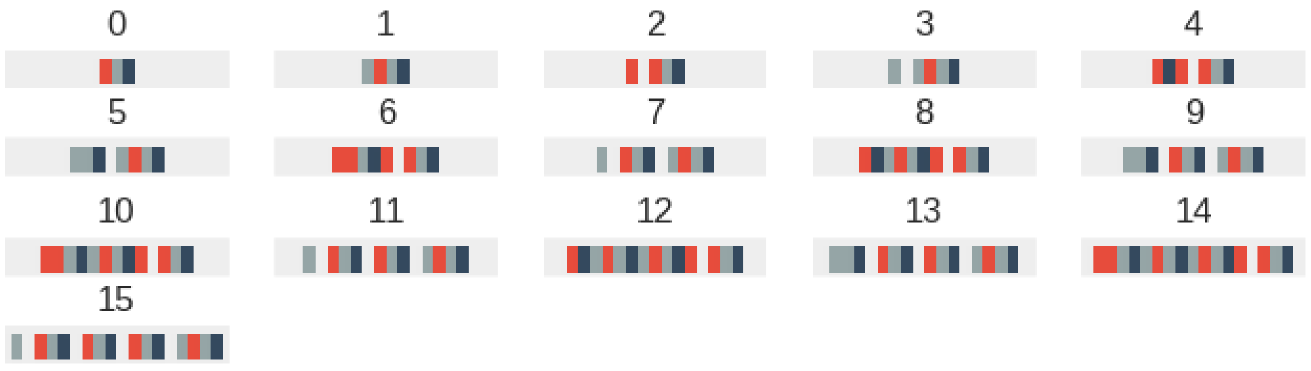

Figure A.25: Another solution to the ”Tricolor” replication.