Morphozoic, Cellular Automata with Nested Neighborhoods as a Metamorphic Representation of...

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Morphozoic, Cellular Automata with Nested Neighborhoods as a Metamorphic Representation of Morphogenesis

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Abstract

A cellular automaton model, Morphozoic, is presented. Morphozoic may be used to investigate the computational power of morphogenetic fields to foster the development of structures and cell differentiation. The term morphogenetic field is used here to describe a generalized abstraction: a cell signals information about its state to its environment and is able to sense and act on signals from nested neighborhood of cells that can represent local to global morphogenetic effects. Neighborhood signals are compacted into aggregated quantities, capping the amount of information exchanged: signals from smaller, more local neighborhoods are thus more finely discriminated, while those from larger, more global neighborhoods are less so. An assembly of cells can thus cooperate to generate spatial and temporal structure. Morphozoic was found to be robust and noise tolerant. Applications of Morphozoic presented here include: (1) Conway's Game of Life, (2) cell regeneration, (3) evolution of a gastrulation-like sequence, (4) neuron pathfinding, and (5) Turing's reaction-diffusion morphogenesis.

Keywords: Morphogenesis, Cellular automata, Moore neighborhoods

Introduction

Morphogenesis is a biological process by which cells move and differentiate into organs and tissues through genetic expression and collaborative, often physical mechanisms. They become different kinds of cells, perhaps as many as 7000 kinds in our bodies (Gordon, 1999). One of the most persistent concepts of morphogenesis is the morphogenetic field (Beloussov, Opitz & Gilbert, 1997; Alberts et al., 2002; Levin, 2011, 2012; Morozova & Shubin, 2012; Vecchi & Hernández, 2014; Beloussov, 2015) with clinical significance for human birth defects (Opitz & Neri, 2013). A morphogenetic field is a region of an embryo that has the potential to develop into a specific structure. How this happens has been subject to much investigation and debate. Some mechanisms are better understood than others. As discussed in (Tyler, 2014), which reviews the full panoply of models of morphogenetic fields, we have added the idea that a morphogenetic field is the trajectory of a two dimensional differentiation wave that triggers a step of differentiation in each cell it traverses (Gordon, 1999; Gordon & Gordon, 2016b, a).

While the mechanisms behind the transformation of an egg into an embryo (embryogenesis) and then to an adult organism have traditionally been of great interest to biologists, as a pattern formation problem it is equally intriguing to computer scientists. Part of the allure involves the spontaneous attainment of order of great complexity from geometrically simple beginnings. Even though one of the founding fathers of computer science (Leavitt, 2006; Hodges, 2014; Tyldum, 2014), Alan Turing proposed a plausible model for understanding one level of the self-organizing aspect of morphogenesis (Turing, 1952; Gordon, 2015), the process of phenotype-building has a "ghost in the machine" (Koestler, 1967), a cybernetic aspect (Gordon & Gordon, 2016a; Gordon & Stone, 2016) that has gone underappreciated.

Recent chemical experiments have revealed that while Turing's original reaction-diffusion equations portray certain aspects of morphogenesis, they do not account for heterogeneity (Tompkins et al., 2014) or the multistep hierarchical differentiation of cells into different types (Gordon, 2015). In this study, we propose that given the right representation, simulated morphogenesis can yield solutions that are biologically plausible. Our approach, *Morphozoic*, models a hierarchical structure of cellular communities. Computationally, these communities are nested versions of Moore-like neighborhoods. A Moore neighborhood is the set of cells that are immediate neighbors to a cell, so in a two-dimensional square array the Moore neighborhoods contain eight cells (Weisstein, 2016b). In Morphozoic, a single higher-level cell houses an entire lower-level Moore neighborhood, down to single cells, and a set of lower-level neighborhoods compose a higher-level neighborhood (Gordon & Rangayyan, 1984a, b). While this serves as a constraint on cell-cell communication, it also serves as top-down information. This top-down information, when coupled with local, bottom-up information at different spatial scales, provides us with a mechanism for strongly emergent phenomena (Holland, 1992).

We originally called such nested neighborhoods "adaptive neighborhoods" in the context of image processing, because around each pixel a Moore neighborhood size was chosen that best fit the local features of the picture (Gordon & Rangayyan, 1984a) (Gordon & Rangayyan, 1984b). The field of adaptive neighborhood image processing now has over 400 publications, and an independent discovery

of the idea has extended the idea in many additional directions (Katkovnik, Egiazarian & Astola, 2006). In the field of cellular automata, adaptive neighborhoods have been used in the sense of changing neighborhood type rather than size (Mofrad et al., 2015). Our approach of nested neighborhoods has been combined with cellular automata for edge detection (Liu et al., 2012) and rule identification (Adamatzky, 1997; Sun, Rosin & Martin, 2011; Zhao, Wei & Billings, 2012). Irregular (Batty, 2003) and "extended" (Guan & Clarke, 2010) Moore neighborhoods have also been used for geographic cellular automata, though not with the nesting idea in mind. Irregular, grown adaptive neighborhoods have been called coalitions in cellular automata (Burguillo, 2013). Morphozoic appears to be unique in using nested neighborhoods, not to find an optimal neighborhood of a cell, but to provide information at many scales to that cell. It thus permits the study of local/global interactions.

Computer modeling of biological systems is widespread (Wyczalkowski et al., 2012; Tanaka, 2015). The Morphozoic approach is based on the Cellular Automaton (CA) architecture which exhibits computational universality (Dobrescu & Purcarea, 2011) (Wolfram, 2001) that is not well understood in the context of biological development. The aim of the Morphozoic project is to build an abstract model of morphogenetic fields to explore its computational capabilities. While the model may lead to some insights into biology, this is not a central goal of the project. Simulations presented here suggest that the model can be used to produce general self-organizing structures. In particular, many aspects of modern human life involve local/global interactions, so Morphozoic may contribute to the social sciences (Batten, 2001). We also show how Morphozoic may be used to reverse engineer a sequence of state changes of a system and derive an approximation to the rules governing that system. Morphozoic may therefore be used for reverse engineering (Gordon & Melvin, 2003; Deutsch, Maini & Dormann, 2007; Elmenreich & Fehervari, 2011; Lobo & Levin, 2015).

Because of its local/global construction, Morphozoic may be a step towards meeting the challenge posed by Russ Abbott:

"...when a glider appears in the Game of Life, it has no effect on the how the system behaves. The agents don't see a glider coming and duck. More significantly we don't know how to build systems so that agents will be able to notice gliders and duck. It would be an extraordinary achievement in artificial intelligence to build a modeling system that could notice emergent phenomena and see how they could be exploited. Yet we as human beings do this all the time" (Abbott, 2006).

The Morphozoic platform can model a wide range of natural and artificial phenomena, but the question remains whether or not the software can exhibit biological realism. Certainly in terms of approximating morphogenesis, it is not clear whether patterns formed and identified by Morphozoic are produced by biologically-realistic mechanisms. However, in the realm of biological realism, Morphozoic is consistent with similar approximations of biological complexity. Particularly at the level of interacting cells, morphogenesis and Morphozoic alike exhibit what Abbott (Abbott, 2006) calls 'epiphenomena'. These epiphenomena, or emergent outcomes of collective interactions between agents, are as biologically realistic at the macro-scale as gene action is at the micro-scale. However, as morphogenesis is non-reductive (Abbott, 2006; Gordon & Gordon, 2016a), it becomes difficult to make exact predictions of behavior in existing biological systems. What makes for an excellent naturalistic pattern replication

mechanism (Wolfram, 1984) might make for a poor descriptor of unfolding processes in the frog embryo.

Biological realism in modeling involves the degree to which selectively adding in features of the system you are attempting to model produces a useful representation. At a macro-level of description, Morphozoic exhibits *a priori* biological realism (Bourgine & Lesne, 2010) that captures the higher-order dynamics of a biological system rather than the lower-level causal mechanisms of complexity (Ruxton & Saravia, 1998). *A priori* realism incorporates known features in a minimal and abstract fashion (Bourgine & Lesne, 2010). In cases where the underlying system has many moving parts and layers of complexity, a high degree of abstraction is required to avoid transcomputational limits (Bremermann, 1967; Ashby, 1968; Gordon, 1970; Bower, 2005). Transcomputational limits are of particular concern in biological systems, where the myriad sources of variation can produce a very high dimensional problem space. While abstraction in the face of transcomputational limits is a supposed requirement for biologically-inspired simulations, nevertheless many models of collective behavior (Resnick, 1994) and evolution (Adami, 1998; Alicea & Gordon, 2014) also utilize highly abstract representation while producing realistic biological system dynamics. This is one reason why Morphozoic can reproduce patterns seen in morphogenesis without invoking mechanisms of gene expression.

Another reason why Morphozoic can exhibit “lifelike” patterns is due to the nature of Cellular Automata. In many cases what drives changes in the dynamics of the model are not lower-level control mechanisms, but the order in which key spatial and temporal events play out. While this is important for real biological systems as well, changes to spatial and temporal order of how events are executed lead to synergistic effects in Cellular Automata dynamics (Ruxton, 1996). Furthermore, the timing of events in a Cellular Automata model impact predictive ability, as Huberman and Glance (Huberman & Glance, 1993) have shown by implementing asynchronous behaviors in the Prisoner's Dilemma game. In Morphozoic, we keep the standard features of cellular automata: discrete time steps, each cell changes state simultaneously with all the others, and no cell moves from its initial position. These three aspects are clearly not biological. Lifting these constraints is a topic for future research. Morphozoic provides a rich starting point.

There are also parallels between biological and sociotechnical systems that demonstrate how adaptive behavior might be as much a consequence of temporal evolution than formal biological mechanisms. Sometimes this temporal evolution is intertwined with structural features of the system, such as when scientists can “unboil” an egg and return proteins to their original conformational state (Bijelic et al., 2015). The origin of evolutionary novelties also relies upon how temporal sequences interact with existing variation to produce innovations. This, evolutionary novelties are generated from what is already available through recombination and repurposing (Jacob, 1977). Assembling what already exists into new combinations is called combinatorial innovation, part of something Wagner and Rosen (Wagner & Rosen, 2014) refer to as innovability. Acting as a mechanism for new phenotypic possibilities, characterizing the innovability of emergent systems like Morphozoic might provide a very broad window into the systems-level mechanisms of developmental processes.

Innovability is a key driver in the functional diversity seen in Morphozoic, and can be analogous to the types of developmental plasticity observed in biological systems (West-Eberhard, 2002). In phenomena ranging from axonogenesis to generalized stress response (Bateson et al., 2004; Gluckman, Hanson & Low, 2011; Low, Gluckman & Hanson, 2012), organisms can exhibit a morphogenetic adaptive response to both local and global signals. In this sense, Morphozoic provides a means to explore how the timing and phenotypic consequences of these processes might unfold (Moczek et al., 2011). While Morphozoic does not possess the same mechanisms that drive biological plasticity, phenotypic changes can be approximated using discrete computation. While Morphozoic may be able to approximate the pattern-formation aspects of developmental plasticity, a concept known as the adjacent possible may be used to bridge the gap between biology and simulation. The adjacent possible was originally proposed by Stuart Kauffman as a way to describe possible new states for a system given historical contingency (Johnson, 2010). The adjacent possible is ever-expanding, and this non-random expansion into possibility space is what drives subsequent innovations (Tria et al., 2014).

Fortunately, the cellular automata representation is well-suited to producing novelties that result from interactivity. Identifying the specific mechanisms for the generation of novelties is a relatively unexplored question (Kier, Bonchev & Buck, 2005). How can we discover these pathways and make parallels with developmental and other biological systems? On the one hand, the adjacent possible can be made salient using a method called fitness optimization. This allows us to understand patterns of innovation that conform to the adjacent possible idea as a series of moves towards a fitness peak (or functional optimum). On the other hand, many biological and technological systems also include significant constraints on their evolution such that the states making up the so-called adjacent possible are limited to relatively small portions of the whole system (Solé et al., 2013). One way to investigate these non-innovable portions of the system is to construct a neutral network (van Nimwegen, Crutchfield & Huynen, 1999) that defines all possible configurations of the system. To approximate the full set of possible states (which may or may not be transcomputational), we may rely upon computational information such as the neutral network, cellular automata rules, and knowledge about the constraints a given system might pose. Applying the concept of the adjacent possible then allows us to limit the range of plausible emergent mechanisms in biological and non-biological settings.

Coupling Morphozoic with other computational and data-driven models of embryogenesis may lead us to a middle-out approach (Noble, 2002). The middle-out approach can be defined as a combination of top-down and bottom-up approaches where specification begins at the level where the data are sufficient. Using inferential and other methods, we can then move towards other levels of analysis. This is ideal for systems that are too interactive for systems or reductionist approaches to be effective on their own (Noble, 2002). The middle-out approach is particularly useful to data-driven research in that it strikes a balance between reductionism and integration. As the reductionists have mechanisms, the systems people have overarching descriptions (Kohl & Noble, 2009). Morphozoic occupies a middle-ground between reductionism and integration in the sense that the states of single cells are influenced by local neighborhoods, but that each local neighborhood is interlinked to form a potentially large (global) problem space. This interlinking occurs at many levels, due to the use of nested neighborhoods.

By occupying this middle ground, defined by neighborhoods, we can approach multiscalar biological processes in novel ways (Walker & Southgate, 2009). Multiscalarity can reach 8 orders of magnitude, as in diatoms, for instance (Ghobara et al., 2016).

One of the inspirations for Morphozoic is the *Morphone* model (Portegys, 2002), a programmable, modular signaling system for morphing complex patterns. One of the ways Morphozoic differs from Morphone is in its leveraging of local vs. global signaling fields as computing mechanisms. Another feature of Morphozoic, typical of computing systems but distinct from biological systems, is the use of cell states as signals to other cells instead of supporting separate signaling objects.

Description

Cellular automaton

Morphozoic is built upon a two-dimensional (2D) cellular automaton (CA) architecture. CAs generally have these properties:

- A cell has a state value (e.g. on or off). However, the value can be a more complex entity, such as a real value or vector.
- A cell senses the states of adjacent cells that makes up its *neighborhood*. One example is a 3x3 Moore neighborhood.
- Action rules determine how a cell state changes based on the states of the cells in its neighborhood.

CAs date back to the 1940s and the work of Stanislaw Ulam, who, requiring a model to study the growth of crystals, developed a simple lattice network (Ulam, 1962). At the same time, John von Neumann, Ulam's colleague, was working on the problem of self-replicating systems (von Neumann & Burks, 1966). Von Neumann's initial design was to have robots build new robots out of a “sea of parts”. This proved problematic, and a more abstract and discrete model was later developed that became a foundation for the CA approach. It was Ulam who suggested using a discrete system for creating a reductionist model of self-replication. Von Neumann’s work in self-replication system is similar to what is probably the most famous cellular automaton: the “Game of Life,” (Gardner, 1970) which is presented as an application of Morphozoic in a later section. We introduced long-range interactions in cellular automata in a simple model of two dimensional “snail” morphogenesis, showing they led to more robust pattern formation (Gordon, 1966). Long-range effects are also incorporated into human evacuation CA models (Kaji & Inohara, 2014).

In 2001, Stephen Wolfram’s book *A New Kind of Science* was published (Wolfram, 2001). The book discusses how CAs are relevant to the study of biology, chemistry, physics, and all branches of science. In addition, CAs are relatively easy to create in software and are straightforward in performance evaluation. For these reasons the CA architecture was chosen as a platform for Morphozoic. As

demonstrated in Wolfram's work, CAs can serve as a model of parallel distributed processing that fit many natural systems well. Some of these properties of the physical world:

- Contain a large number of simple parts, called cells, each of which is an automaton. This means it acts on its own (autonomously).
- Parallel operation.
- Global, emergent effects from local interactions.

Each cell (automaton) can respond to external signals in "deciding" what to do. Those decisions are restricted to certain choices, either finite in number or represented by continuous values. For example, CAs can simulate fluid or gas dynamics by storing individual molecules in the cells and implementing particle interactions by the local rules.

One of the main variations of CAs are in the number of dimensions they contain. A one-dimensional (1D) CA is simply a row of cells. A two-dimensional (2D) CA is a grid of cells. Three-dimensional (3D) CAs operate within a volume of discrete cells. The concept of a *neighborhood* is central to the description of a CA, as the states of a cell's neighborhood define the input to the local state transition rules. In a one-dimensional CA, a cell's neighborhood is usually its adjacent cells. In a 2D CA, typical neighborhood configurations are shown in Figure 1. It is also common, as is done for Morphozoic, to include the center cell in the definition of its neighborhood.

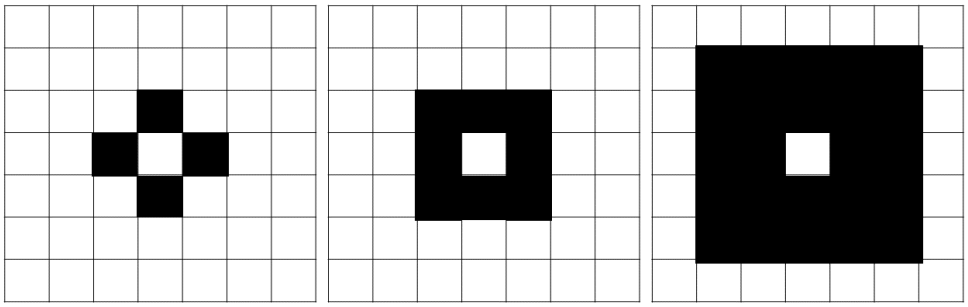

Figure 1– Typical two-dimensional CA neighborhoods. Adapted from Figure 2, Espinola et.al, 2010.

CA cells contain a *state* that can take on values defined by the automaton. For example, a binary state can be considered to be in a 0 (off)/1 (on) state, as shown in Figure 2.

0	0	1	0	1	1
1	0	0	0	1	1
1	0	1	1	1	0
0	0	1	0	1	1
1	1	0	0	1	0
1	1	1	0	0	1
1	0	0	1	1	1
0	0	1	0	1	0

Figure 2 – A 2-dimensional grid of cells, each in a discrete state of "0" or "1". Moore neighborhood of cells shown inside red bounding box. Automaton for Moore neighborhood is denoted with a red circle.

State values change based on transition *rules*. A good way to understand how state transition rules work is to consider a one-dimensional CA with adjacent cell neighborhood, as shown in Figure 3. Using Wolfram's terminology, the eight possible neighborhood state configurations and center cell state transitions can be enumerated. So this rule set is number 30.

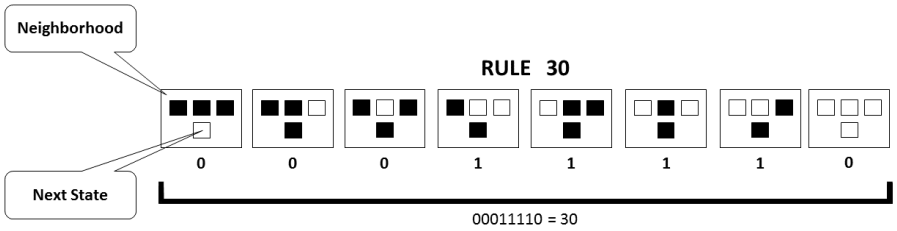

Figure 3 – State transition rule set 30, where 30 base 10 = 00011110 base 2. From (Weisstein, 2016a) with permission per Eric Wolfram's Notice of Copyright http://wolfram.org/copyright.html.

Figure 4 demonstrates how a CA develops over time from a single "on" cell using rule 30. Time advances from top to bottom.

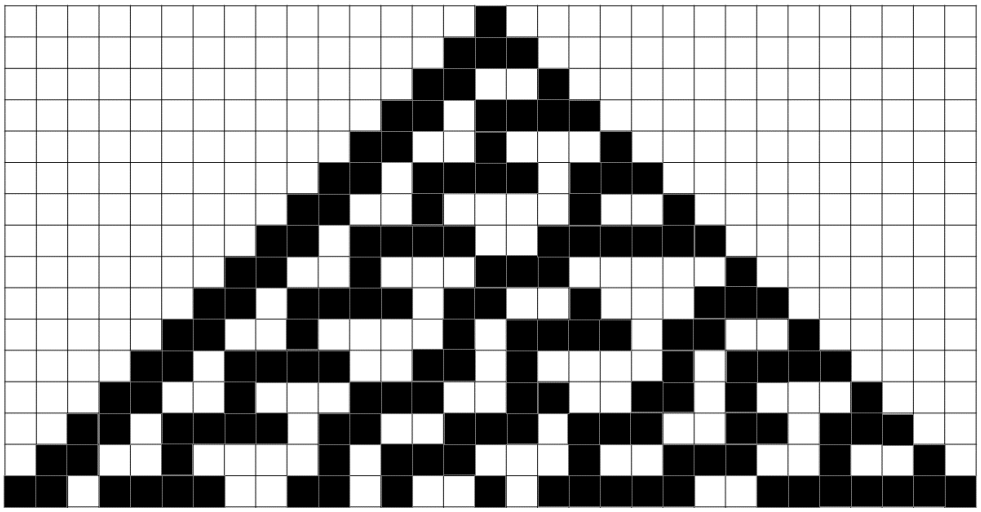

Figure 4 – Application of rule 30. A single cell is turned on (top row) and in the next time step (second row) all of the cells are subjected to rule 30. Two of them change state as a result, leaving three cells turned on in the second row. This process is iterated to generate the third row, etc. Patterns like these are actually generated by the pigment depositing line of cells in marine cone snails (Waddington & Cowe, 1969). The discrete version of such one dimensionally generated patterns became known as Lindenmeyer patterns (de Koster & Lindenmayer, 1987). From (Weisstein, 2016a) with permission per Eric Wolfram's Notice of Copyright http://wolfram.org/copyright.html

There are many other possible rules to compute a cell's state from a group of cells. Consider blurring an image. A pixel's new state (i.e., its color) is the average of all of its neighbors' colors. Most image processing algorithms can be formulated as CAs. The rules define the functionality of the CA.

Variations of CAs

The following are some variations of the CA model:

1. **Non-rectangular grids**. There is no essential reason why a CA must be confined to a rectangular grid or space.

2. **Probabilistic**. The rules of a CA need not necessarily work in a deterministic fashion (Gordon, 1966, 1980). An example is the Stochastic Game of Life (Monetti & Albano, 1997).

3. **Continuous**. The state of a cell can be something other than a discrete value, such as 0 or 1. For example, the values could range between 0 and 1. Of course the rules must then reflect how to calculate these continuous state values. Examples in materials science, traffic flow and earthquake analysis abound (Olami, Feder & Christensen, 1992; Bubak & Czerwiński, 1999; Kitakawa, 2004, 2005; Gosálvez et al., 2009; Ferrando et al., 2011; Ferrando, Gosálvez & Colóm, 2012; Li et al., 2015).

4. **Historical**. In the Game of Life CA, the current state configuration determines the next configuration. However, taking into account historical states is also possible. For example, Portegys and Wiles (Portegys & Wiles, 2004) describe a CA that self-repairs in the presence of noise by use of historical cell states.

5. **Moving cells**. In these examples, cells have a fixed position on a grid, but can move to other grid points (or, equivalently, their states can be transferred to other cells or switched with them) (Gordon et al., 1972, 1975; Chopard, 1990; Fukui & Ishibashi, 1996; Hochberger, Hoffmann & Waldschmidt, 1999; Halbach & Hoffmann, 2005; Moussa, 2005).

6. **Nesting**. Another feature of complex systems is that they can be nested into hierarchies. For example, a city is a complex system of people, a person is a complex system of organs, an organ is a complex system of cells, etc. Cell values that reflect this hierarchical arrangement are possible (Weimar, 2001; Dunn & Majer, 2007; Kiester & Sahr, 2008; Dunn, 2010).

From a more speculative viewpoint (Ilachinski, 2001), researchers have raised the question of whether the universe is a cellular automaton. For example, mathematical models have shown the emergence of "particles" within CAs, such as the gliders in the Game of Life. This leads to conjectures that the natural world, which is well described by physics with particle-like objects, could actually be a CA. This hypothesis has led scholars to a perspective of nature existing within a discrete framework. Edward Fredkin (Fredkin, 1992), a strong proponent, has proposed the "finite nature hypothesis", i.e., the idea that "ultimately every quantity of physics, including space and time, will turn out to be discrete and finite."

Objectives

A main objective is to devise an abstraction that models morphogenesis in a CA using a nested neighborhood approach. As a type of multilayered scheme (Bandini & Mauri, 1999; Dascalu et al., 2011), nested neighborhoods, defined more formally below, are simply neighborhoods contained within neighborhoods, much like Russian matryoshka dolls. Nested neighborhoods provide a straightforward representation of a morphogenetic field that contains a hierarchy of local vs. global information. Information about a more local cell neighborhood having fewer cells is more precise and finer grained than information about a larger, more global neighborhood.

The scheme must be computationally plausible. Neighborhoods of increasing size contain increasing numbers of cells. In order to constrain the potential information explosion, a specific number of bits are used to represent each neighborhood, regardless of its size. The smallest neighborhood is represented precisely; larger neighborhoods are increasingly "fuzzy" because they cannot be completely represented by the available bits. This forms a precision gradient that decreases as the neighborhood grows in size. An intended result of this plan is that more distant cells are sensed in aggregation, as described in the next section.

Additional objectives:

- Compact state change rules.
- Noise tolerant.
- Generalizable from exemplars.
- Evolvable.

Morphogenetic field specification

The morphogenetic field is specified in a CA by equipping cells with these properties:

- A cell state is its *type*.
- A cell emits, senses, and reacts to signals.
- Signals carry information about the types of neighborhood cells.
- A field is the confluence of signals sensed by each cell.

Rules are embodied in *metamorphs*, which encapsulate pattern-matching *morphogens* and cell state change actions.

Morphogen

A "morphogen" abstracts many types of morphogenesis mechanisms: chemical (the classical definition), physical, energy, etc. It also summarizes a morphogenetic field as a set of a cell's nested neighborhoods and their contents. This is shown in Figure 5. A neighborhood consists of an *NxN* set of *sectors* surrounding a lower level neighborhood:

$neighborhood_i = NxN(neighborhood_{i-1})$

where *N* is a fixed odd positive number chosen by the user of Morphozoic, and $neighborhood_0$ is composed of *NxN* elementary cell sectors.

Hence the number of cells in $neighborhood_i = N^i x N^i = N^{2i}$.

A morphogen is composed of a set of nested neighborhoods:

$morphogen(cell) = \{ neighborhood_0(cell), neighborhood_1(neighborhood_0), ... neighborhood_n(neighborhood_{n-1}) \}$

The *value* of a sector is a vector representing a histogram of the cell type densities contained within it:

value(sector) = [density(cell-type$_0$), density(cell-type$_1$), … density(cell-type$_n$)]

The number of cells contributing to the density histogram of a sector of *neighborhood$_i$* = $N^{i-1} x N^{i-1}$

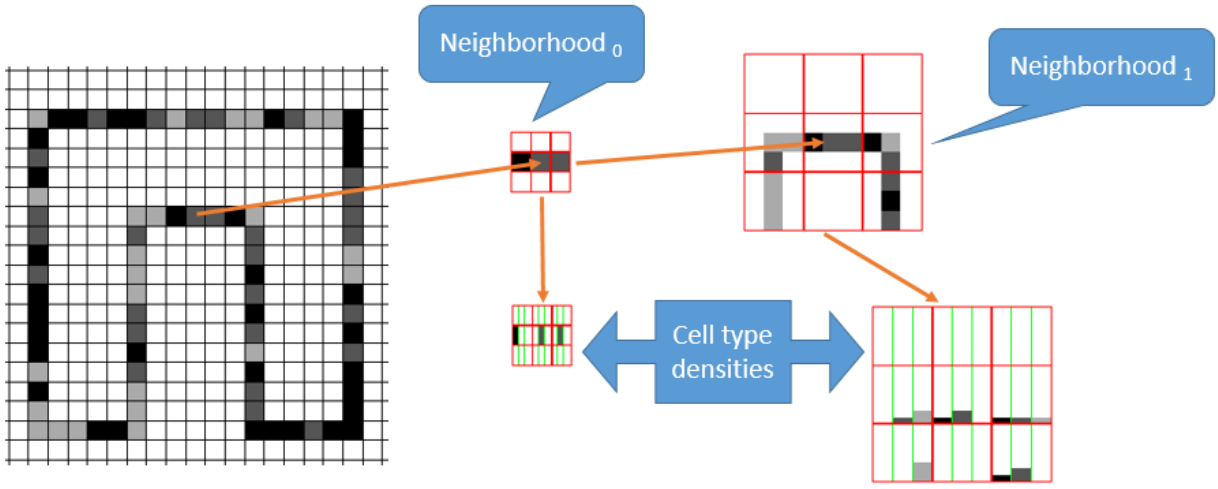

Figure 5 – Morphogen nested neighborhoods.

Metamorph

A *metamorph* represents a cellular automaton morphogen→action agent, defined as a mapping from a morphogen to a cell type.

Generation

A set of metamorphs describing a pattern of cell activity can be generated from manual input or a programmed sequence of cellular automaton transitions. For example, the Game of Life application uses the programmed Game of Life rules to process the cell states. As the CA changes, the neighborhoods for each cell are used to construct morphogens, and the cell type transitions associated with the morphogens are actions. The morphogens and actions are composed into metamorphs.

Execution

Once generated, the metamorphs can be independently used to "execute" the application. Metamorph execution consists of creating a morphogen for each cell in the grid and comparing each of these morphogens to the stored set of morphogens contained in the generated metamorphs, where the distance between them is given by:

$$distance(metamorph_i, metamorph_j) =$$

$$\sum_{x}^{neighborhoods} \sum_{y}^{sectors} \sum_{z}^{cell\ types} abs(cell\ type\ density_{i,x,y,z} - cell\ type\ density_{j,x,y,z})$$

The metamorph having the least morphogen distance is chosen as the cell action.

A unique feature afforded by the use of a distance metric to match morphogens is a noise-tolerant, self-healing capability. Metamorphs act on cells according to neighborhood similarity, which steers cell states toward patterns stored in the metamorphs. This feature is a hallmark of biological systems, and is quite distinct from typical rigid CA rule formulations, such as the Game of Life (see applications), where a minor introduction of noise often results in global disruptions.

Artificial neural network implementation

A compact, fast, and noise tolerant representation of metamorphs can be implemented by an artificial neural network (ANN), a biologically-based learning machine that is particularly adept at classifying input patterns into output categories (Haykin, 2011).

ANN background

ANNs are loosely modeled after the neuronal structure of biological nervous systems but on smaller scales. A large ANN might have thousands of processor units and interconnections, whereas a human brain, for example, can have 86 billion neurons. An African elephant brain contains 267 billion neurons (Wikipedia, 2016b), and human cerebral cortex contains 150 trillion synaptic interconnections (Drachman, 2005). ANN architectures often functionally diverge from their biological counterparts in important ways, including how learning is implemented.

An ANN is a subset of a general computing model known as connectionism. A connectionistic model features an interconnected network of simple units that produce emergent properties that are beyond the capabilities of the individual units (Medler, 1998). In the emergent respect, that the proverbial whole is greater than the sum of its parts, an ANN is similar to a cellular automaton.

A prevalent type of ANN is the multilayer perceptron (MLP). MLPs are organized in layers, shown in Figure 6. Layers are made up of a number of interconnected neurons. Patterns are presented to the network via the input layer, which connects to one or more hidden layers where the actual processing is done via a system of weights associated with the connections. The hidden layers then connect to an output layer where the output is represented by the activation of one or more neurons.

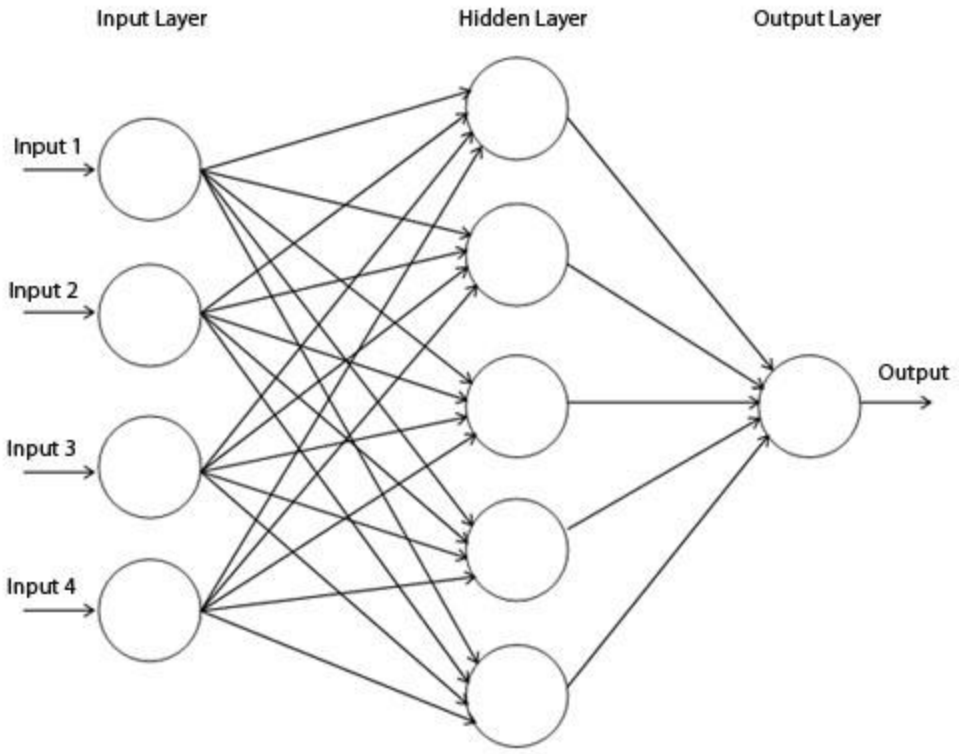

Figure 6 – Multilayer perceptron. From (Cazala, 2015) with permission of Juan Cazala.

A *weight* value is associated with each connection in the network. The weights are multiplied by the outputs of the source neurons, the sum of which is input to an *activation function*, which computes a neuron's output.

Activation functions are typically sigmoid shaped, such as the *logistic* function shown in Figure 7. Here the output switches smoothly from 0 (off) to 1 (on) over an interval controlled by the β parameter. An important property of an activation function is that is it differentiable, which allows a network to be trained through learning.

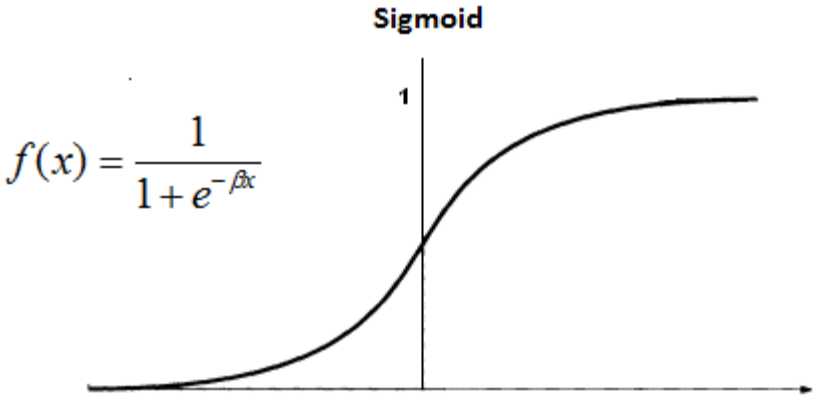

Figure 7 – Logistic activation function. From (Sayed, 2016) with kind permission of Saed Sayed.

Learning is the process of modifying the connection weights to produce outputs that differ least from "correct" outputs, i.e. minimized error. When the correct outputs are known, this type of learning is called *supervised learning*. Learning typically entails *backpropagating* the output error from the output to input neurons to modify the weights of the connections such that the error is reduced in subsequent computations. The most common modification algorithm for this is the *delta rule*.

Training is a process that involves repetitive runs of input-output patterns through the network with an application of the learning rule performed for each pattern. A run through an entire training set is called an *epoch*. ANNs, like their biological counterparts, are known for their ability to produce correct outputs given noisy or similar inputs. After training, a separate test set of patterns with input variations can be evaluated to assess the effectiveness of training.

There are a number of ANN variations. For example, the activation function can be a Gaussian function instead of a sigmoid one. ANNs with many layers are also possible. In general these are known as *deep learning* networks. In a *convolutional* network, an input layer neuron feeds only a subset of neurons in the next layer. This resembles the architecture of the human retina. An important ANN variation, capable of learning input-output sequences such as those found in speech patterns, are called *recurrent* ANNs.

Implementation

By squashing the morphogen sector values into an input vector and considering the cell types as a set of outputs, an ANN can be trained to learn a set of metamorphs such that a morphogen derived from a cell in a CA will map to the metamorph closest matching it. This is shown in Figure 8.

The advantages of using an ANN are threefold:

1. Speed: Instead of searching a set of metamorphs during execution for the closest morphogen, an ANN performs a cascading set of arithmetic calculations to arrive at an output.
2. Compact representation: An ANN is capable of retaining a large number of input-output mappings in the form of interconnection weights.
3. Generalization capability: An ANN is capable of classifying inputs that are similar to training inputs. This capability will be exploited in subsequent applications.

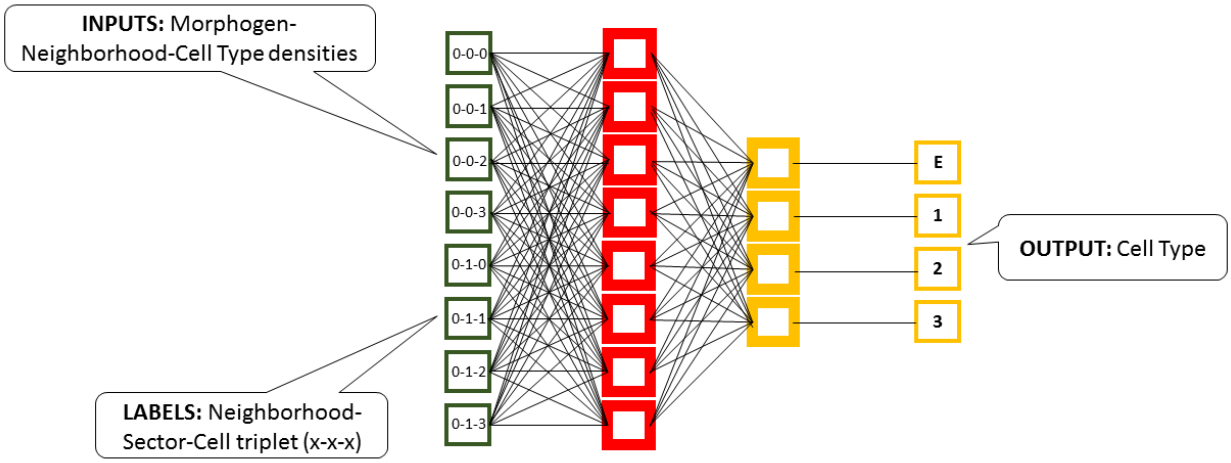

Figure 8 – Neural network implementation.

Results

Various features of Morphozoic are illustrated by the following applications.

Conway's Game of Life

This well-known CA (Gardner, 1970) was chosen as a baseline capability test for Morphozoic. In the Game of Life (GoL), cells are in a rectangular array on a "game board". Each cell is either in an "alive" or "dead" state. The state change rules are as follows:

1. Any live cell with fewer than two live neighbors dies, as if caused by under-population.
2. Any live cell with two or three live neighbors lives on to the next generation.
3. Any live cell with more than three live neighbors dies, as if by overcrowding.
4. Any dead cell with exactly three live neighbors becomes a live cell, as if by reproduction.

A GoL "game" starts with an initial configuration of alive and dead cells. The rules are then applied to the cells at each time step. Usually, if the initial configuration is random, the pattern of live and dead cells appears to change chaotically for a while, then resolves itself into isolated clusters of cells that cycle through a repeating series of states.

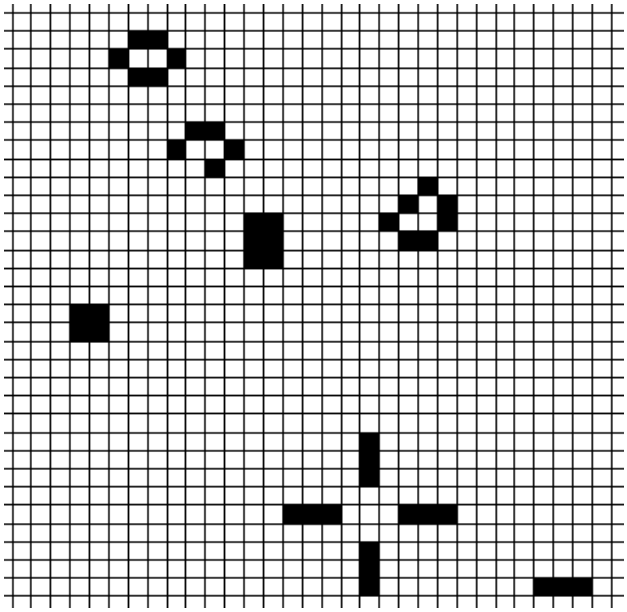

Figure 9 – A Game of Life configuration.

A sample GoL configuration is shown in Figure 9. Despite its simple rules, the GoL produces many dynamic self-sustaining patterns (and is capable of producing an unlimited number of such patterns). One class of pattern, called “gliders”, move across the game board as they go through their state changes and interact in various ways with other clusters when collisions occur (Rendell, 2002). More complex configurations called “guns” are a special type of self-sustaining pattern that produce gliders at a specific rate. Using gadgets such as these it has been shown that a single-tape Turing machine can be simulated by GoL (Rendell, 2002). In complexity theory, a set of rules that manipulates the state of a system is described as Turing complete if it can simulate any single-tape Turing Machine. To demonstrate the Turing completeness of another computational system all one needs to do is show that it is capable of simulating an existing Turing complete system.

Examples of Turing complete systems include most commonly used programming languages, which span paradigms such as procedural (C), functional (Haskell), and object-oriented (Java). A language’s Turing completeness is determined by whether it has the ability to branch conditionally and load/store an arbitrary number of variables. These two features, inherent to general purpose languages, can be implemented in other paradigms using analogous structures such as using recursion in Haskell to implement repetition. Turing completeness research has resulted in the discovery of more and more simple systems that hold these properties. In fact, GoL is not the only cellular automata that has been proven to be Turing complete nor is it the simplest.

The elementary cellular automaton Rule 110, whose state transition rules are stated in Table 1, has also been shown to be Turing complete (Cook, 2004). Unlike GoL, Rule 110 functions in only one dimension, each cell’s next state results only from the current states of its two neighbors.

$B_0\,B_1\,B_2$	111	110	101	100	011	010	001	000
B_1'	0	1	1	0	1	1	1	0

Table 1. State transition from B_1 to B_1' given all possible starting states.

While proving that simple cellular automatons such as GoL and Rule 110 are Turing complete does not allow us to compute in novel or more efficient ways, it does allow us to demonstrate the Turing completeness of other systems such as Morphozoic. Proving that Morphozoic is Turing complete is significant because "Turing completeness" means that it is a universal computer. Given enough memory, Morphozoic would be able to perform any computation that any other Turing complete system is capable of. This says nothing about how efficiently the computation will be done; it only says that the computation *can* be done.

For Morphozoic, we "reverse engineer" a complete set of GoL rules, consisting of 512 3x3 Moore neighborhood configurations. Generating a metamorph for each rule, the configurations were correctly processed, both in the lookup and ANN implementations. Therefore, it follows that Morphozoic is also Turing complete. From the perspective of modeling complex systems like embryos, this means that Morphozoic is capable of modeling anything that can be computationally modeled.

Cell regeneration

The Morphozoic algorithm is capable of modeling cell regeneration. In order to demonstrate this, an apparatus was devised that also highlights the functionality of nested neighborhoods. Figures 10 and 11 show the apparatus. The automaton is trained to regenerate either the horizontal bar on the right side of Figure 10 or the vertical bar on the right side of Figure 11 beginning with the central block configurations on the left side of the figures, respectively. The shaded borders are the distinguishing features that determine regeneration direction: vertically shaded borders train for a horizontal bar and horizontally shaded borders train for a vertical bar.

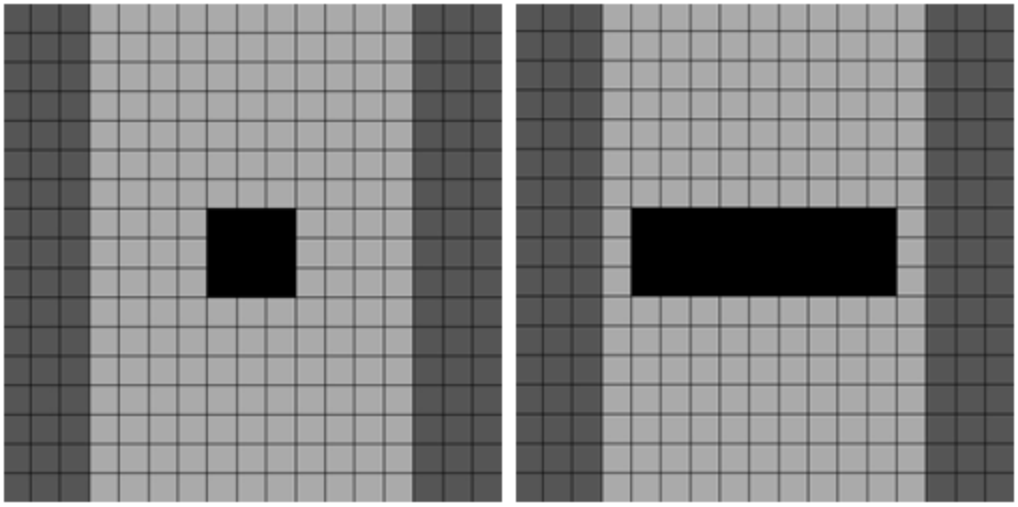

Figure 10 - Horizontal bar. Left: begin. Right: goal.

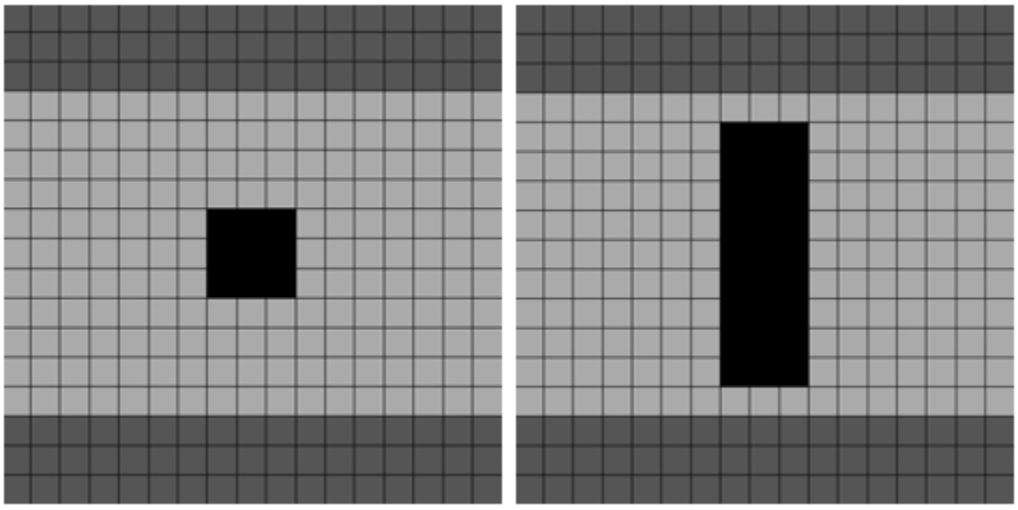

Figure 11 - Vertical bar. Left: begin. Right: goal.

To spotlight the results, only cells in the central 9x9 area in are allowed to create metamorphs during training, and thus cells only in this area are allowed to regenerate by modifying their type values. Two settings of the neighborhood dimension and number of neighborhoods were defined. The *unnested* setting was a single 9x9 neighborhood. The *nested* setting was three nested 3x3 neighborhoods. The unnested and nested automata thus equally contained 81 variable values. However, the nested automaton neighborhoods span an area of 27 cells while the unnested automaton spans only 9 cells. The nested automaton affords the extended range by aggregating cell values.

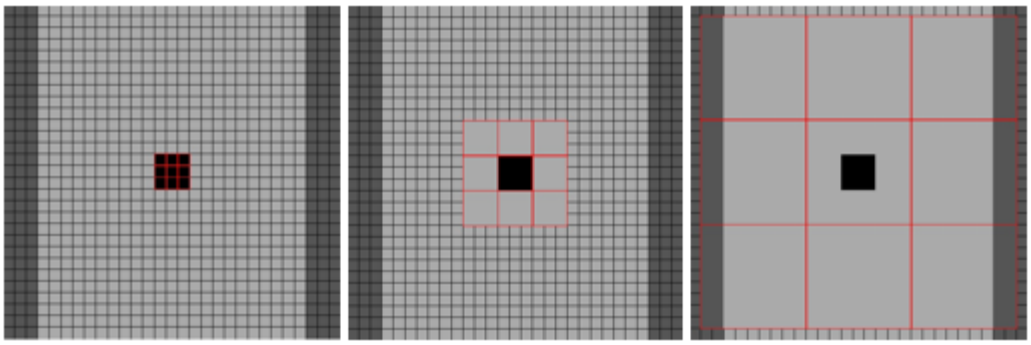

Figure 12 – nested morphogen fields: left=3x3, center=9x9, right=27x27

The automata were trained and tested for a variety of border lengths, which are manipulated by changing the dimensions of the grid: the larger the grid, the longer its borders. And as the border lengths increase, the distances from the central block of regenerating cells to the borders increase, eventually passing out of range of the morphogenetic fields associated with the metamorphs. This can be seen in Figure 12, which from left to right shows the morphogenetic field sizes for the 3x3, 9x9, and 27x27 nested neighborhoods. It can be seen that only the 27x27 neighborhood intersects with the left-right border, allowing morphogens associated with the central cells to generate the correctly aligned bar. Morphogens associated with the 3x3 and 9x9 neighborhoods do not intersect the border cells, and thus cannot determine the correct orientation.

For each border length setting, the automata were sequentially exposed to the correctly oriented bars for the vertical and horizontal borders, causing the creation of metamorphs that generate appropriate cell types. A test is correspondingly in two parts: the central block with vertical borders followed by the central block with horizontal borders. A successful test is defined as the regeneration of the correct bars for both parts.

The results are shown in Table 2 for border length increments of four cells. Both the unnested and nested automata correctly process the first two border lengths. However, at the third length, the unnested automaton cannot detect the borders and thus fails to regenerate both bars correctly. Eventually the border recedes beyond the range of the nested automaton as well, indicated in the last row of the table.

Border length	Unnested neighborhoods	Nested neighborhoods
17	✓	✓
21	✓	✓
25	×	✓
29	×	✓
33	×	✓
37	×	✓
41	×	×

Table 2 - Cell regeneration results.

The cell regeneration presented here can also be understood as a type of tropism, wherein a directional movement or growth takes place in response to an environmental stimulus. Phototropism, for example, is a response to light (Goyal, Szarzynska & Fankhauser, 2013). Another biological counterpart involving cell (re)generation stimulated by fields of chemical signals is paracrine signaling for wound healing (Hocking & Gibran, 2010; Dittmer & Leyh, 2014). Stem cells migrating to wound sites release bioactive factors that orchestrate wound healing.

When tissues are wounded, they are healed via a regenerative process called epithelialization (Hocking & Gibran, 2010). During this process, it has been found that stem cells, particularly mesenchymal stem cells (MSCs) aid in the speed of wound healing by releasing growth factors and other extracellular factors that facilitate regeneration (Hocking & Gibran, 2010). In general, stem cells are functionally plastic, and can differentiate into a variety of functional cell lineages depending on where they are recruited and the functional context. During organ regeneration, bone marrow stem cells migrate to sites that are damaged to provide various roles in the regeneration process (Morigi et al., 2004). It is this functional context where the parallels with Morphozoic's generative process can be found. For example, MSCs often act through paracrine signaling rather than direct replacement of the cells making up damaged tissue (Bruno et al., 2013) .

Stem cells also have the capacity to self-renew, which allow them to proliferate and thus persist for many more divisions than differentiated cells. Perhaps more importantly, stem cells can manipulate their local environments to favor regeneration (Dittmer & Leyh, 2014). This is done by acquiring the gene expression patterns of their new defined fates, as well as producing a host of secretion factors. It is this secretome (Salgado & Gimble, 2013) that most strongly influence the extracellular environment, and can act to coordinate the behavior of cells and tissues at multiple scales. Influence of the local environment is also accomplished via paracrine signaling (Baraniak & McDevitt, 2010), which involves short-range chemical signaling of growth factors between cells. In a very simple manner, Morphozoic

can mimic these signaling mechanisms, and the architecture of Morphozoic could be used to implement these mechanisms at multiple spatial scales.

Cell regeneration is concerned with the restoral of missing information using nearby available information. A related process, digital image inpainting (DII) is a computer algorithm that restores missing information of images such as those of old oil paintings. A biological counterpart occurs in human visual systems as well in the form of blind spots (Satoh, 2012). As an illustration of the Morphozoic cell regeneration capability applied to image restoral, consider the problem of restoring an image from its edges, as shown in Figure 13.

Figure 13 – Lenna image with edges (Wikipedia, 2016a).

This is done by casting the original image and edge-detected image into a CA grid. The edge cells, shown in the upper left part of Figure 14 (in reverse color for contrast), form an outline of the source pattern. The original image, shown in the bottom right of Figure 14, forms the target pattern. Only the dark edge cells are allowed to morph into target cells. With this restriction, five morphing steps are necessary to complete the transition.

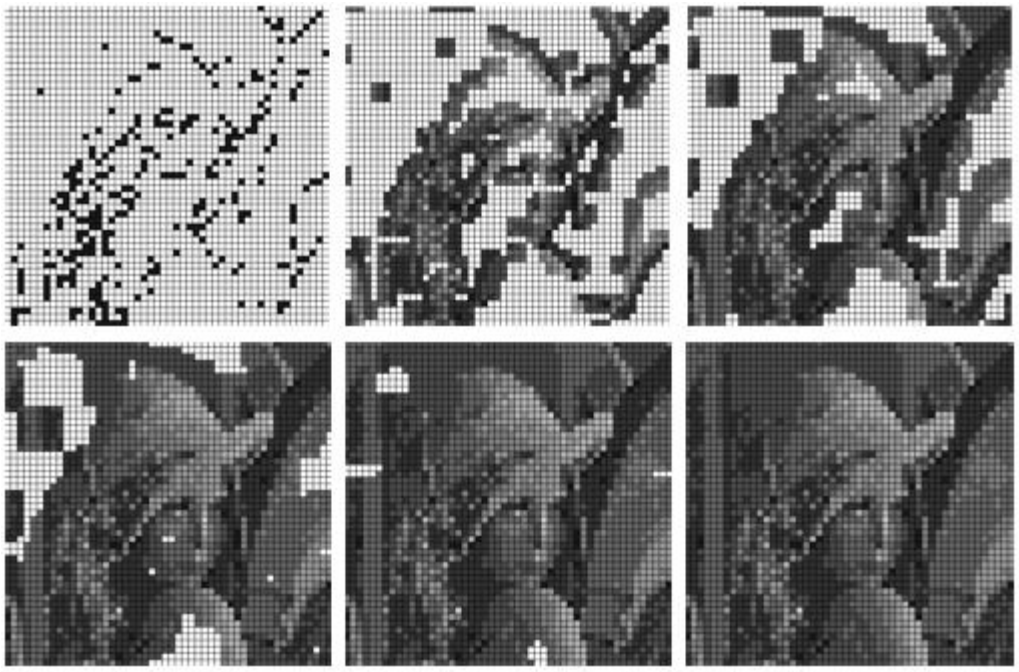

Figure 14 – Step-by-step image restoral from edges.

Gastrulation evolution

Background

There have been a number of attempts to model gastrulation and related developmental processes. Developmental phenomena such as cleavage, blastulation, and gastrulation have been modeled using a physical cellular model that indirectly assumes how genetic mechanisms effect the timing of these processes (Drasdo and Forgacs, 2000). A more direct technique would involve the use of Genetic Algorithms (GAs). GAs are a type of evolutionary computation that focuses on the construction and optimization of programs using natural selection. In this case, natural selection act to select programs that meet or exceed the criteria to reproduce and/or maintained in a population of programs. GAs have been used in conjunction with Young's cellular automata to approximate the reaction-diffusion driven biological pattern formation and replicate morphogenetic fields (Gravan and Lohoz-Beltra, 2004). Because they are an instance of adaptive computing, there is the potential for broader application of GAs to problems of biological development As an optimization procedure, GAs provide an adaptive method that can find solutions despite a rugged search landscape (Bornholdt, 1998). This is analogous to how biological populations evolve solutions to adaptive problems in a *de novo* fashion. We can successfully approximate complex, emergent phenomena in development specifically and biology more generally by more closely examining the relationship between computational representation and biological complexity.

A GA consists of three parts: a genetic representation, a set of operators for mutation and/or crossover operator, and a selection criterion (Holland, 1992). The algorithmic representation (genome) often

consists of one or more chromosomes, while each chromosome consists of several genes. A genetic representation is a computational abstraction of a genome, each gene representing a compact encoding of some aspect or feature in a given system. Each gene consists of serial bits and acts as a bit register, which can be used to encode a wide variety of problems. This allows us to capture the power of population dynamics and heredity rather than expression of genes, although specialized genetic algorithms (Ferreira, 2001) can incorporate gene expression. In general, using genetic algorithms as a form of theoretical inquiry allows us to replicate the dynamics of a given biological system, which in turn allows us to better understand the complexity of the underlying system (Steventon and Arias, 2016).

The essential component of a genetic algorithm is the mutation and/or crossover operations. While mutation consists of bit flipping, recombination consists of exchanging entire blocks of bits either within or between programs. In both cases, an operator introduces variation in the function of a program. This variation is then selected upon based on fitness criterion, but is also subject to historical constrains of the problem space. This allows for the self-organization of patterns to emerge (Nizam and Shanmugham, 2013) without breaking the code or destroying the structure of the initial program. One way in which GAs avoid code fragility is to start with a population of programs that exhibit differential reproduction. In this way, a genetic algorithm selects from a variety of potential solutions. A related issue is the maintenance of structure and complexity in a naturally-selected program space is the existence of building blocks (Forrest and Mitchell, 2014). This is similar to modularity in biological evolution, in which parts of the program are protected from future evolutionary change (Wagner and Altenberg, 1996).

All of these issues figure prominently into the approximation of gastrulation as a developmental process. GAs are particularly good at finding heuristic solutions to problems residing in a large possibility space, so they are likewise suited to simulating instances of biological self-organization where an exact solution is not required. This is particularly true of simulating large problem spaces for where biological experimentation would yield no clear solution. The problem of emergence in biological self-organization can be viewed in terms of computational complexity (Grover, 2011). In gastrulation, we can see the usefulness of both properties, in addition to the usefulness of incorporating gene expression into a multi-scale model (Kaandorp et.al, 2012). Biological self-organization also relies on rules and constraints rather than explicit instructions.

Implementation

Gastrulation is a process by which the cells of an embryo form an invagination in an early spheroid shape in the course of tissue differentiation. A simple Morphozoic model of this is shown in Figure 15. This configuration was formed through a progression of cell “divisions” starting from a single central cell. Morphozoic generated metamorphs from a programmatically produced sequence. Two nested 3x3 neighborhoods were required; one neighborhood was found to be insufficient to reproduce the desired output. Once generated, the metamorphs executed the sequence correctly.

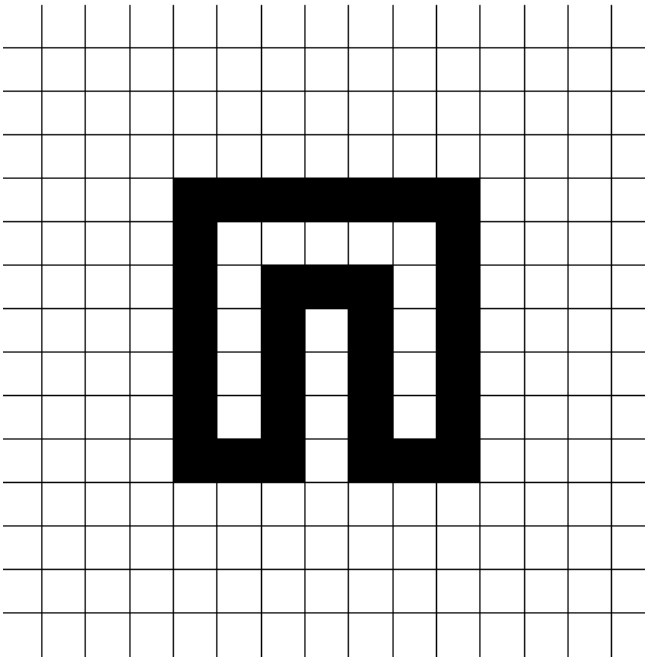

Figure 15 – Gastrulation configuration.

A model that purports to explain the workings of morphogenesis at any level of abstraction should be evolvable. In order to demonstrate the mutability and evolvability of Morphozoic, a genetic algorithm (GA) was used to evolve a population of “organisms” to gastrulate successfully. The fitness function was a count of the number of matching cell types summed over the sequence of cell type transitions.

Each population member contained metamorphs that were initially constructed by randomly pairing morphogens generated from a programmed gastrulation sequence with actions from the sequence. The number of metamorphs in each member was determined by the number required to execute the sequence.

After a subset of the population was selected as fit members, the population was replenished with mutants and offspring of fit members. Offspring were created by mating randomly chosen parents members and performing a crossover operation on their metamorph sets. Crossover consisted of supplying the child with a set of metamorphs randomly selected from its parents. Mutants were created from individual fit members by discarding all metamorphs that were not executed and replacing them with random ones.

Additional GA parameters:

- Population size = 50
- Fit population size = 10
- Number of generations = 50
- Number of offspring from matings = 20

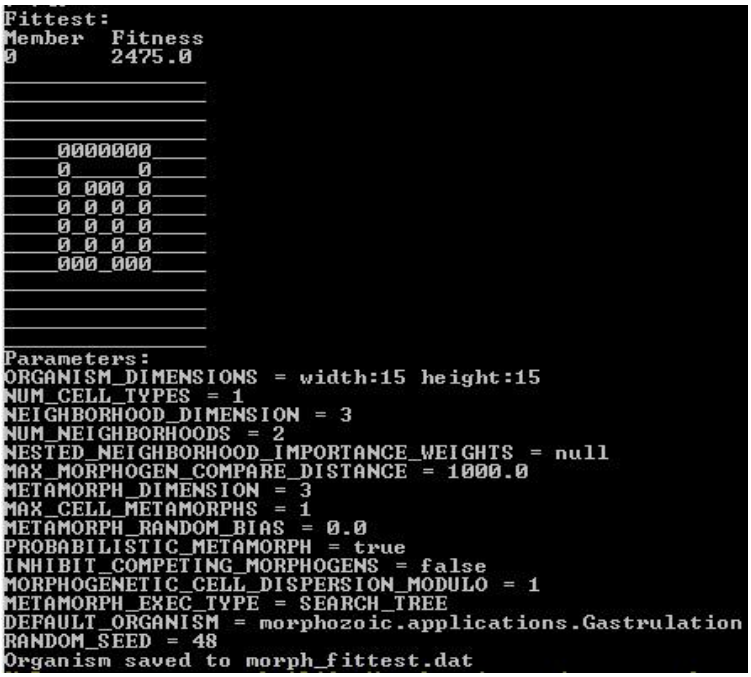

Figure 16 – Gastrulation evolution results.

As Figure 16 indicates, the GA produced the required gastrulation morph sequence. The computation was done in approximately 12 hours on standard desktop computer.

Neuron pathfinding

Also called axon guidance, neuron pathfinding is a process by which axons are guided by chemical signals to target neurons, a process essential for the formation of organized neural networks (Tessier-Lavigne & Goodman, 1996). While cellular automata have been used to simulate similar “branching” phenomena (Markus, Böhm & Schmick, 1999), the generalization of reverse engineered rules is a novel application.

One of the benchmarks presented here is that of neuron pathfinding. Morphozoic is able to accomplish this gradually by exploiting the organizational feedback of cellular growth and spatial gradients embodied in the metamorphs. In biology, neuron pathfinding is accomplished a bit differently, instead using chemotropic mechanisms to guide axons to their target. Tropic cues are directional cues initiated by various stimuli. In the case of chemotropic cues, chemical signals and gradients (e.g. the axonal growth cone) guide regenerating tissues in the direction of its target (Huber et al., 2003). The chemotropic mode of action has not only been shown to exist in developmental morphogenesis (Tessier-Lavigne et al., 1988), but during tissue regeneration as well (Alto et al., 2009).

To simulate this, three types of cells are used: source neuron, target neuron, and axon. These can be seen in Figure 17. In this application, source neurons are allowed to have multiple axons. Metamorphs were generated from programmatic sequences of axon growth. For execution, however, the

metamorphs were used to train an ANN (see Figure 8), which classified actions based on pattern-matching morphogens.

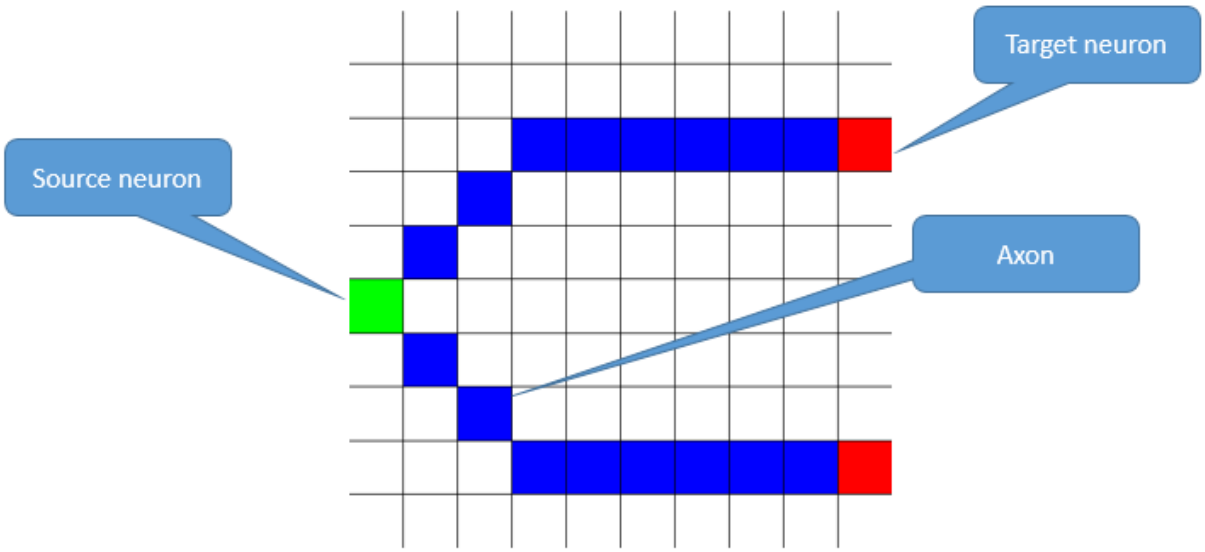

Figure 17 – Neuron pathfinding example.

The training set was created by growing axons from source to target neurons. The source and target neurons were randomly placed along the left and right sides of the grid, respectively. Metamorphs were then generated from multiple random configurations.

For testing, source and target neurons were randomly placed, morphogens generated from cell neighborhoods, and axons grown by pattern-matching the learned patterns. The challenge here is that axons must be grown from source to targets in different positions than those for which training was done, so training must generalize to handle novel neuron positions. The employment of an ANN as a classification mechanism was useful to accomplish this.

This procedure was done for a single source neuron, one and two target neurons, and with one, five, and ten training set exemplars. A successful trial is defined as axons connecting to the target neurons. Ten trials were run for each parameter configuration.

The results are shown in Figure 18. As might be expected, performance for the single target neuron exceeded that for two targets, the latter having a greater number of possible configurations. The number of exemplars also had a significant beneficial effect: one exemplar was insufficient to produce any successes for the two target neuron case.

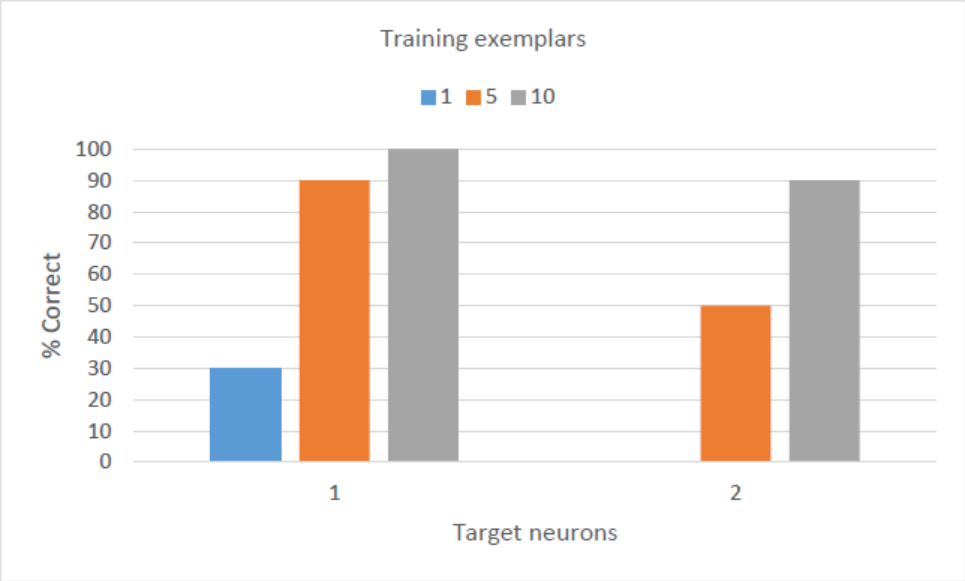

Figure 18 – Neuron pathfinding results.

Turing's reaction-diffusion morphogenesis

Alan Turing is credited with pioneering a mathematical formulation of morphogenesis generally known as a reaction-diffusion system (Turing, 1952). This system consists of a set of dynamically coupled substances that, depending on parameters, are capable of producing various complex patterns, such as stripes, spots, and spirals. Figure 19 shows a "cheetah coat" pattern generated from a random initial pattern of three cell types.

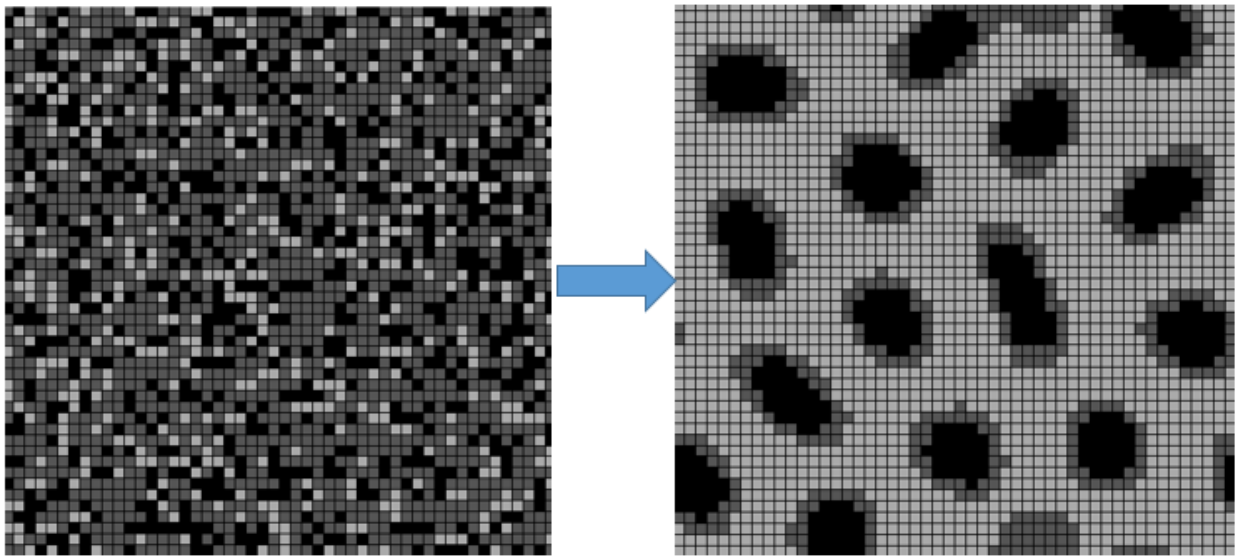

Figure 19 – Reaction-diffusion morphogenesis of a "cheetah coat" pattern from random values.

This application is a comparison with this well-known specialized morphogenesis algorithm. Metamorphs were generated from the Turing reaction-diffusion morphogenesis. These were used to train an ANN to learn appropriate cell type changes. To test, a freshly randomized pattern was generated and the metamorph pattern-matching mechanism executed. A typical result is shown in Figure 20. While not as smooth appearing as the original, the spotted pattern is distinctly visible.

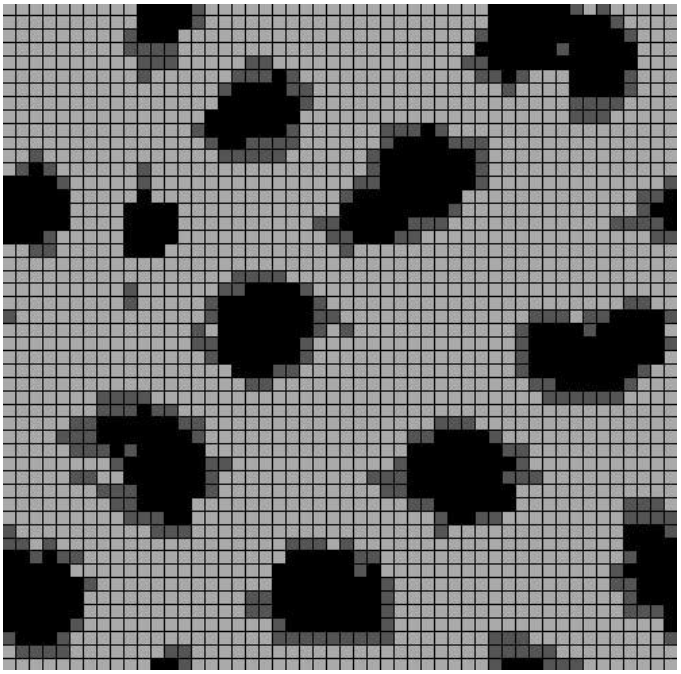

Figure 20 – Simulation of reaction-diffusion morphogenesis.

Conclusions

Biology presents us with numerous cases of morphogenetic fields as a morphogenesis mechanism. The particular mechanisms and the depth of knowledge of these cases varies widely. Morphozoic is an attempt to implement an abstraction of the functional commonality of morphogenetic fields as a mechanism for self-organizing computation.

Morphozoic is a novel embodiment of a number of capabilities that are useful for morphogenesis: flexibility, compact and economical computability, evolvability, and generalizability, especially in association with the artificial neural network implementation. The cited applications were chosen to demonstrate these properties.

Future directions

- **Neighborhood sector value:** The assignment of a value to a sector could be any function of the types of its cellular components: average, mode, winner take all, etc. An alternative is to look at the change of cell type as an image processing operation, such as taking a Laplacian, Sobel and other

edge enhancements, starbyte transformations (Sivaramakrishna & Gordon, 1997; Sivaramakrishna, 1998), contrast enhancement (Gordon & Rangayyan, 1984b, a), etc.

- **Field signal strength and cell type variability:** If cell types were continuous quantities instead of discrete, a straightforward proportional mapping of morphogen similarity to cell type value would be possible. On a related, more subtle possibility, morphogenetic fields are signaling constructs. Signals can vary in some ways, such as amplitude, while retaining invariant signatures, such as frequency spectra for electromagnetic waves. This suggests that variable action potentials proportional to field strength could be a fruitful topic for research. For example, might scaled, fractal-like structures be morphed?
- **Dynamic/temporal fields:** Limiting morphogenetic fields exclusively to spatial representations restricts the model to a state machine. Dynamic fields that incorporate temporal information could also be explored (Portegys & Wiles, 2004; Martínez, Adamatzky & Alonso-Sanz, 2013). This could take the form of metamorphs that contain past neighborhood patterns or hierarchical streams of neighborhoods that embody context.
- **Fluid three-dimensional fields:** A major reason that the cellular automaton architecture was chosen was that it provides a straightforward mapping of local and global morphogenetic fields. However, a fixed two dimensional grid is not a crucial feature of the Morphozoic model. The fluid three dimensional medium that biological systems operate in points to an opportunity for the model to explore.

Relevance to artificial intelligence

Morphozoic is also relevant for artificial intelligence (AI). AI research to a great degree focuses on the brain and behaviors that the brain generates. But the brain, an extremely complex structure resulting from millions of years of evolution, can be viewed as a solution to problems posed by the environment. There is a common and somewhat ironic tendency to describe AI inputs and outputs in human cognitive terms, i.e. post-processed brain output, such as symbolic variables (Hoffman, 2009).

An alternative approach, suggested by morphogenesis, is to view the environment as set of local/global, spatial/temporal signal fields, and that the processing of fields is what spurs brain development. Organisms are capable of performing amazing feats, such as navigation and nest-building, by the sensing of unique environmental signals, such as polarized light, magnetism, and chemical scent trails. Morphogenesis makes plain that signal fields can have powerful computing capabilities. Perhaps it is worth exploring artificial intelligence as a solution to environments composed of these fields. As Edmund Sinnott, author of *Plant Morphogenesis* (Sinnott, 1960), suggested, morphogenesis may be the key to understanding intelligence (Sinnott, 1961; Sinnott, 1962b; Sinnott, 1962a; Sinnott, 1966), starting with plant intelligence (Mancuso & Viola 2015).

In keeping with nature's penchant for extending rather than replacing, the sponge-like shape of the mammalian neocortex can be seen as symbolically apropos. For its purpose might be to soak up signals from far reaches of time and space and render them, as though yet near and present, to the old brain whose instinctual role has little changed over eons. The environmental gradients that clearly drive the

behavior of simpler creatures then became internalized in the nervous systems of more neurologically complex ones.

The Morphozoic Java code is available here: https://github.com/pascualy/Morphozoic.

Morphozoic was developed in conjunction with these community projects that model and simulate the *C. elegans* nematode worm:

- DevoWorm (Alicea et al., 2014; Alicea, 2016)
- OpenWorm (Szigeti et al., 2014)

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