Asynchronous, irregular automata nets: the path not taken

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Abstract

This is a prelude to, and an extension of the original paper Artificial tissue models (Stark, R., 1994. The topology and analysis of asynchronous processes. http://www.math.usf.edu/~stark/documents). However, this exposition is designed for a broader audience — anyone working in biological information processing. A primary objective is to demonstrate that irregular asynchronous automata nets, as opposed to cellular automata, are a realistic approach to modeling biological information processing. Also, new material is presented. Sections 1 and 2 review the early history of von Neumann's attempt to explore biological information processing and finally the emergence of cellular automata. The history is guided by the question of why John von Neumann knowingly (we believe) compromised his investigation of biological information processing by falling back to the model we now know as cellular automata. Section 3 defines and explores examples of cellular automata and artificial tissue. Sections 4 and 5 contain philosophical observations which unify our paper, and propose an answer to the original question. A new model for Turing's leopards' spot problem is presented. The asynchronous models are defined by a cell program and a local communications protocol only. Computational freedom comes from asynchronous activity, while global organization emerges from the entropy reducing nature of the cell programs. © 2000 Elsevier Science Ireland Ltd. All rights reserved.

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1. Introduction

Cellular automata — a mathematical model of large numbers of very simple, interacting, finite-state information processors — developed in the imagination of Hungarian-American mathematician John von Neumann (1903–1957). He was inspired by the work of McCulloch and Pitts (1943), Turing (1952), and Wiener (1961), and motivated by a desire to understand biological information processing — especially self-reproduction (von Neumann, 1966).

The original kinetic model, developed in conjunction with Burks (1970) was physical in nature and so not easily investigated mathematically. Later, von Neumann, influenced by his friend Stanislaw Ulam (Aspray, 1999), simplified and streamlined the original model/approach. The result is the cellular automata (CA) model. The CA model’s streamlining consists of synchronous activity by cells, and homogeneous interactions be-

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between cells. Communication is homogeneous if for every pair \(x, y\) of cells, there is a graph automorphism (i.e. a function \(a: G \to G\) which maps the graph onto itself while preserving edges) and satisfies \(a(x) = y\).

A cell’s communications protocol is a function which reduces every multiset of neighboring states to a single input-value from the set the set \(Q\) of cell states and inputs. Activity consists of communication followed by an opportunity to change state. Activity is synchronous if each cell is active at each time. This is the model we call cellular automata. In both cellular automata and artificial tissues, cell programs are identical. A program is a finite-state automaton \((Q, z)\) where \(Q\) is a set of states/messages, \(z: Q^2 \to Q\) is the state-transition function, \(\mu: \mathcal{H}(Q) \to Q\) is the communications protocol, and \(\mathcal{H}(Q)\) the set of \(Q\)’s multisets.

The CA model flourished in mathematics and computer science. Results were established using well-known mathematical techniques. Mathematicians and theoretical computer scientists wrote and published thousands of scholarly papers (a recent search of MathSciNet turned up more than 4000 items!) However, success came at a cost. The assumptions upon which tractibility depended were biologically invalid. Papers in quality journals, using the dynamics of cellular automata to support biological conjectures reach their conclusions only as a consequence of biologically flawed assumptions. Thus, as a model for biological information processing, CA models are fatally contaminated.

This is the path that was taken. The alternative assumes asynchronous activity and irregular interactions between automata. This would have been a difficult path to follow — especially in the years before desk-top workstations and recent advances in mathematical dynamics — but it would have been true to biological paradigms. For example, consider cardiac or epidermal tissues. These tissues are sets of cells joined by communication. Communication is along irregular lines (automorphisms are non-existent), is bidirectional, anonymous, strictly local, and asynchronous. Further, globally shared memory is not present. Each cell has a finite set of states and a small set of, variably many, spatial neighboring cells. Epidermal and heart tissue, with cells communicating via gap junctions, inspired this model. Such communication is primitive compared with that of neural networks. Recent references include Science (1999a,b) and Baigent et al. (1998).

The artificial tissue model differs from biological reality in that it is simpler than real tissues. Generally, real tissues may be dominated by a single cell type, but more than one cell type (i.e. program) will be present, more than one type of communication will be used, and global structures (such as the cardiac pacemaker) may be present. However, our meager assumptions are biologically acceptable, and so positive results established using artificial tissue will be biologically consistent.

This expository paper explores the early history of cellular automata in Section 2, and examples from both paths are presented in Section 3. Of special interest, from the path not taken, is a new approach to Turing’s famous leopards’ spots problem. Web references to simulations of this and other artificial tissues (i.e. asynchronous automata nets are given. Finally, key features of the nature of the path not taken are discussed in Section 4. Sections 3 and 4 address issues raised in Section 2 by illustrating that the path not taken is the biologically-appropriate path.

I thank Arthur Burks, Herman Goldstein, Ron Graham, Paul Halmos, Chris and Sharon Stark, Yuri Gurevich, Ava Bozoki, Freeman Dyson and Austin Hershel, for responding to requests for historical information and help in general. Necessarily, many names, and results have been omitted. However, the bibliography includes starting points for further study which can correct this deficiency.

2. Historical observations

By all accounts, von Neumann’s cellular automata were to have first been studied in the discrete case and then in the continuous case. Concerning this, he wrote: ‘they [the models] will be of a much less combinatorial [i.e. discrete] and much more analytical [i.e. continuous] character’.

Further, by starting with the discrete case and
moving toward the continuous, the power of analysis — ‘the technically most successful and best elaborated part of mathematics’ — could be used (Aspray, 1999). According to Burks:

‘Von Neumann thought that automata mathematics should be closer to the continuous and should draw heavily on analysis. He thought that the specific problems of automata theory require this, and he felt that there is a general advantage in an analytical as opposed to a combinatorial approach’ (Burks, 1970).

Stan Ulam was also thinking about cellular automata, perhaps even before von Neumann. Although, as the following Ulam quotation indicates, nothing was ever written down.

‘I remember also (it must have been sometime in 1929 or 1930) that he [Mazur] raised the question of the existence of automata which would be able to replicate themselves, given a supply of some inert material. We discussed this very abstractly and some of the thoughts which we never recorded were actually precursors of theories like that of von Neumann on abstract automata’ (Burks, 1970).

However, von Neumann never developed a continuous theory of automata. Shortly after his Hixon lectures in 1948, Ulam convinced von Neumann to abandon the continuous approach in favor of the discrete. Ulam ‘suggested that a cellular framework would be more amenable to logical/mathematical treatment’ (Goldstine, 1972). As far as a time frame for the shift of emphasis, Ulam writes:

‘After the war and before his illness, we held many discussions on these problems. I proposed to him some of my own ideas about automata consisting of cells in a crystal-like arrangement’ (Ulam, 1976; p. 280).

Emphasis has been added because similar wording appears in (Schrödinger, 1944; chapter 6), and because it is suggestive of CA’s communications automorphisms.

Von Neumann’s reasons for choosing what he called the crystalline case were twofold. First, ‘the general possibilities are about the same in both cases’. Considering the very substantial differences known to exist between the global dynamics of the two, his comment may have referenced a particular phenomenon which was not recorded, or he could have been misunderstood. However, I doubt that this is what he believed.

Second, (echoing Ulam) ‘the continuous case is mathematically more difficult than the discrete.’ This is certainly true. However, John still seemed to think that the continuous case was important:

‘…if and when the appropriate analytical methods to deal with the continuous case are developed, this case will be more satisfactory and more broadly and relevantly applicable than the crystalline case’ (von Neumann, 1963).

Von Neumann knew of the entropy of information, and of Schrödinger’s earlier conjecture on the ability of (Boltzmann/Gibbs) entropy to manage the incredibly complex, and nearly chaotic activity, of living systems. It is alleged to have been von Neumann who informed Claude Shannon of the thermodynamic nature of his developing information theory, particularly the entropy function. It seems likely that got the idea from Leo Szilard.

The Markov chain analysis (Ulam, 1972; Stark, 1994a,b) necessary to support the analytical approach to his investigation was certainly within his reach. A basic 0, 1 law (Stark, 1994b, The Global Behavior Theorem of Section 4) which has recently served as a key to mathematical investigations, and substantially decreased the difficulty of realistic modeling, is based on Markov chain analysis. So, I believe the tools needed to begin a valid approach, to biological information processing in simple tissues, were present in von Neumann’s mind.

He just didn’t have the time to put them together. His untimely death prevented development of the continuous model and perhaps it was Stan’s prescience of this that led him to the discrete model. According to Goldstine:
von Neumann seemed to regard automata theory as a means of studying biological processes as well as a source of mathematical ideas:

‘Their role in mathematics presents an interesting counterpart to certain functional aspects of organization in nature. Natural organisms are, as a rule, much more complicated and subtle, and therefore much less well understood in detail, than are artificial automata. Nevertheless, some regularities which we observe in the organization of the former may be quite instructive in our thinking and planning of the latter; and conversely, a good deal of our experiences and difficulties with our artificial automata can be to some extent projected on our interpretations of natural organisms’ (Toffoli and Margolus, 1987; Serra and Zanarini, 1990)

After von Neumann’s death, Ulam was inspired by discoveries in molecular biology during the 1960s, and continued their investigation of biological aspects of computation:

‘After reading about [the biological developments] which were coming fast, I became curious about a conceptual role which mathematical ideas could play in biology. If I may paraphrase one of President Kennedy’s famous statements, I was interested in ‘not what mathematics can do for biology but what biology can do for mathematics’. I believe that new mathematical schemata, new systems of axioms, certainly new systems of mathematical structures will be suggested by the study of the living world.’ (Ulam, 1972)

Like the new mathematics created in response to the physicists’ theory of general relativity:

‘It appears that experimentation on models of games played by self-organizing living material through chemical reactions in living organisms will lead to novel abstract mathematical schemata.’ (Aspray, 1999)

von Neumann’s understanding of information processing in biological paradigms may be seen in his early work on automata. For example:

‘…[O]rganisms can be viewed as [being] made up of parts which, to a certain extent, are independent elementary units. … [A major part of the problem of automata] consists of how these elements are organized into a whole…” (von Neumann, 1948; p. 289).

‘Independence’ implies asynchronous activity, and the issue of ‘organization’ is most interesting in the irregular and asynchronous case where the lack of rigorous mid-level structure is the origin of the mystery of emergent global behavior. The computational importance and power of biological systems is a major theme in his work. For example:

‘… [The ENIAC weighs 30 tons [27 000 kg] and dissipate[s] 150 000 watts,... while the human nervous system, which is functionally about a million times more powerful], weighs a pound or two [1 kg, and dissipates about 50 watts]… [T]he ENIAC … handles merely 700 [bits] of information…” (von Neumann, 1948; p. 301)
Impressed by McCulloch & Pitts’ neural networks, he envisions a logical approach to understanding automata and biological information processing:

‘... [T]he logic of automata... will be of a much less combinatorial, and much more analytical, character. In fact,... [I] believe that this new system of formal logic will move closer to... thermodynamics... that part of theoretical physics that nearest... to manipulating and measuring information.... ’ (von Neumann, 1948; p. 304).

A recent reference for logical approaches to biological systems is Duan et al. (2000).

Von Neumann’s interest in understanding self-reproduction was the result of an apparent inconsistency in the observed fact of self-reproduction:

‘There is a... ‘vicious circle’ in nature, the simplest expression of which is the fact that very complicated organisms can reproduce themselves.... When an automaton performs certain operations, the operations must be expected to be of a lower degree of complexity than the automaton itself.... [I]t would therefore seem that a certain degenerating tendency must be expected, some decrease in complexity as one automaton makes another.... [I]t is in clear contradiction with... nature.... For the question which concerns me here, that of the ‘self-reproduction’ of automata, Turing’s universal machine is too narrow in one respect only. His automata are purely computing machines.’ (von Neumann, 1948; p. 312 and 315).

At first glance, a similar inconsistency appears in the universal but finite Turing machine. Contrary to intuition, it can simulate every other Turing machine. Von Neumann hoped to generalize Turing’s construction and proof of universality to encompass self-reproduction. But, at first he saw it as an extension from computation and information to physical structure.

The vicious circle appears again in self-reproduction’s apparent violation of the Second Law of Thermodynamics — also noted by Schrödinger.

Among this law’s various statements are... In a closed system (i.e. one in which neither energy nor information enter the system) entropy (i.e. disorder) increases. A transformation whose only final result is to transfer heat from a body at a given temperature to a body of a higher temperature is impossible (Clausius).

Notice that the transformation prohibited by Clausius would increase order and decrease entropy. An enlightening and beautifully written exposition on thermodynamics is The Refrigerator and the Universe (Goldstein and Goldstein, 1993).

Thermodynamic aspects of biological information processing, now seem to be the key to organizing asynchronous totally distributed automata nets. I am speaking here of cell programs which locally reduce [a] Shannon entropy of neighboring cell states — i.e. which increase [some type of] order. These programs are then linked by a form of cell-to-cell communication capable of extending the developing local order to larger neighborhoods like the previously mentioned crystal-like arrangement. Thus, the asynchronous global behavior of a tissue is directed thermodynamic mechanisms. This idea may have its origins, and certainly gained its notoriety, in Erwin Schrödinger’s famous 1944 lectures on the nature of life at Trinity College’s Institute for Advanced Study in Dublin (Schrödinger, 1944; chapter 6).

After von Neumann’s death, Ulam suggested the following approach to understanding asynchronous models. It is appropriate for dealing with thermodynamic issues:

‘... In order to make the ‘almost always’ precise, one needs to have a measure in the space of all possible outcomes of a branching process...’ (Ulam, 1972; p. 285).

The first author of this paper has begun developing this approach — using two product spaces of Markov chains (Stark, 1994b). The first consists of chains of random sets of active individuals, the second consists of all possible runs of the process. Each chain in the first obviously determines a chain in the second. An interesting measure on the process’ runs, defined by this mapping from first to second, captures the role of cell memory. Using these tools, emergent properties
(which are first-order and dense and open) of artificial tissues are proved to occur with probability 1.

3. Examples: synchronous and asynchronous

The two paths are contrasted in the examples sketched in this section. The path not taken, by von Neumann, is asynchronous — illustrated in a new solution to the famous leopards’ spots problem. The path taken is synchronous with homogeneous communications. It is illustrated in Conway’s Game of Life¹ and the ripple adder. Definitions are implicit in these examples. But most important, the asynchronous models are shown to be unnatural.

The Game of Life is a specific cellular automaton invented by mathematician John Conway (Gardner, 1970). It runs on an infinite two-dimensional array of cells, \((m, n)\in\mathbb{Z}^2\), with 0, 1-values \(C_{m,n}\). Each cell \((m, n)\) interacts with eight neighbors in terms of their 0, 1-values (Table 1).

> According to the global 0, 1-assignment, \(C\), a cell \((m, n)\) is either occupied \((C_{m,n} = 1)\), or vacant \((C_{m,n} = 0)\). At each moment, the current colony consists of the cells with value 1.

Three rules are applied synchronously to determine the next colony. Death: If an occupied cell has fewer than two or more than three neighbors, then the organism dies (for fewer than two neighbors, of loneliness; for four or more, of overcrowding). Survival: If an occupied cell has two or three neighbors, it survives to the next generation. Birth: If a vacant cell has three neighbors, then it becomes occupied. In other words, if \(C'_{m,n}\) is the value of \((m, n)\) at time \(t = 0, \ldots, i + 1, \ldots\) and \(\sum C'_{m,n} := C'_{m-1,n-1} + \ldots + C'_{m+n+1,n+1}\) is the sum of the eight neighbors’ values, then the next value at \((m,n)\) is:

\[
C'_{m,n} \begin{cases} 
C_{m,n} & \text{if } \sum C_{m,n} = 2 \\
1 & \text{if } \sum C_{m,n} = 3 \\
0 & \text{otherwise.}
\end{cases}
\]

For example, a \(4 \times 4\) subarray of cells could experience the change in global state outlined in Table 2. The fat arrow, \(\Rightarrow\), is used to represent steps in global computations, converting one global state into its successor.

Conway’s model is strong enough to encode Turing machines (Wolfram, 1994) and their computations, so it is universal in that every deterministic serial computations can be programmed in a two-dimensional cellular automaton. A few webpages on the Game of Life and cellular automata, with links to others, are given in (WWW pages on cellular automata). The ripple adder is a linear array of cells:

\[
\ldots(n + 1), \ldots, + 1, 0, -1, \ldots, (n - 1)\ldots
\]


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Table 1
A 3 × 3 patch of an array of automata \((m, n)\), and their states \(C(m', n')\) for Life

| \(C_{m-1,n-1}\) | \(C_{m-1,n}\) | \(C_{m-1,n+1}\) |
| \(\ldots\) | \(C_{m,n}\) | \(C_{m,n+1}\) |
| \(C_{m+1,n-1}\) | \(C_{m+1,n}\) | \(C_{m+1,n+1}\) |
| \(\ldots\) |

Table 2
A sequence of \(4 \times 4\) patches of global state values in a run of Life

| 0 0 1 0 | 0 1 0 0 | 0 0 1 0 | 0 0 0 0 | 0 0 0 0 |
| 1 0 1 0 | 0 0 1 1 | 0 0 0 1 | 0 1 0 1 | 0 0 0 1 |
| 0 1 1 0 | 0 1 1 0 | 0 1 1 1 | 0 0 1 1 | 0 1 0 1 |
| 0 0 0 0 | 0 0 0 0 | 0 0 0 0 | 0 0 1 0 | 0 0 1 1 |
Activity and communication move information from right to left. In acting synchronously, this cellular automaton adds binary real numbers. At time $t$, $i_n^t$ is an input bit, $c_n^t$ a carry bit, and $m_n^t$ a memory bit. Initially, every $c_0^0 = m_0^0 = 0$ and real binary inputs are written in $[\ldots, i_n^0, \ldots]$. At subsequent steps, $m_{n+1}^t$ is computed from $B_n^t$, $c_{n+1}^t$ from $B_{n-1}^t$, and $i_{n+1}^t$ is externally determined. Specifically:

\[
c_{n+1}^t = (i_{n-1}^t c_{n-1}^t + i_{n-1}^t m_{n-1}^t + c_{n-1}^t m_{n-1}^t) \mod 2
\]

\[
m_{n+1}^t = (i_n^t + c_n^t + m_n^t) \mod 2.
\]

For example, the sum of successive inputs $\frac{2}{3} = (0.0011100\ldots)_2$ and $\frac{3}{8} = (11.1110\ldots)_2$ is computed as in Table 3.

In these arrays, the decimal point is an imaginary place keeper and does not correspond to any cell. The $m$-row in the last global state is the sum $(100.0001100111\ldots)_2 = 42_{10}$. The following example of pattern construction in asynchronous and irregular networks relies on local mechanisms only. There is no global synchronization of cellular activity, no globally shared memory, and no regularity in communications structure.

We compensate by replacing the global tissue structure by a cell program and a local-communications protocol which is entropy (Shannon and Weaver, 1963) non-increasing and so eventually decreasing. This local reduction of entropy spreads through the network like crystalization in a supersaturated solution. As it spreads, the structure of the local graph emerges in the global graph. This is Schrödinger’s concept of life (Murphy and O’Neill, 1995) expressed in our terms.

Global states should now be thought of as functions $\bar{s}: (V,E) \rightarrow (Q, \rightarrow)$ from the tissue’s communication graph to the cell state-transition graph. An edge $xy \in E$ is unbroken by $\bar{s}$ if $\bar{s}(x) \rightarrow \bar{s}(y)$ — notice that this includes $\bar{s}(x) = \bar{s}(y)$. Generally, entropy reducing asynchronous processes move global states toward graph homomorphisms. Then once a homomorphism has been reached, subsequent global states are necessarily homomorphisms. $\Rightarrow$ preserves homomorphisms. It is possible to view the following leopards’ spots program as a homomorphism seeking process, but at first it may be best to see them simply as entropy reducing processes.

Runs of processes are paths through $(Q^V, \Rightarrow)$ the global graph. Thus, the global attractors of $(Q^V, \Rightarrow)$ are disjoint sets of homomorphisms. With probability 1, asynchronous runs will be trapped by an attractor (Stark, 1994a,b). Several simulations of other asynchronous processes, programmed in MAPLE, may be found on the Internet (Stark, 1999).

A new solution to the leopards’ spots problem. Turing (1952) raised and solved the problem of a distributed process capable of generating large patterns, leopards’ spots, from a homogeneous initial global state (Fig. 1). His solution used a

### Table 3

A binary ripple adder summing $\frac{2}{3}$ and $\frac{3}{8}$

<table>
<thead>
<tr>
<th>$[\ldots, 0.0001100111\ldots]$</th>
<th>$\Rightarrow$</th>
<th>$[\ldots, 0.0111000000\ldots]$</th>
<th>$\Rightarrow$</th>
<th>$[\ldots, 0.0000000000\ldots]$</th>
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<td>$[\ldots, 0.0001100111\ldots]$</td>
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<td>$[\ldots, 0.0111011000\ldots]$</td>
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...
mechanism based on the diffusion and reaction of reactants in a fragment of Euclidean space. It has since been verified in vitro (Lengyel and Epstein, 1991), and is related to the well-known spiral patterns seen in the Belousov–Zhabotinsky reaction.

The solution presented here is based on entropy reduction at the level of individual asynchronously active cells. The communications graph is somewhat random. However, the entropy being reduced is defined in terms of graph labelings, \( \bar{s} \), and a fixed state coloring \( \sigma: Q \to \{ \text{red, yellow, blue} \} \). Given \( s \in Q \):

\[
\sigma(s) = \begin{cases} 
\text{red}, & \text{if } s = 2 \\
\text{yellow}, & \text{if } s = 4, 5, \text{ or } 6, \\
\text{blue}, & \text{if } s = 0, 1, \text{ or } 3 
\end{cases}
\]

Now this cell program allows transitions \( \bar{s}' = \bar{s}' + 1 \) in which the number of edges (of both graphs) broken by \( \sigma \cdot \bar{s}' + 1 \) decreases. This process is theoretically capable of generating wallpaper style patterns of any design.

For a cell \( c \), its state \( s \), its neighbors’ states \( n_s \), \( s \)'s color \( r \), and neighbors colors \( n_r \): \( c \) is stable if the state is a graph homomorphism and one of the following is satisfied:

Fig. 1. Leopards' spots as a global state on 333 cells.
Stable cells do not change state when active. Cells in state 3 cannot be stable, so global halting states cannot contain state 3. With one exception, an unstable cell will move from state \( s \) to \( (s + 1) \text{mod} 7 \). Stable global states contain isolated red cells, surrounded by blue cells each of which touches a red and a yellow cell, all other cells are yellow. The colors red, blue and yellow are the visible cell values (phenotypes?), while the states are hidden variables (genotypes?) which store information which is not displayed.

As more cells eventually become stable, the Shannon entropy decreases. The sample space consists of the nine ordered pairs of colors. Initially, the measure gives each pair a probability of \( \frac{1}{9} \). But the process eliminates certain color pairs: 

- \([\text{red, red}], [\text{red, yellow}], [\text{yellow, red}]\),
- \([\text{yellow, yellow}], [\text{blue, red}], [\text{red, blue}]\),

become either very probable or very improbable. As global stability is approached, these probability measures evolve, and their associated Shannon entropy decreases. Decreasing entropy is equivalent to the development of a pattern.

A simple measure-theoretic argument (Stark, 1994a,b) proves that with probability 1 this process will eventually halt. Halting states depict a rough leopard-spot pattern.

4. The nature of asynchronous processes

Synchronous activity, in the rigorous sense defined here, is not seen in nature, at least not in the interactions of sets of cells, animals, etc. But this perfect synchronization is present in the state dynamics of computer chips. In the absence of human intervention and invention, nature is asynchronous.

But, contrary to the conclusions one might jump to, asynchronous activity is the source of the power of biological information processing. There are global transitions that are possible only by asynchronous activity. Consider the three-cell tissue:

\[
G = (\{a, b, c\}, E) \quad \text{where} \quad E = \{ab, bc, ca\}
\]

with \( Q = \{0, 1\} \).

It is given the cell program that changes from \( s \) to \( (s + 1) \text{mod} 2 \) if there are two distinct values among neighbors. The global transition \( [0, 1, 1] \Rightarrow [0, 0, 0] \) is the result of activity in which only \{\(b, c\}\} are active.

Both the synchronous and serial global graphs are subgraphs of the asynchronous global graph. So, every global computation is a run of an asynchronous computation. The key to creating/understanding/programming meaningful asynchronous computations is in controlling \( \Rightarrow \) by the cell program and communication. Specifically, communication and state-transitions must be programmed to be entropy reducing — in the sense of some local measure. Although I have no proof, I believe that in a network with a strongly connected cell–cell communication, a cell program and communication protocol that is locally entropy reducing will eventually produces global behavior that is entropy reducing and so is meaningful/patterned in some sense.

Entropy reducing mechanisms are seen in biological systems whenever ATP (or some similar triphosphate) is dephosphorlated to deliver the energy required for a biological process. So an energy input is associated with the reduction or maintenance of entropy at a less than maximal level. Without this, the existence of such programs and protocols would contradict the second law. Shannon entropy and the second law of thermo-
dynamics, in the context of information processing, are well developed by Bennett (1982) and Feynman (1996). These sources explain how an input of information may be substituted for the energy input mentioned above. An asynchronous process is non-deterministic, and so the set of infinite runs may be viewed as a subset of a product space. There is a theorem that crystallizes these ideas for the entropy of first-order properties.

Imagine, on our product space, a first-order logic of properties of runs, a product topology, and a product measure. A property (of runs) is dense and open if, given a finite initial segment of a run, it is possible to extend it to an initial segment with the property, and once an initial segment has the property every extension of it has the property.

4.1. Global behavior theorem

Theorem 4.1.1. Every dense and open first-order property of an asynchronous process occurs with probability 1.

Proof. Definitions, proofs, examples, and applications can be found in Stark (1994a,b).

The global behavior indicated for the asynchronous process of this paper is an immediate consequence of this theorem.

5. Conclusion

The modeling of known, or proposed, biological information processing mechanisms as asynchronous automata nets is a source of valuable insights. Interested readers are sincerely invited to communicate their suggestions, questions, corrections, and other comments to the first author. As for the original question, we conclude that von Neumann’s choice was motivated by the need to deliver a viable mathematical model before his time ran out.

References


