

Research Article

Functional Information of a Driven Cellular Automaton

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1. Independent researcher

For decades cellular automata (CA) simulations have proven versatile in modeling a wide range of natural phenomena due to their limited dimensionality and ability to allow adjustment of the small number of parameters that control self-organization. In this study, a model was designed that extends the self-organized phase of the automaton by keeping a single cell in a permanently active state. After interacting with over 400,000 initial configurations of randomly placed standard automata cells surrounding the perennial cell, 351 unique stable structures were created by the end state of evolution. These structures are analyzed with the goal of quantifying their complexity beyond the expected selection bias inherent in CA. A correlation was established between the average number of generations required to construct each structure and its complexity as measured by functional information theory. This link between information measured in bits and construction in generations quantifies the computational work performed by the state transition rule of the CA. Because complexity is often in the eye of the beholder, the correlations developed in this work remove observer bias from the often-difficult task of defining complexity generated by self-organized processes in nature.

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1. Introduction

“Everybody talks about the weather, but nobody does anything about it”¹. However, one man, John von Neumann – called ‘The Man from the Future’ by a biographer^[1] – did begin work in the late 1940s that continues to contribute to our understanding of this most complex of nature’s systems, the weather^[2]. The many interacting components of the atmosphere surrounding the geosphere, impacted by solar radiation and influenced by gravity, creates the weather and prompted von Neumann, among several

others, to consider if the first somewhat-programable computer – the ENIAC (Electronic Numerical Integrator and Computer) – could become a forecasting tool if they could create a model adapted to use this tool. The effort required modifying the equations known at the time to govern atmospheric phenomena to methods suitable for numerical solutions because they were analytically intractable at the scale and complexity of even a local weather event. By 1951 they achieved some success in creating a model of several weather events whose computed behavior closely matched the real-world event. They had predicted the weather, but only after it had occurred, hence hindcasting.

Progress in understanding complex weather systems since the time of von Neumann has been made and accurate forecasting is now common, but much work remains in many other fields where the principles in nature that create the emergence of self-organized structures continue to tax the analytical tools of science^[3]. Identifying the control parameters is often where the hard work begins in understanding these systems. The action of self-organization often emerges during phase transitions – think of liquid water becoming ice – as the system reaches a critical point. This is why for decades cellular automata (CA) simulations have proven versatile in modeling a wide range of natural phenomena due to their limited dimensionality and ability to allow adjustment of the small number of parameters that control self-organization. The technique of using CA to model nature was also originated by von Neuman, with inspiration provided by Stanislaw Ulam^[4]. Examples of CA applications include traffic flow^[5], fluid dynamics^[6], biology^[7], urban planning^[8], epidemiology^[9], self-reproduction^[10], artificial chemistry^[11], quantum mechanics^[12] and autopoiesis and multicellularity^[13].

In previous research^[14] I demonstrated how a modified version of Conway's Game of Life (GoL)^[15], called perennial evolution (PE), can create stable and increasingly complex geometric structures in phases of evolution from random initial configurations. This evolution, while non-Darwinian, is characteristic of complex systems with the ability to “dissipate energy or to maximize entropy production through patterning”^[16] even though thermodynamics plays no role in PE dynamics. PE is identified as *driven* because it continually injects order during evolution by keeping a CA cell or structure permanently active while maintaining and often extending the system's dissipative action due to the physics of its state transition rule (STR)^[17]. The structures created in PE display a selection bias and a variable chemistry-like reactivity, acting as an artificial chemistry.

As an elaboration on my previous work, where several of the frequently occurring GoL still life structures were used as artificial molecules, the current project considers how to first build artificial molecules from

a single perennial cell. This new model is analogous to how the primordial elements created by stellar evolution in the early universe^[18] eventually gave birth, over cosmological ages, to minerals that formed the geospheres of planets^[19] in continuing phases of structure building^[20]. When these structures, considered as artificial molecules, and their history of formation are analyzed by the methods of functional information (FI) theory^[21], a new understanding of self-organization and complexity is obtained for this driven CA. The goal of this work is to gather Insights from the application of FI to CA to provide new opportunities for modeling complex systems.

2. The Perennial Evolution Construction Process

In contrast to Conway's canonical GoL (CE), PE defines two types of objects (*active grid cells*) that can exist as shown in Figure 1, functioning as two-dimensional analogs of atoms that can bond and become structures representing *artificial* molecules. It is the construction process of this bonding and the resulting selection bias toward certain geometric forms that is the focus of this research and not insights into the physics of creation of *real* molecules.

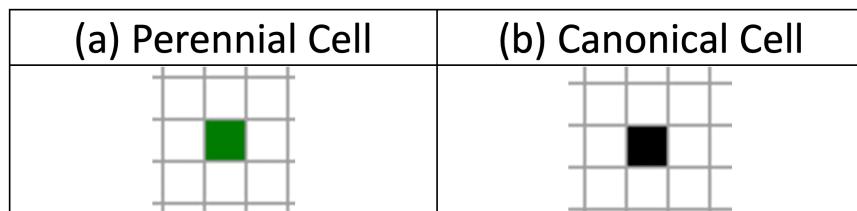


Figure 1. Atomic Components. Two building blocks for construction of artificial molecules in PE. The terms 'cell' and 'atom' will be used interchangeably in this model.

The bonding is controlled by the physics of the STR that acts synchronously in discrete steps (*generations*) on all cells in the grid (*universe*) defined by the following rules:

1. Each inactive cell is defined as having the potential to become an active canonical cell and will become active if it has 3 active neighbors, otherwise it remains inactive.
2. A canonical cell that is active remains active during evolution if it has 2 or 3 active neighbors, otherwise it becomes inactive; this rule combined with rule 1 is often expressed using the nomenclature B3/S23 where 'B' signifies born and 'S' survive.

3. A perennial cell cannot be created by the STR but is manually introduced into the initial configuration of canonical cells prior to the beginning of a phase of evolution. A perennial cell is permanently active throughout all generations and can have as many active canonical neighbors at the cardinal and intercardinal directions of the cell (the Moore neighborhood) as rules 1 and 2 will allow.
4. A collection of canonical cells bound to a single perennial cell resulting from the action of rules 1, 2 and 3 is considered a molecular object if it becomes a static geometric structure during evolution and remains static until the universe reaches an end state. This end state occurs when the density of active cells in the evolving automaton reaches a constant or periodic value, but the molecule itself must be static. Also, the structure must have bonds connecting all the cells within the molecule, i.e., it must be a 'strict still life' as defined by the GoL ([Still Life](#)) consisting of only one 'island'.

Many familiar GoL still life will be created in PE because rules 1 and 2 are identical with the CE rules. However, structures will also be created that cannot exist without a single perennial cell and these objects will have a special focus in the analysis of this research and referred to as PE molecules.

An example of PE construction is shown in Figure 2 where the creation of a molecule is demonstrated in an initial phase of structure building.

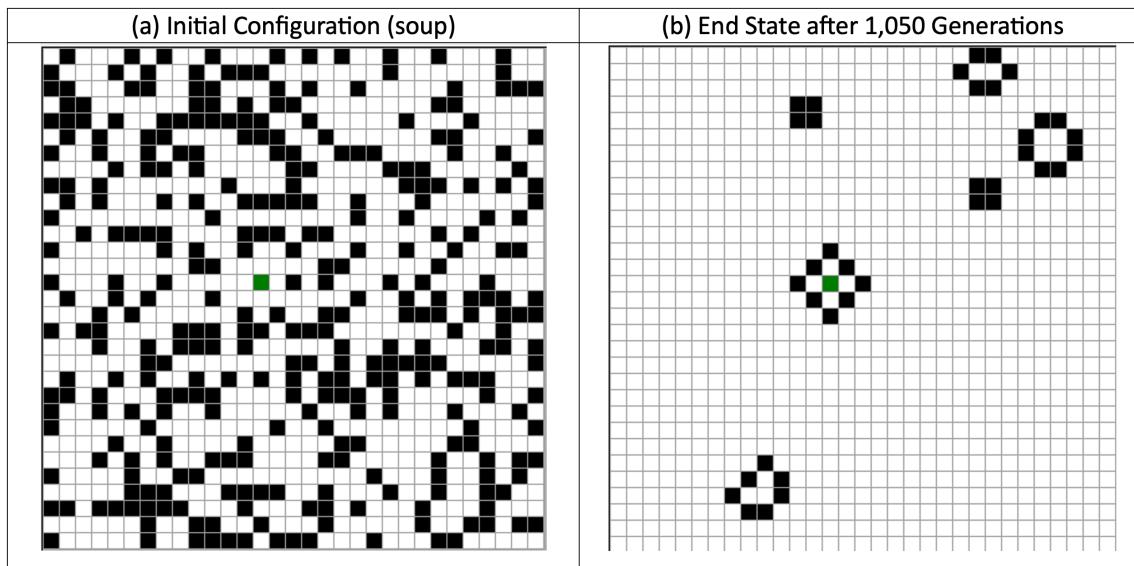


Figure 2. Perennial Evolution. A single perennial atom within a random soup of canonical atoms in (a) evolves after 1,050 generations to a static density in (b) creating a stable structure modeled as a molecule that could not exist without the perennial cell; this PE molecule is named a ‘Diamond’. The universe size for this simulation is a 30 X 30 toroidal grid with an initial density of active cells in (a) of 35%.

With few exceptions it is common in PE for an embedded perennial cell to extend the number of generations for a random initial configuration of canonical cells to reach a static end state as compared with the same soup without the perennial cell. As an artificial chemistry this phenomenon can be viewed as the reactivity of the perennial cell – a type of catalytic effect – with the canonical cells. For example, in Figure 2, the soups in (a) without the perennial cell reached a static end state in 180 generations as compared to the 1,050 when a perennial cell is present. This catalytic effect, an extension of the region of dissipation during evolution where the rates of change per generation between active cells becoming inactive (death) and inactive cells becoming active (birth) are competing is the region of self-organization that exhibits power law behavior^[22]. See Appendix A1 for more details and how these death/birth rates, called a dissipation factor (DF) can be measured and correlated with the number of generations that a soup requires to reach a static end state.

3. Molecular Phenomenology

Statistically significant patterns of molecular construction in PE are only revealed from evolution of a large set of initial state configurations (soups). Each soup contains a single perennial cell embedded

among randomly positioned canonical cells. The total number of initial soups in the dataset for this project was 416,000 and each soup was set to evolve up to a maximum of 2,000,000 generations. Most of these soups (401,275) reached an equilibrium state prior to the maximum generation limit and those that did not reach equilibrium or were periodic were discarded from analysis. The initial soups were divided into 300 subsets to allow computation on a cluster of desktop computers. A toroidal grid size of 30 X 30 for each soup with an active cell density of 35% was chosen based on the fact that GoL dynamics are scale-invariant relative to grid size^[23] and the initial soup density is in the range where self-organized criticality is optimal^{[24][25]}. This choice also helped minimize the total data processing time to 1,715 hours.

The expected results of the dataset were the creation of molecules but 42.79% of the 401,275 soups did not produce any structure: the perennial cell remained unbound to canonical cells. However, 229,570 of the initial configurations, or 57.21%, produced a total of 351 molecular-like, stable objects with 186 qualified as PE molecules, unique from CE still life. The software developed for this project creates a signature for each molecular object that defines its unique geometry and in Figure 3 the number of signatures discovered per subset is presented.

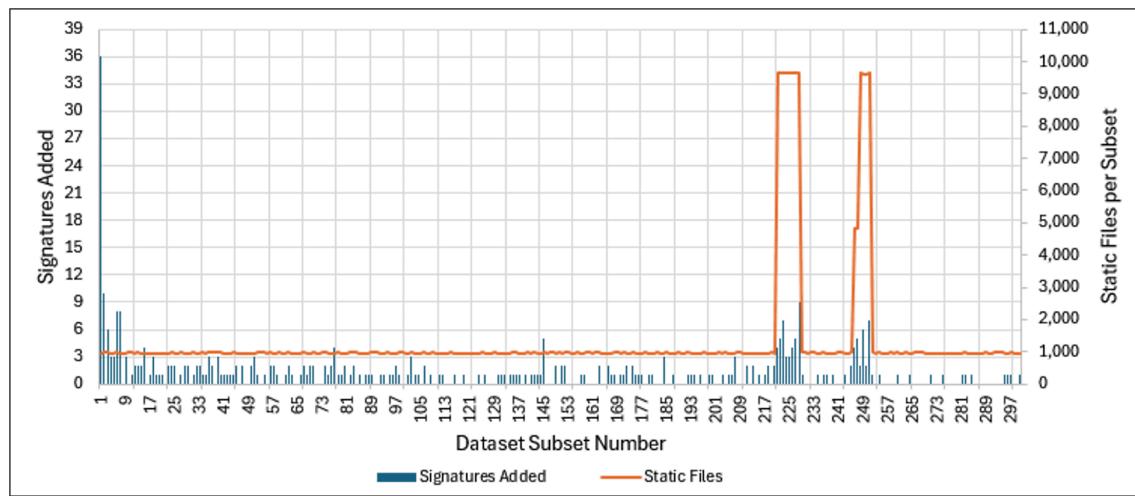


Figure 3. Discovery of Molecular Signatures. The first subset discovered 36 molecules, and the subsequent number discovered rapidly declined. Subsets 1 to 220 each contained 1,000 initial soups and some subsets following this range had a larger number of soups as can be seen by the number of static files produced from evolution on the secondary Y-axis. The total number of subsets was 300.

3.1. Molecular Families

An organizational scheme of molecules into families, based on the number of canonical cells per molecular structure, was developed as limits to the variety of artificial molecules that can exist within a family of a defined size were discovered. The smallest family size was 3 canonical cells bound to the single perennial cell and the largest was 19, however no molecules were discovered for sizes 16 or 18. An overview of family statistics is shown in Figure 4.

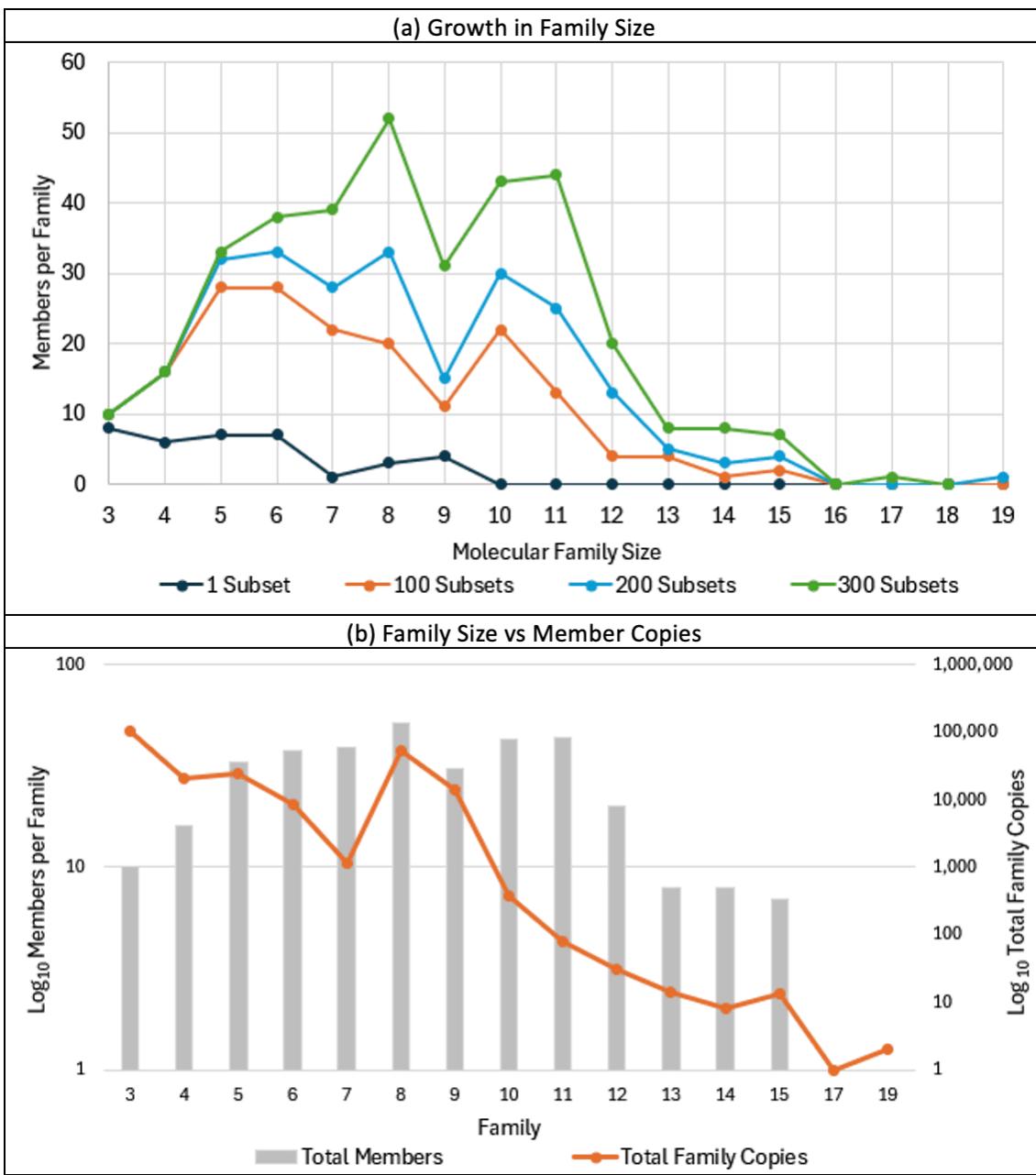


Figure 4. Family Statistics. In (a) 351 molecular-like structures were gradually created per subset with 186 qualified as PE atoms; the family sizes 16 and 18 are shown only to emphasize that they contained no structures. In (b) any correlation between the number of copies of molecules per family versus the family size is not apparent in this data although there is a general falloff after family 9 as the size increases. Family 8 contains the PE molecule shown in Figure 2 (b) named a Diamond.

3.2. Minimum Molecular Size Limit

Molecular-like structures of less than three canonical atoms cannot exist in PE nor in CE as illustrated in Figure 5.

	(a)	(b)	(c)	(d)	(e)
Initial State					
End State					

Figure 5. Minimum Molecular Size. In (a) the end state is not a molecule. In (b) this structure becomes the classic period 1 oscillator known as a Blinker in CE and is thus not stable nor qualifies as a molecule. In (c) a stable Block is formed and in (d) a stable Tub. The end state of (a) through (d) occurred in a single generation while in (e) the end state was reached in 1,278 generations from evolution with a random soup of canonical cells in which the perennial cell was embedded; the state shown here is generation 1,277. (The Block and Tub were also created from random canonical soups with a single embedded perennial cell but shown here in a simplified form of creation.)

The Block and Tub are part of a family identified as P_1C_3 since they contain 3 canonical cells bound to the single perennial atom, but they do not qualify as PE molecules since they can be created in CE. More on the PE molecule (e) in the next section.

3.3. Isomers in Families of Molecules

In addition to the minimum size of a molecule, many molecules in a family can appear in several orientations relative to the grid as two-dimensional spatial isomers (stereoisomers). For example, family P_1C_3 contains 8 stereoisomeric members as shown in Figure 6.

Molecular Structure							
Copies Created	217	211	209	204	202	201	197
Bond Location	NE	SW	SW	NE	SE	NW	SE

Figure 6. Family P₁C₃ Stereoisomers. The perennial cell's bond location to a canonical cell varies among these molecules corresponding to the intercardinal directions of the Moore neighborhood. Rotation and/or reflection with respect to the XY-Plane of any one of these molecules demonstrates the structure's isometry. The total number of copies for all forms of this molecule is 1,622. This geometric form is unique to PE since it can't exist without the perennial cell.

Stereoisomers reveal that for a given family, e.g., P₁C₃, there is a limit to the number of unique structures that can exist within a family of a specific number of canonical cells. If a molecule like those in Figure 6 is manually assembled where the first canonical cell is bound to the perennial cell's north binding location, the structure is not stable as seen in Figure 7.

Initial State	Generation 1	Generation 2	Generation 3	End State at 168 Generations
				

Figure 7. Nonstable Hypothetical P₁C₃ Object. A binding to the north of the perennial cell – as well as a binding to the east, south, or west – in the absence of any other canonical cells in the universe, results in the initial state evolving to a static configuration in 168 generations, but a stable molecule is created. The behavior of this object results from the driven nature of PE where the presence of a perennial cell with only a few canonical cells injects order as the universe evolves.

The position of the canonical cells bonded to the perennial cell in Figure 7 illustrates how critical geometry is to the final state of such an object. This sensitivity to position, a result of the STR that governs atomic bonding, is demonstrated in the possible number of isometric forms for other families as seen in Figure 8.

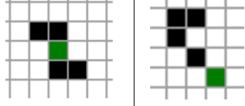
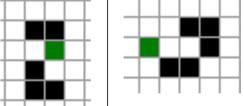
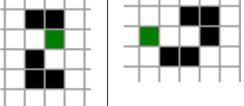
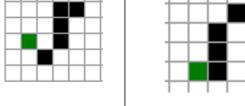
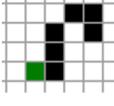
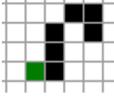
Family	P ₁ C ₄		P ₁ C ₅			P ₁ C ₆
Molecular Structure						
PE Atom?	True	True	False	True	True	False
Forms Detected	4	8	4	8	8	8

Figure 8. Isometric Molecules. In family P₁C₄ the two isomers complete the possible number of structures that can exist in this family (the Boat, discussed shortly, in its 4 forms are the remaining molecules in this family). The repeated appearance of 4 and 8 forms of structures is a function of the CA neighborhood with its 8 possible directions of bonding.

3.4. Selection Bias

A subset of the 351 created molecules is shown in Figure 9 and represents 97.67% of the total molecular copies. This subset of 21 molecules is ranked from left-to-right by the number of copies for each molecule and will be a primary focus for analysis.

Family	3	8	3	5	4	5	9	6	5
Molecule									
Name	Block	Diamond	Tub	Beehive	Boat	Barge	Yacht	Loaf	Ship
PE Rank	1	2	3	4	6	10	12	16	20
GoL Rank	1	n/a	6	2	4	10	134	3	5
Copies	94,219	53,337	10,696	5,839	5,055	4,460	3,480	2,042	1,855
Other Forms and Copies				 5,835	 5,031	 4,257	 3,474	 2,038	 1,853
					 5,010		 3,432	 1,979	
						 4,960	 3,425	 1,963	

Figure 9. Frequently Occurring Molecules. The PE rank is for the primary orientation of molecules with more than one form. The GoL rank of still life is based on a [frequency class](#) relative to the Block, the most common object in CE as well as PE. The Diamond is the only PE molecule in this collection and the others follow the standard CE naming convention ([still life names](#)) except for the 'Yacht' whose GoL name (Barge Siamese Loaf) is not used because I needed a shorter monicker for ease of reference.

PE did produce CE structures within the top 10 frequently occurring GoL still life though in a slightly different order and the Yacht's occurrence frequency is indicative of some of the differences between CE and PE. Of course, the Diamond as a PE molecule shows that the physics of PE differs from CE, and these differences will be examined in the sections ahead.

4. Analysis: Functional Information Theory and Molecular Construction

The phenomenology presented in the previous section demonstrates that the selection bias of PE is different from CE and the appearance of molecules unique to PE was also noted. Quantifying these aspects of PE is the task of this section and includes a detailed analysis of the molecular construction process responsible for these observations.

4.1. Function Information Defined

In Hazen's study on complexity in patterning systems^[26] FI is defined as a "degree of function (E_X) [that is] a quantitative measure of a configuration's ability to perform the function X". In PE, this function is the system's ability to create stable artificial molecules, and the "quantitative measure" is given by the formula:

$$I(E_X) = -\log_2[F(E_X)] \quad (1)$$

In Equation 1, $F(E_X)$ is the "fraction of all possible configurations of the system that achieves a degree of function $\geq E_X$ " and is referred to as the Functional Information Detection Ratio (FIDR) in this research and is a measure of the frequency of occurrence of objects created by the system. In the context of PE, the "degree of function" is a measure of the action performed by the STR to form a stable molecule^[27] with ≥ 3 active canonical cells with a single perennial cell as demonstrated above in Figure 5. The 401,275 configurations (from the initial 300 subsets of soups) are the "all possible configurations" where each configuration could result in the creation of a molecule, even though only 229,570 configurations did create a molecule and achieve the defined degree of function. However, FI considers the larger value discussed in Section 3 of 401,275 soups as representative of the state of knowledge about the system prior to any evolutions of the automaton, that is, all configurations are initially equally likely to produce molecules of the defined degree of function because the probability distribution of the system is uniform – and unknown – prior to any evolutions being performed^[28]. Once evolution begins, information about the system increases with the value of $I(E_X)$ in bits a measure of this new information, quantifying the computational work performed by the STR to produce a molecule. It is also important to consider the fact that the functional information of a molecule – in this case, an artificial one – is not the property of a molecule in isolation, "but of the ensemble of all possible sequences, ranked by activity"^{[21][29]}. This activity of the environment is shown in Figure 10 where the FI values for each of the 351 molecules are displayed.

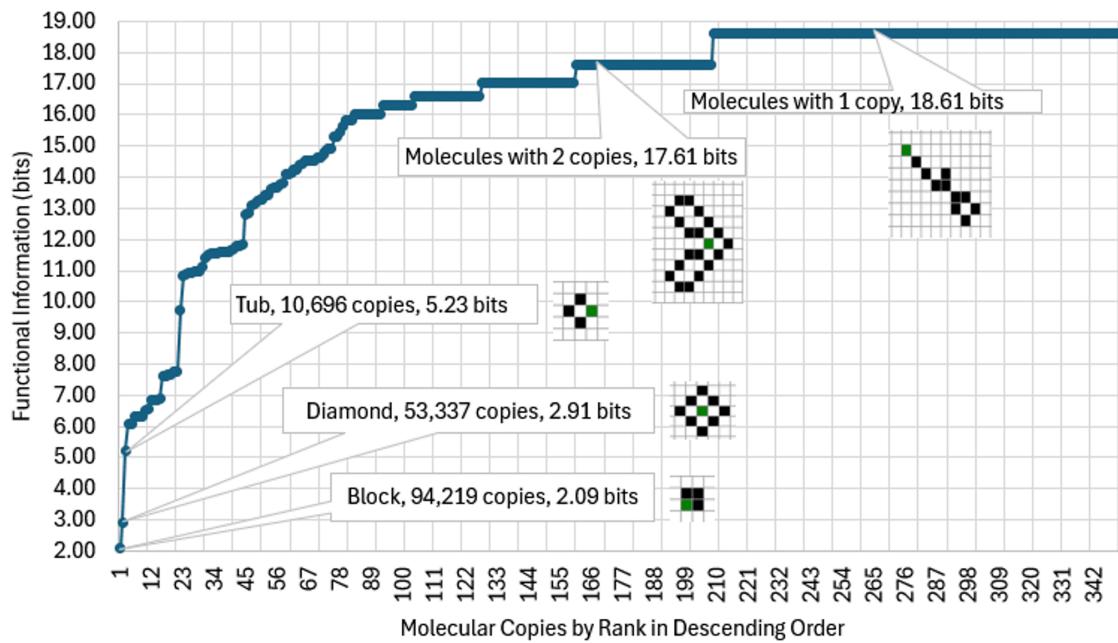


Figure 10. Functional Information for all CE and PE Molecules. Three of the most frequently occurring molecules are shown along with two of the less frequent to visually illustrate the differences in complexity. The Diamond and the two molecules shown with 2 copies and 1 copy are among the 186 PE structures that can't exist in CE.

While the images of the several molecular structures in Figure 10 yield a limited intuitive picture of complexity along the lines of the time-worn saying, “I know it when I see it”, additional quantification of complexity can be derived from the relationship of the FI values to the construction process that created each molecule.

4.2. Complexity and Molecular Construction

As the FI value of a molecule increases, the frequency of its occurrence decreases, i.e., its probability of forming from a random configuration of canonical cells surrounding the single perennial cell decreases (FIDR decreases). Given that a lower FI value defines a less complex structure, can this FI value be correlated with the quantity of computation work performed during the soup’s evolution? Stated in terms of a hypothesis, does a less complex molecule require fewer generations to form during evolution than a more complex molecule?

To test this hypothesis, the software created for this project was designed to record the minimum, maximum, and average number of generations for each molecule’s creation for each soup in which it was

generated and is defined as construction steps (CS). The CS values (min, max and average) are different from the number of generations that the random soup requires to reach its end state, rather it is a measure of the generational value when the molecule first forms and remains a strict still life until the end state is reached. For example, the Block, the most frequently occurring molecule, and the least complex, has a range of CS values as shown in Figure 11.

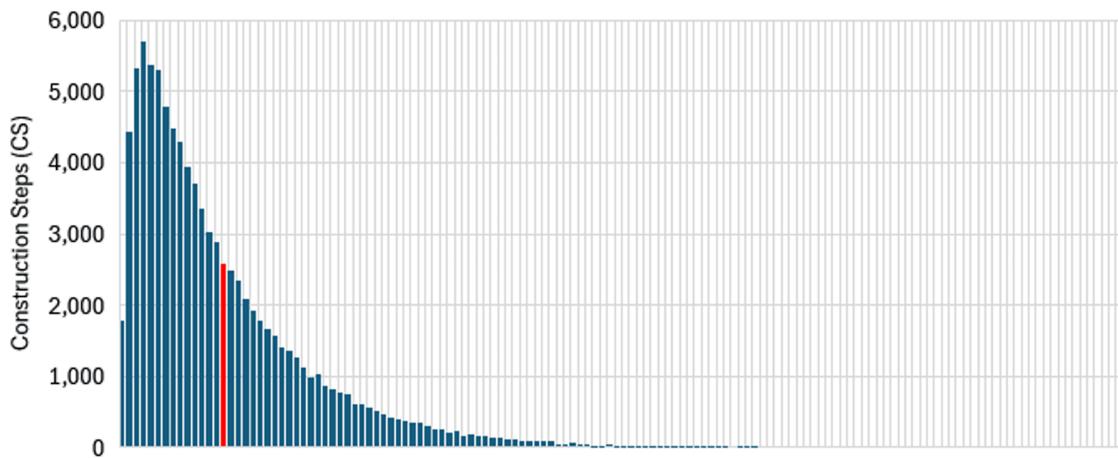


Figure 11. Block's CS Values. The minimum CS is 4 and the maximum 7,171 with an average of 749.22 generations as shown by the red column in the histogram. This result represents the range of CS values for all 94,219 random soups that created the Block. The histogram's horizontal axis contains bins of size 52 but the bin ranges are not shown due to space limitations on the page.

The other 20 frequently occurring molecules (see Figure 9) have similar skewed (long tail) histograms of CS values that represent the nature of CA evolution whose variation in construction steps is highly contingent on initial conditions and analytically unpredictable.

It is tempting to consider, for the finite environment that has been tested, that the minimum CS value is equivalent to Kolmogorov complexity^[30], i.e., the shortest program description^[31] in bits that can produce a molecule is a measure of its complexity. Since the algorithmic nature of the STR is an evaluation of each cell's active or inactive state – a binary choice – then the trend of minimum CS values might be like the trend in F_i values that increase as a molecule's complexity increases. However, a minimum CS value is only one instance of evolution, but the F_i values are representative of the activity of the total environment, namely all the configurations that produced a molecule. In this case, the average CS values for each molecule – and this governs the entire set of configurations for a molecule – when

converted to average construction steps per molecular copy have a common dimension with the FIDR in Equation 1 that produces the FI value for a molecule. As an example, the Block with an average CS of 749.22 generations for all 94,219 copies yields a new metric called the Construction Index (CI) of $749.22/94,219 = 0.008$ and its FIDR is $94,219/401,275 = 0.2348$. This consideration yields the CI values for all 21 of the frequently occurring molecules as shown in Table 1.

Name	Detections	FIDR	FI	Min CS	Avg CS	Max CS	CI
Block	94,219	0.23480	2.09	4	749.22	7176	0.0080
Diamond	53,337	0.13292	2.91	13	761.61	9075	0.0143
Tub	10,696	0.02666	5.23	7	746.32	6580	0.0698
Beehive 1	5,839	0.01455	6.10	9	751.77	5677	0.1287
Beehive 2	5,835	0.01454	6.10	12	755.65	6043	0.1295
Boat 1	5,055	0.01260	6.31	10	738.47	7626	0.1461
Boat 2	5,031	0.01254	6.32	8	729.91	7157	0.1451
Boat 3	5,010	0.01249	6.32	7	748.76	6180	0.1495
Boat 4	4,960	0.01236	6.34	10	752.95	6104	0.1518
Barge 1	4,460	0.01111	6.49	16	739.44	6156	0.1658
Barge 2	4,257	0.01061	6.56	13	752.47	5200	0.1768
Yacht-1	3,480	0.00867	6.85	15	757.82	5957	0.2178
Yacht-2	3,474	0.00866	6.85	19	734.44	4779	0.2114
Yacht-3	3,432	0.00855	6.87	19	745.89	5732	0.2173
Yacht-4	3,425	0.00854	6.87	20	768.49	4850	0.2244
Loaf 1	2,042	0.00509	7.62	11	751.93	5757	0.3682
Loaf 2	2,038	0.00508	7.62	27	753.90	5293	0.3699
Loaf 3	1,979	0.00493	7.66	24	755.31	6145	0.3817
Loaf 4	1,963	0.00489	7.68	9	721.81	5885	0.3677
Ship 1	1,855	0.00462	7.76	18	755.12	6218	0.4071
Ship 2	1,853	0.00462	7.76	15	770.63	6157	0.4159

Table 1. Molecular Construction Parameters and FI. There is an inconsistent rise in Min CS values as the FI values increase, however the calculated CI values appear to be correlated with the FI values.

When a scatter plot of CI vs FIDR is produced for all the molecules in Table 1 a high degree of correlation is revealed in Figure 12.

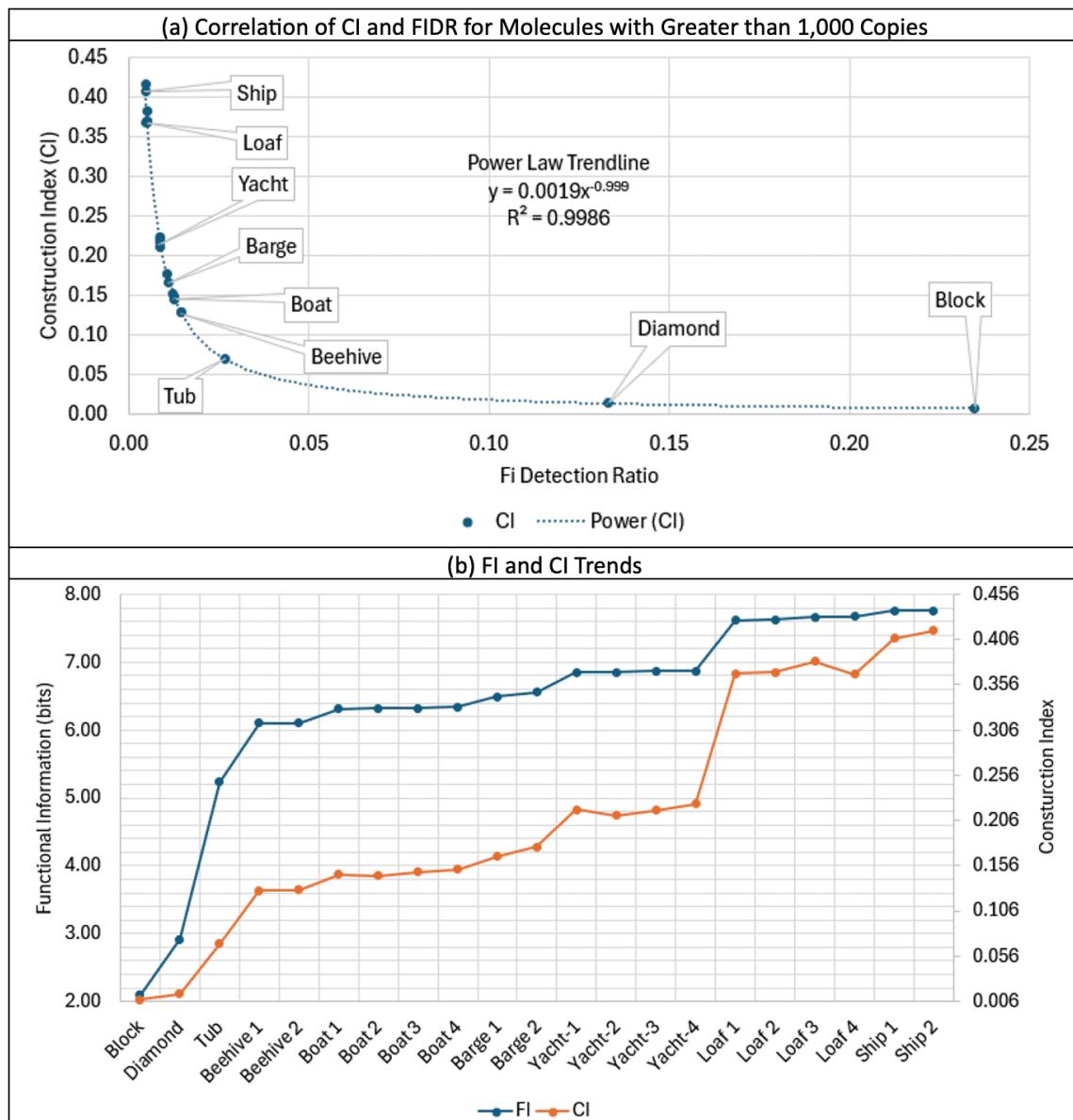


Figure 12. Construction and Functional Information. In (a), to eliminate visual clutter, those molecules with multiple orientations only have their most frequent example labeled. (See Appendix A1 regarding the power law trend in (a) that was discussed regarding Figure 2). Based on this correlation, in (b) the scalar CI values, while not commensurate with the logarithmic FI values and thus shown on a secondary Y-axis, exhibit the same trend toward increasing values.

As the number of copies of a molecule decreases, for example with the several forms of the Loaf and Ship in Figure 12 (b), the CI trend shows more variability. This is a result of a weaker correlation between CI and FIDR and this variability increases as seen in Figure 13 where molecules with greater than 100 copies are included.

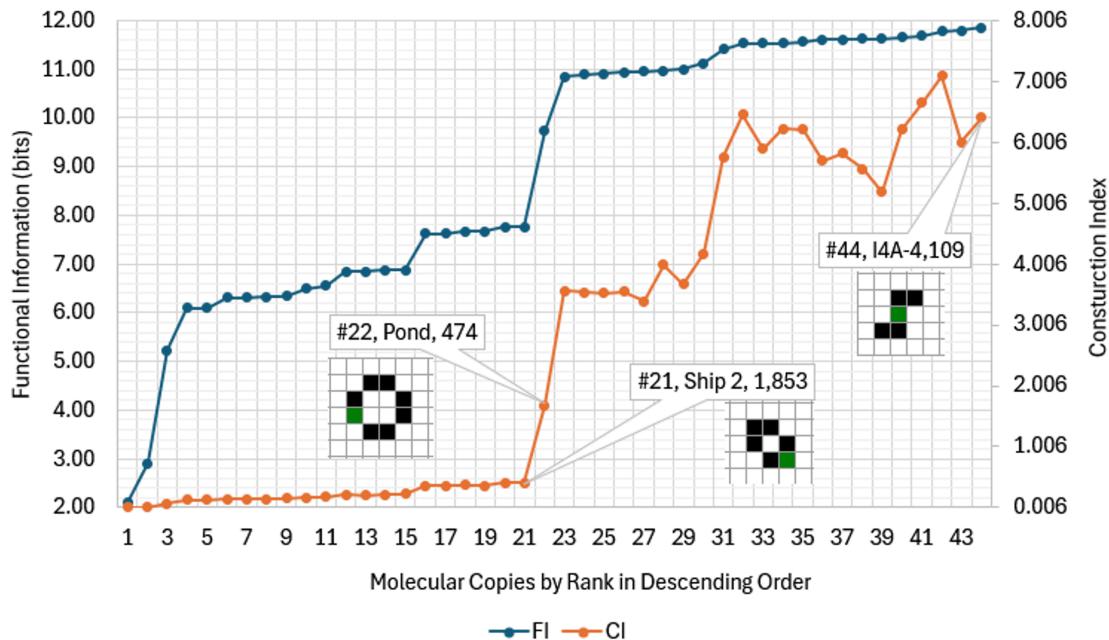


Figure 13. FI and CI Trends for Molecules with Greater than 100 copies. The first 21 molecules are those shown in Figure 12 with greater than 1,000 copies where Ship 2 has 1,853 copies. After the molecule numbered by rank as 22, a GoL Pond, with 474 copies, the variability of the CI trend increases. The final molecule, 44 with the name 'I4A-4' has 109 copies and is a PE molecule belonging to family 4, previously described in Figure 8 as having 3 isometric siblings.

In Appendix 2 additional graphs of FI/CI trends are shown for molecules with greater than 1 copy and a graph for all 351 molecules. Upon examining these graphs, it is obvious that the strength of the correlation between CI and FIDR governs that of the CI trend relative to FI, such as those 21 molecules shown in Figure 12. This observation is supported by the average CS values and their standard deviation for the range of molecules as shown in Table 2.

Molecular Rank	Number of Copies	Average CS	Reference
1 to 21	Greater than 1,000	750 ± 12	Figure 12
22 to 44	100 to less than 1,000	763 ± 58	Figure 13
45 to 208	2 to less than 100	754 ± 346	Appendix 2 Figure A2-1
207 to 351	1 copy	796 ± 616	Appendix 2 Figure A2-2

Table 2. Variation in Construction Steps. The Construction Index (CI) is computed from the average number of Construction Steps (CS) for a molecule divided by its number of copies. As evidenced by the standard deviation shown in the Average CS column, as the number of copies decreases, the correlation between FI and CI trends degrades, resulting in the variability seen in the referenced graphs.

The hypothesis state at the beginning of this section “does a less complex molecule require fewer generations to form during evolution than a more complex molecule?” has been found to be valid within the constraints described in Table 2. A complete list of all 351 molecules (structure and associated construction parameters) in spreadsheet format is available as Supplemental Information (All Molecules.xlsx). Additional aspects of complexity are explored in the next section.

4.3. Complexity and Molecular Geometry

The driven CA in this project produced two types of molecules: CE molecules whose form could exist without the PE atom – many of these are the well-studied GoL still life – and PE molecules that can only exist because of the presence of a PE atom. Figure 14 displays the differences in FI values for these two types of molecules.

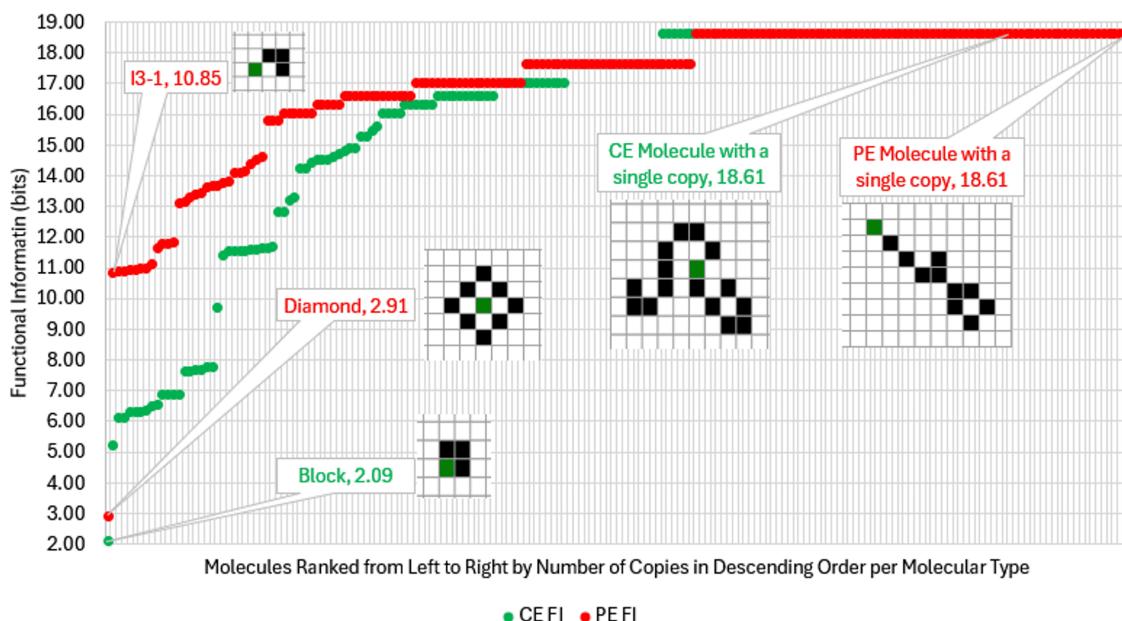
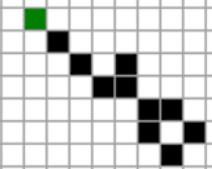
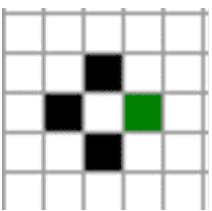
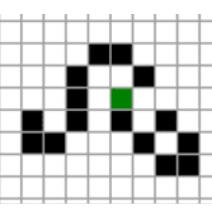
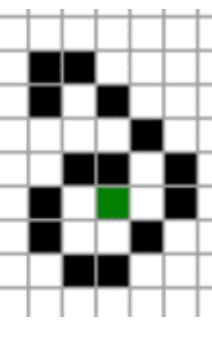
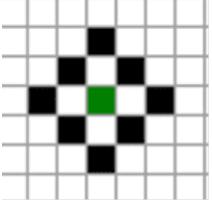
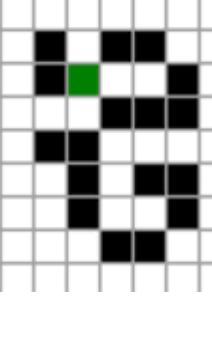


Figure 14. FI values for CE and PE molecules. Of the total 351 molecules 165 are CE and 186 PE. Several of these two types of molecules are shown on the graph. The molecule labeled 'I3-1', first encountered in Figure 6 concerning isomers in families, is typical of many forms in several families where a single bond between a PE and CE atom makes the structure stable; of the 186 PE molecules, 79 exist in this configuration.

Of primary interest in this section are the various geometric forms of molecules and their relationship to the 'binding strength' of the PE Atom due to the STR (Section 2) where it can have as many active canonical neighbors as the B3/S23 rule will allow. Of course, the term 'binding strength' is an analogy for valency in CA and not an inherent property of the atoms themselves since all binding results from the STR over the evolutionary period of the soup in which the molecule is created. How the number of bonds for each PE atom in all 351 molecules affect the final geometric configuration of a molecule and the subsequent FI value is shown in Table 3.

PE Atom Bonds	Molecule Type	Number of Molecules	Range of FI Values in Bits	Least Complex Example	Most Complex Example
1	PE	79	10.85 to 18.61		
2	CE	78	5.23 to 18.61		
3	CE	87	2.09 to 18.61		
4	PE	85	2.91 to 18.61		

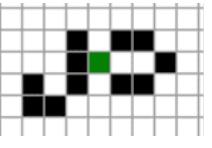
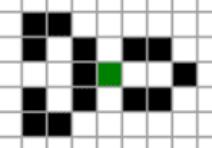
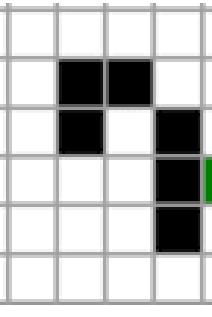
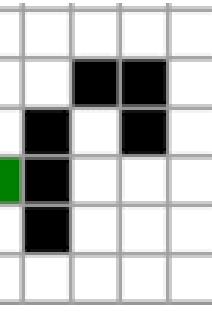
PE Atom Bonds	Molecule Type	Number of Molecules	Range of FI Values in Bits	Least Complex Example	Most Complex Example
5	PE	21	17.03 to 18.61		
6	PE	1	18.61		

Table 3. Complexity and PE Atomic Bonds. All bond values produced molecules with the largest FI values, but the bond values 5 & 6 only were able to produce PE molecules of high complexity compared with the lower bond values. Complexity in this table is quantified by the functional information value in bits.

The largest FI value of all the molecules is 18.61, quantifying the rarity and complexity of a molecule that was created with a single copy out of the 401,275 random soups that created the entire collection of 351. Among all those with this value (18.61), 79 were PE and 64 CE molecules. The fact that CE molecules with an FI value of 18.61 could have been created in the GoL without a perennial atom means that the presence of a perennial atom and its associated 'binding strength' does not contribute to the complexity of a molecule as defined by functional information theory; it does, however, result in a unique geometry for those 79 PE molecules that have only a single bond to their PE atom.

4.4. Frequency of Occurrence Differences of CE Molecules

As noted in Figure 9, PE created several of the top 10 GoL still life with a different rank compared to their GoL rank – supposedly – due to the presence of the perennial cell within the random soups of canonical cells. Table 4 list metrics relevant to addressing the doubt raised in the preceding sentence where the frequency of occurrence given by the FIDR is correlated with the PE rank but not the GoL rank.

Name	FI	CI	GoL Rank	PE Rank	Detections	FI Detection Ratio	GoL Relative Frequency
Block	2.09	0.008	1	1	94,219	0.234799	0.496000
Beehive	6.10	0.129	2	4	5,839	0.014551	0.263000
Loaf	7.62	0.368	3	16	2,042	0.005089	0.077600
Boat	6.31	0.146	4	6	5,055	0.012597	0.071700
Ship	7.76	0.407	5	20	1,855	0.004623	0.049400
Tub	5.23	0.070	6	3	10,696	0.026655	0.016600
Pond	9.73	1.681	7	22	474	0.001181	0.015200
Long Boat	11.57	6.219	8	35	132	0.000329	0.005030
Ship-tie	18.61	1485.000	9	307	1	0.000002	0.002550
Barge	6.49	0.166	10	10	4,460	0.011115	0.001060

Table 4. Rank Variations in PE Compared with the Canonical GoL. The data in this table is sorted by 'GoL Rank' in ascending order and for those molecules with multiple forms it includes only the form with the largest number of copies. The 'GoL Relative Frequency' is from the [LifeWiki](#) of common still life objects. On the referenced web page, the relative frequency is listed, for example with the Block, as '1 in 2.0141' that equals the value 0.496000 shown above; the other values were derived in the same manner.

The first observation from Table 4 is that FI values are not increasing relative to the GoL rank: hence the complexity of a molecule as defined by functional information theory is not increasing with their GoL rank. The effect of the CE vs PE rank is shown in the graphs of Figure 15 for the relevant metrics in Table 4.

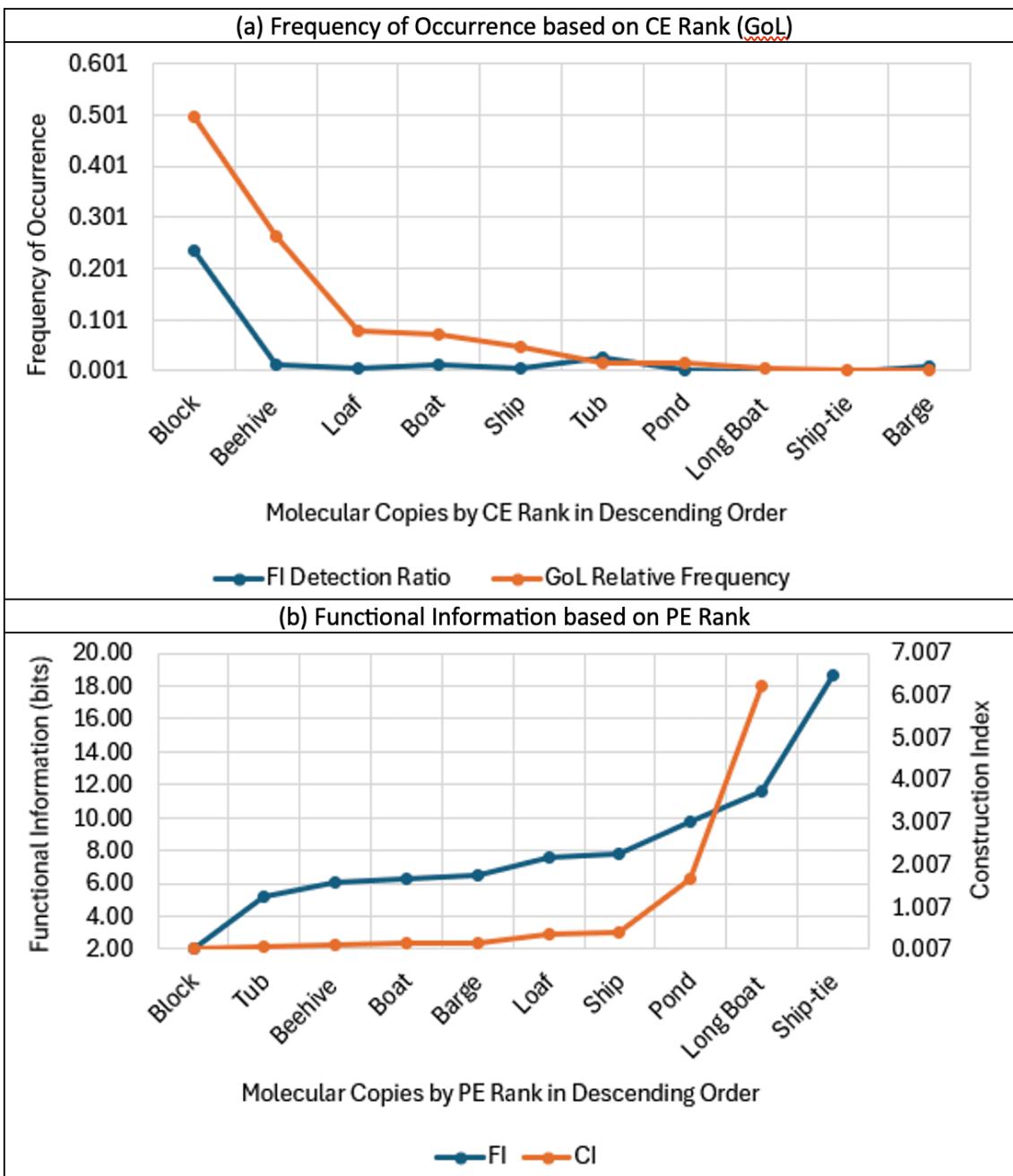


Figure 15. Frequency of Occurrence and FI Trends. In (a) the two trends have a similar trajectory, but the PE FIDR trend is lower for several molecules compared with the GoL relative frequency. In (b) the PE-derived construction index for these molecules has the type of correspondence with the FI values that was previously observed in this research. Note that the CI for the Ship-tie has been omitted since with only a single copy, the average construction steps that allow a CI to be computed aren't representative; the Pond and Long Boat also have a high CI standard deviation due to their low number of copies in Table 4.

The PE FIDR values in Figure 15 (a) reflect the PE frequency of occurrence from the 401,275 initial configurations while the CE rank is determined by the GoL relative frequency based on the evolution of 573,875,593,643,279 soups that produced 7,106,831,604,941,148 still life objects as reported in the [LifeWiki Catalogue](#) with standard GoL evolution governed by the STR B3/S23 rule without a perennial cell. Therefore, the presence of the single perennial atom in the random soups of canonical atoms influenced the self-organization of each soup's evolution in PE. This effect is measured by the dissipation factor (DF), described in Section 2, resulting in each soup on average having a slightly longer period of structure building. In this case, the perennial atom increased the dissipation by approximately 12% relative to the soups without the perennial atom that created the CE version of the structures in Figure 15 (see Appendix 3 for derivation of the 12% value). While it isn't analytically possible to determine the actual contingent events during evolution of these soups that resulted in the PE rank differing from the CE rank, the presence of the perennial cell is the primary cause. I am tempted to say Q.E.D. at this point but the power-law behavior of a cellular automaton's self-organization probably hides additional causal factors that have yet to be discovered, such as the diverse geometry of what I've called molecules. This is work for a future project.

5. Discussion and Outlook

Perennial evolution as analyzed in this project by functional information theory revealed the connection between the information-centric work of the STR, measured by FI in bits, with the average number of construction steps resulting in a stable molecule's frequency of occurrence. While the concept that a function can be equated with the stability of a geometric object might, at first glance, seem trivial, this concept in other work^[32] has proven useful in enabling metrics that quantify complexity. The model created for this project, and the software developed to work with the model, was designed to search for these type correlations. The derivation of a construction index (CI) based on the average construction steps and the number of copies of a molecule is a key metric resulting from the model. As was seen in Table 2, the degree of correlation of CI to FI is dependent on the existence of a large statistical dataset of initial configurations. This fact is always a challenge in working with cellular automata generating stable end states from random initial configurations. One could always desire more data, but this ambition requires extensive computational resources that are often limited by hardware and time. Were the 401,275 initial configurations sufficient? In the case of those molecules shown in Figure 12 with greater than 1,000 copies it proved to be.

The selection bias demonstrated by the collection of molecules with many copies was expected since PE is based on the canonical GoL with a similar bias: the molecules unique to PE were the surprise. The 79 PE molecules that achieved stability via a single bond to the perennial atom (Table 3) certainly appear to exhibit a visually fragile stability, but their high FI values remove observer bias and provide a quantification. In work not yet reported, I created an additional 100 subsets of data that increased the total initial configurations by 96,543. The result of this increase did not change the relative frequency of occurrence of the reported molecules described in this work but did create 35 new molecules. Of these 35 new discoveries 18 were very similar to what had been previously created with a single PE bond; some were simply new isometric forms of previous molecules. Thus, the capacity for diversity in perennial evolution would appear limited, even for those molecules with only a single bond creating stability. While the FI values of molecules will increase with additional subsets of initial configurations, it is not certain that their diversity increases despite an increase in complexity as quantified by functional information theory.

Perennial evolution, as mentioned throughout this work, drives a cellular automaton to longer phases of self-organization due to the catalytic effect of a permanently active cell as described in Figures 2, 7, and 15. This phenomenon could be explored for other models of natural systems and, with the techniques developed in this work, yield insights into their complexity. Consider the molecules created in this project: could two interact to create a bonded pair analogous to the way minerals are formed? For example, minerals form over a long period of geological time during which thermodynamic and gravimetric churning introduce phase changes^[32]. These phase changes could be represented as the conversion of molecules to a fully perennial form as shown in Figure 16. In this state the molecules interact without any soup of canonical cells and form new stable structures.

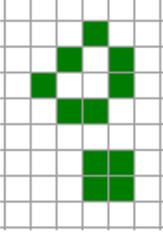
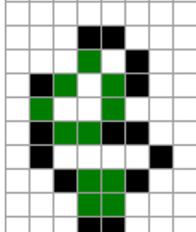
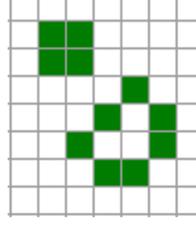
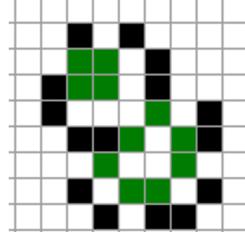
(a) Initial State	(b) End State after 3,099 Generations	(c) Initial State	(d) End State after 78,559 Generations
			

Figure 16. A Loaf and Block as Interacting Molecules. The relative location of the two molecules shown in (a) vs (c) results in different end state structures as well as differences in the length of self-organized construction as measured in generations.

This project has demonstrated one method of application of cellular automata to the quantification of complexity, and future possibilities remain to be explored. Good hunting to all those who share in this quest.

Appendix

A1. Dissipation Factor and Generations

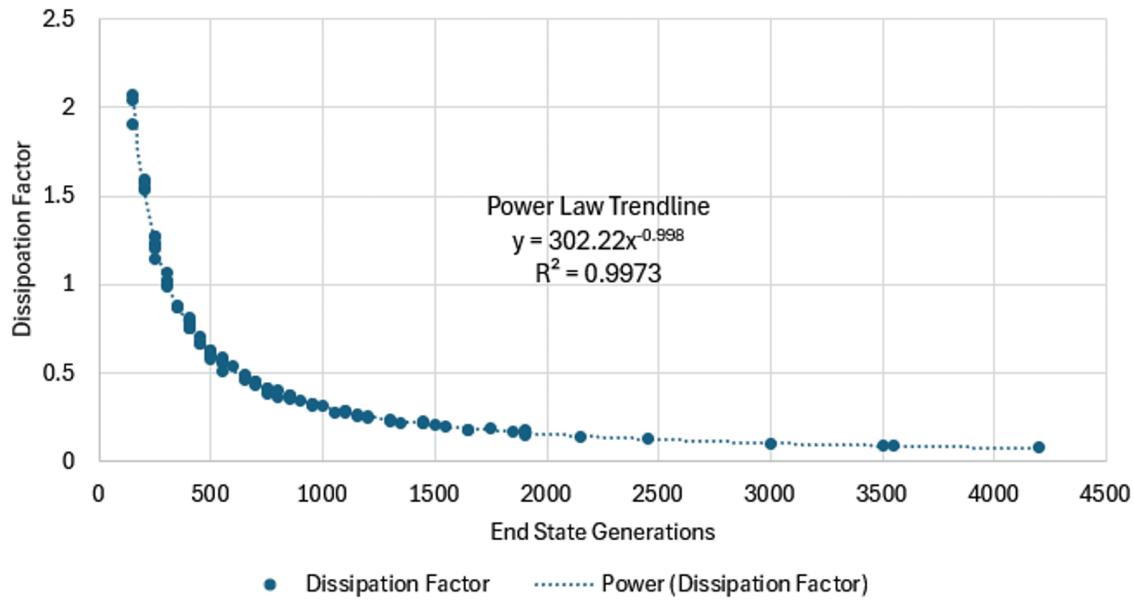


Figure A1-1. Correlation of Dissipation Factor and Generations. The data in this graph is from a subset of 100 of the 94,219 soups that created the Block; each soup evolved to its end state.

In a previous study on PE a dissipation factor (DF) is defined as the difference in the rate per generation of active cells becoming inactive versus inactive cells becoming active over the course of a universe's evolution to a static end state^[14]; for more details see Appendix A1 in the referenced article.

A2. Additional FI/CI Graphs

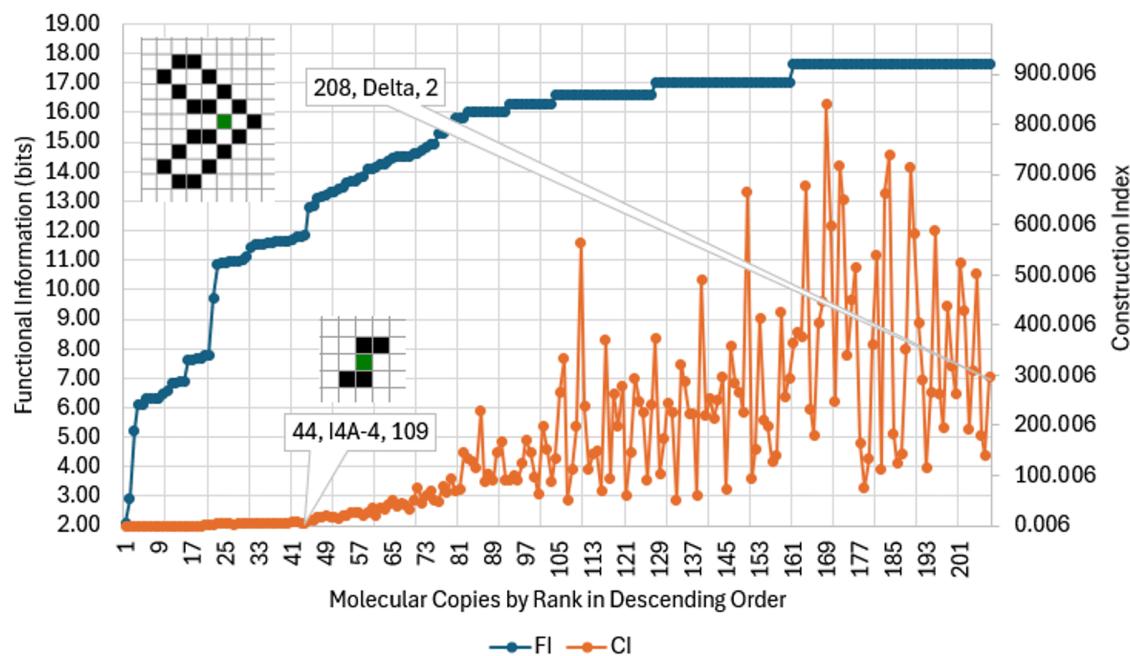


Figure A2-1. FI and CI Trends for Molecules with Greater than 1 copy. This graph shows 208 of the 351 molecules. Number 44 was at the end of the graph in Figure 15 in the main text and number 208, the Delta, is the last of those molecules with greater than 1 copy.

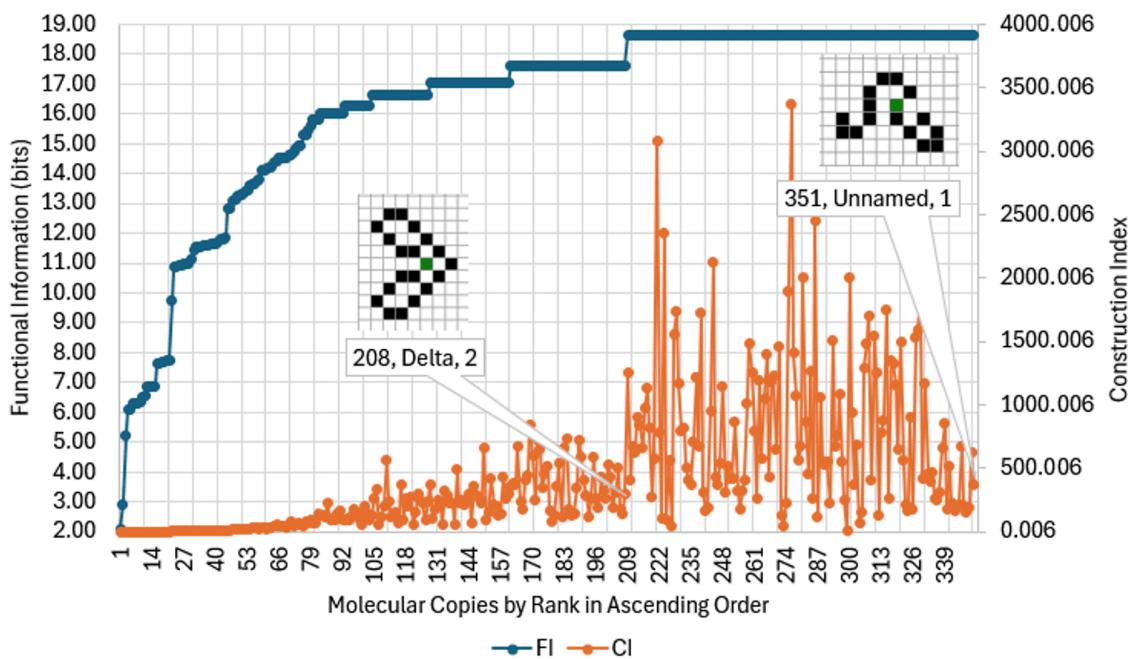


Figure A2-2. FI and CI Trends for Molecules all 351 Molecules. The Delta molecule is the last one on the previous graph, A2-1, and the final molecule, number 351, is unnamed and shown above.

A3. Dissipation Factor Calculations

In section 4.4, where Figure 15's trend of frequently occurring top 10 GoL still life is described, the reference to an 12% increase in dissipation is from the Table A3-1.

GoL Rank	PE Rank	Name	Detections	DDF (%)	DDF Std Dev
1	1	Block	94,219	7.4372	96.1086
2	3	Beehive	5,839	3.0636	106.4108
3	15	Loaf	2,042	4.9605	96.1767
4	5	Boat	5,055	5.6703	101.8834
5	19	Ship	1,855	5.6560	97.0259
6	2	Tub	10,696	6.3793	90.9229
7	22	Pond	474	13.1621	96.6839
8	35	Long Boat	132	16.2559	76.3516
9	307	Ship-tie	1	53.4264	0.0000
10	9	Barge	4,460	4.1806	99.5850

Table A3-1. Differential Dissipation Factors (DDF). The average DDF for all the soups is 12.02%.

DDF is computed by measuring the DF rate for each soup that created a molecule above by reconstructing the soup as a pair of soups, one with and the other without the perennial atom, and $DDF\% = ((DF_{SOUP} - DF_{SOUP + PE\ ATOM}) / DF_{SOUP}) * 100$. The Ship-tie skews the average slightly higher since many soup pairs are needed to provide a representative average value. See [14] for examples concerning the origin, use, and meaning of DDF as an analytical metric.

Statements and Declarations

Funding

No specific funding was received for this work.

Potential competing interests

No potential competing interests to declare.

Data and Code Availability

The software and source code developed for this project are open-source and available for download via [GitHub](#).

Use of AI in Research

Google's Gemini large language model was used to discover peer-reviewed resources for a portion of this research.

Footnotes

¹ This quotation, attributed to Mark Twain, has a deeper history – see [Bartleby](#).

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Supplementary data: available at <https://doi.org/10.32388/HX4713>

Declarations

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