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 complex 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 an automaton by keeping a single cell in a permanently (perennial) active state. After interacting with over 400,000 initial configurations of randomly placed standard automata cells surrounding the perennial cell, hundreds of unique and geometrically complex 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 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 frequently 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

Quantifying complexity created by the emergence of self-organized structures in nature tax the analytical tools of science. In a seminal review by Rupe & Crutchfield[1] they comment that “After more than a century of concerted effort, physics still lacks basic principles of spontaneous self-organization”. Identifying the control parameters is often where the hard work begins in understanding these systems where self-organization 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. Examples of CA applications include traffic flow[2], fluid dynamics[3],

biology[4], urban planning[5], epidemiology[6], self-reproduction[7], artificial chemistry[8], quantum mechanics[9] and autopoiesis and multicellularity[10].

In previous research[11] I demonstrated how a modified version of Conway's Game of Life (GoL)[12], 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"[13] 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 extending the system's dissipative action due to the physics of its state transition rule (STR) [14]. 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[15] eventually gave birth, over cosmological ages, to minerals that formed the geospheres of planets[16] in continuing phases of structure building[17]. When these structures, considered as artificial molecules, and their history of formation are analyzed by the methods of functional information (FI) theory[18], 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.

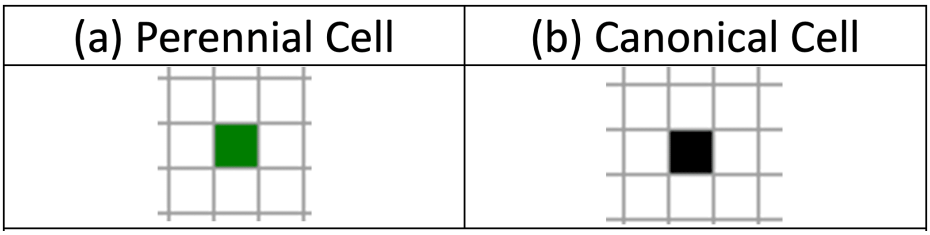


**Figure 1. Atomic Components.** Two building blocks for construction of artificial molecules in PE. The terms 'cell' and 'atom' will be used interchangeably in this model.

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.

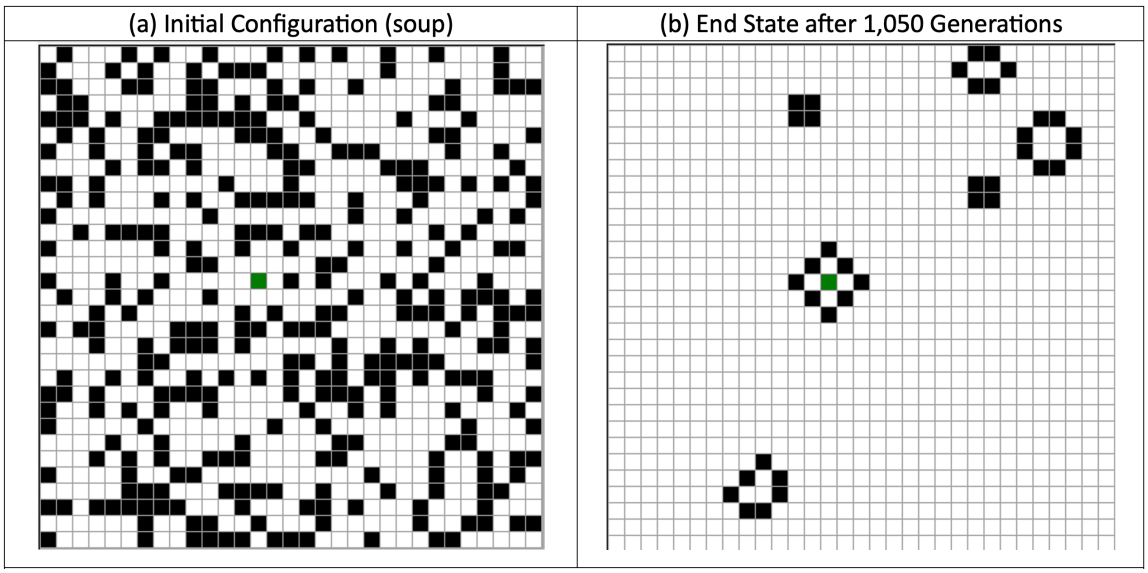


**Figure 2. Perennial Evolution**. A single perennial atom within a random soup of canonical atoms in (a) evolves after 1,050 generations to a static density in (b) creating a stable structure modeled as a molecule that could not exist without the perennial cell; this PE molecule at the center of the grid is named a 'Diamond'. Several other classic CE still life also appear at the end state. 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[19]. 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[20] and the initial soup density is in the range where self-organized criticality is optimal[21][22]. 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.

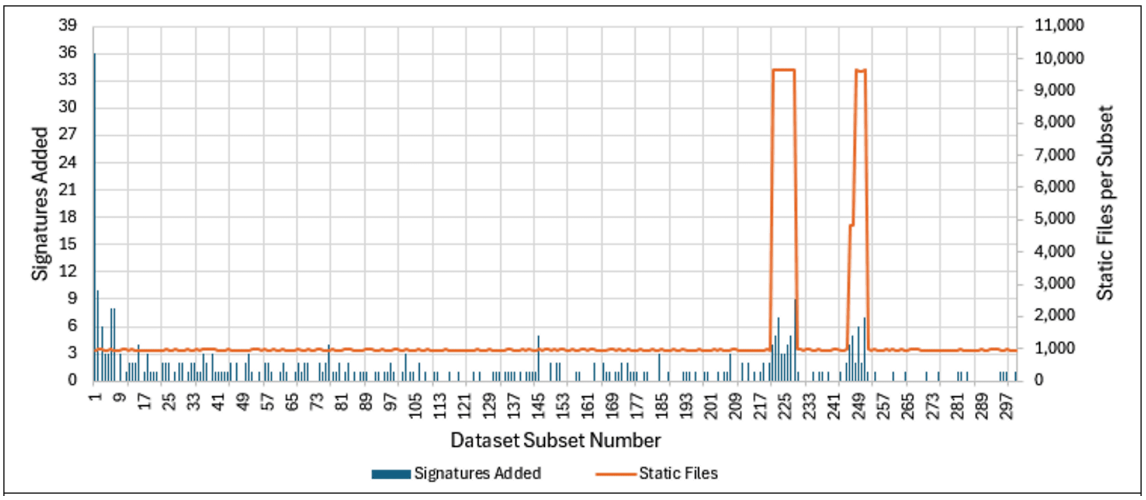


**Figure 3. Discovery of Molecular Signatures.** The first subset discovered 36 molecules, and the subsequent number discovered rapidly declined. Subsets 1 to 220 each contained 1,000 initial soups and some subsets following this range had a larger number of soups as can be seen by the number of static 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.

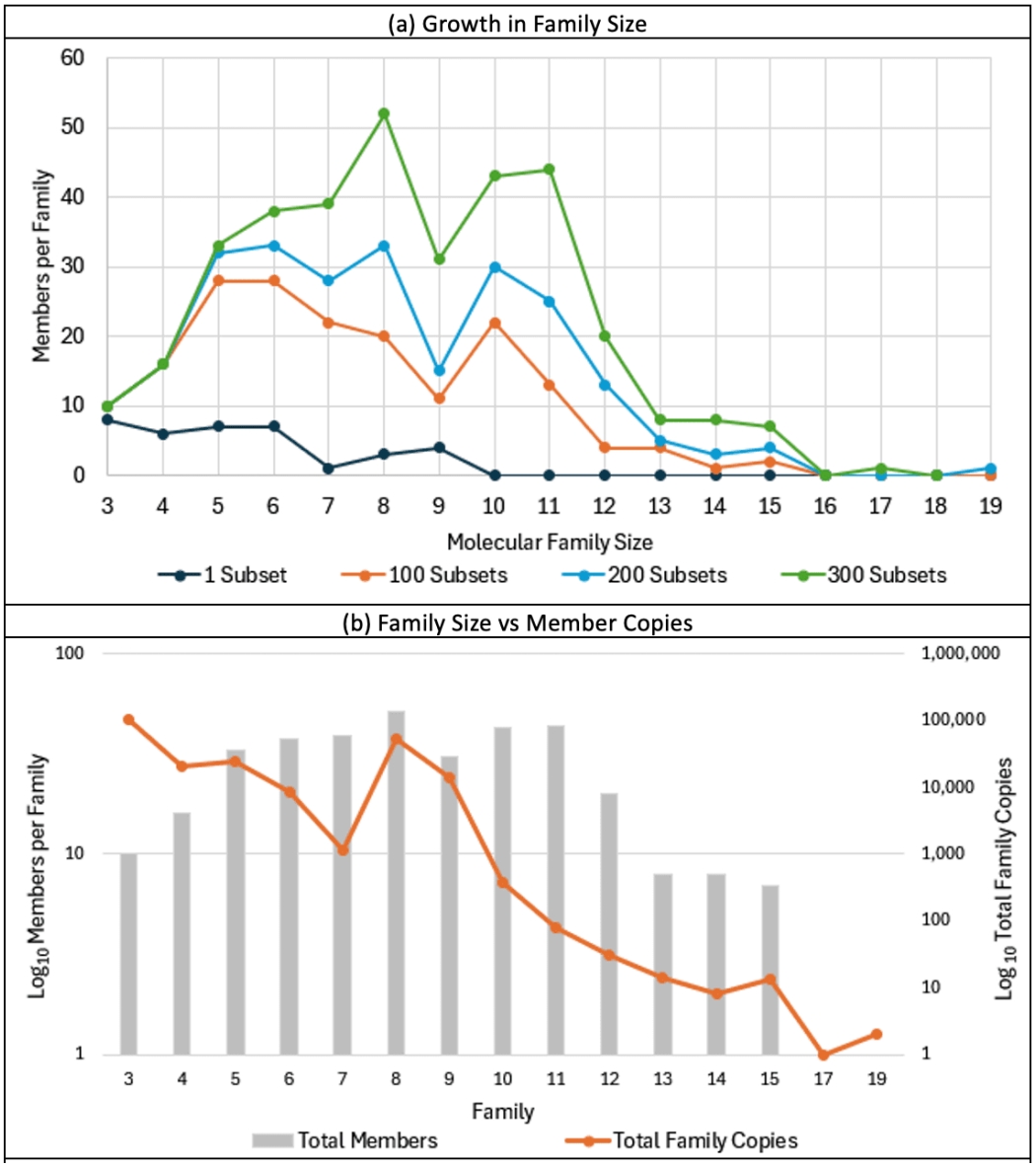


**Figure 4. Family Statistics**. In (a) 351 molecular-like structures were gradually created per subset with 186 qualified as PE atoms; the family sizes 16 and 18 are shown only to emphasize that they contained no structures. In (b) any correlation between the number of copies of molecules per family 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.


doi.org/10.32388/HX4713.2

### *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.

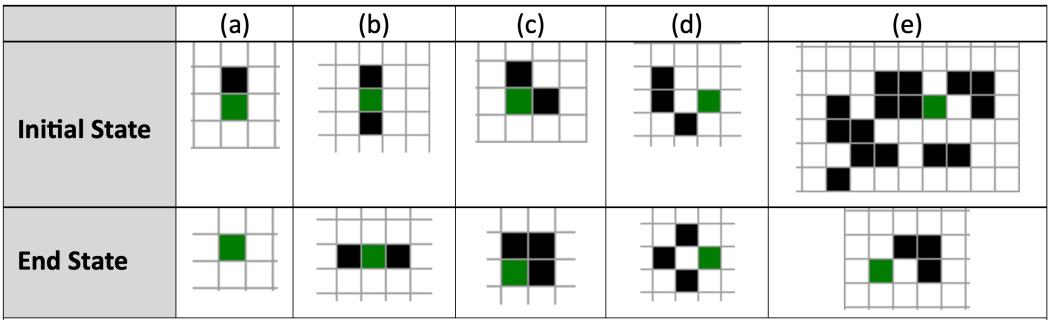


**Figure 5. Minimum Molecular Size.** In (a) the end state is not a molecule. In (b) this structure becomes the classic period 1 oscillator known as a Blinker in CE and is thus not stable nor qualifies as a molecule. In (c) a stable Block is formed and in (d) a stable Tub. The end state of (a) through (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 initial state shown 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.


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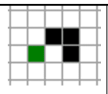
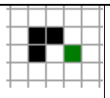
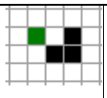
| Molecular Structure |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| **Copies Created** | 217 | 211 | 209 | 204 | 202 | 201 | 197 | 181 |
| **Bond Location** | NE | SW | SW | NE | SE | NW | SE | NW |

**Figure 6. Family $P_1C_3$ 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., $P_1C_3$, 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.

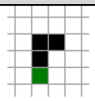
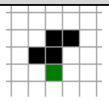
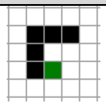
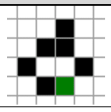
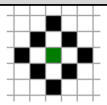
| Initial State | Generation 1 | Generation 2 | Generation 3 | ..... | End State at 168 Generations |
|---|---|---|---|---|---|
|  |  |  |  | ..... |  |

**Figure 7. Nonstable Hypothetical $P_1C_3$ 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 the evolution shown in Figure 7 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. In this context the single PE atom acts as a catalysis within the CA universe of potential canonical atoms, reacting at a rate governed by the STR.

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 by the possible number of isometric forms that can exist for other families as seen in Figure 8.


doi.org/10.32388/HX4713.2

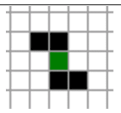
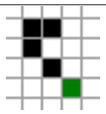
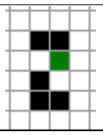
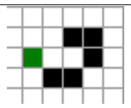
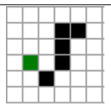
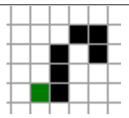
| Family | $P_1C_4$ | | $P_1C_5$ | | | $P_1C_6$ |
|---|---|---|---|---|---|---|
| Molecular Structure |  |  |  |  |  |  |
| PE Atom? | True | True | False | True | True | False |
| Forms Detected | 4 | 8 | 4 | 8 | 8 | 8 |

**Figure 8. Isometric Molecules**. In family $P_1C_4$ 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 of analysis.

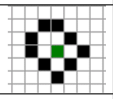
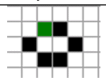
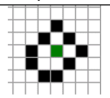
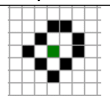
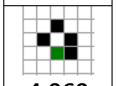
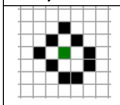
| Family | 3 | 8 | 3 | 5 | 4 | 5 | 9 | 6 | 5 |
|---|---|---|---|---|---|---|---|---|---|
| Molecule |  |  |  |  |  |  |  |  |  |
| Name | Block | Diamond | Tub | Beehive | Boat | Barge | Yacht | Loaf | Ship |
| PE Rank | 1 | 2 | 3 | 4 | 6 | 10 | 12 | 16 | 20 |
| GoL Rank | 1 | n/a | 6 | 2 | 4 | 10 | 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 relative frequency described in the LifeWiki and applies to all orientations. *The 'Yacht', whose GoL name is 'Barge Siamese Loaf' is not used because I needed a shorter monicker for ease of reference.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PE did produce many CE structures within the top 10 frequently occurring GoL still life though in a slightly different order relative to their GoL rank. 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[23] 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:

$$I(E_X) = -\log_2[F(E_X)] \tag{1}$$

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, defining 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[24] with $\geq 3$ 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[25]. 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”[18][26]. This activity of the environment is shown in Figure 10 where the FI values for each of the 351 molecules are displayed.

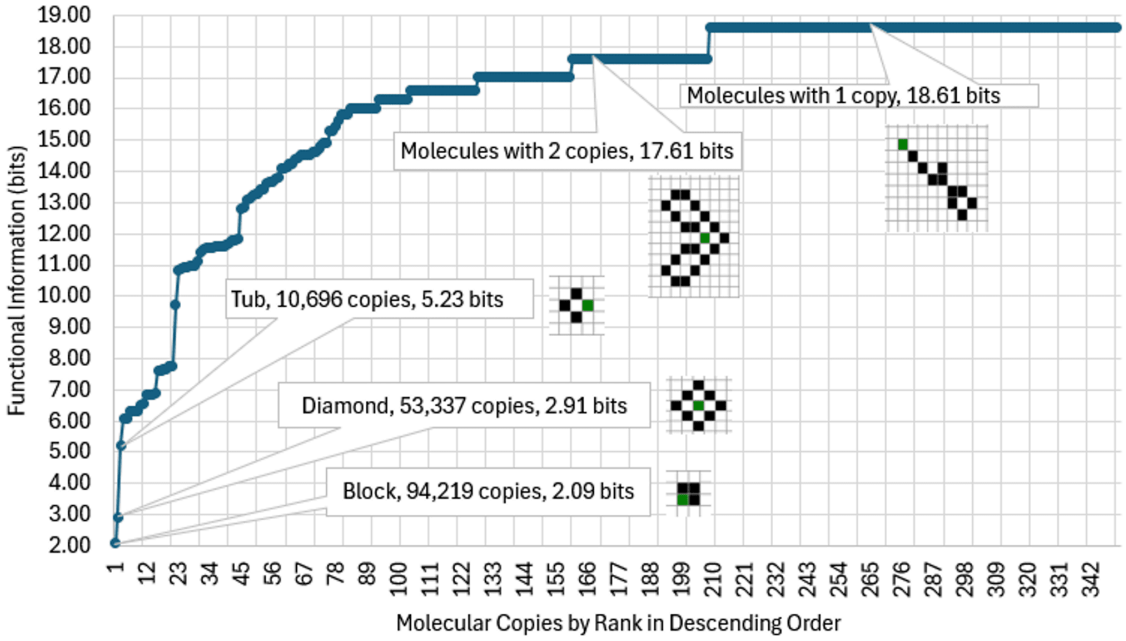


**Figure 10. Functional Information for all CE and PE Molecules.** Three of the most frequently occurring molecules are shown along with two of the less frequent to visually illustrate the differences in complexity. The Diamond and the two molecules shown with 2 copies and 1 copy are among the 186 PE 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. i.e., the 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.

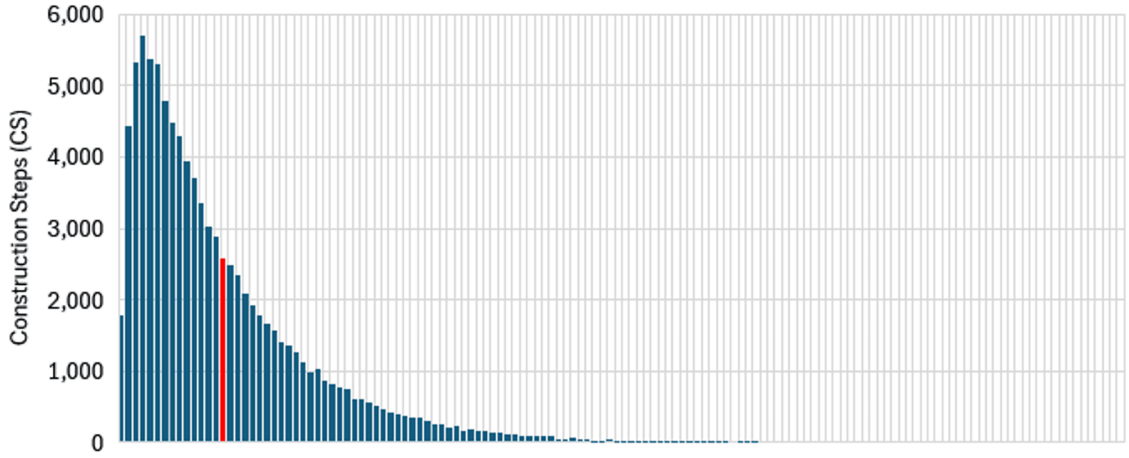


**Figure 11. Block's CS Values**. The minimum CS is 4 and the maximum 7,171 with an average of 749.22 generations as shown by the red column in the histogram. This result represents the range of CS values for all 94,219 random soups that created the Block. The histogram's horizontal axis contains bins 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[27], i.e., the shortest program description[28] 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 Fi values that increase as a molecule's complexity increases. However, a minimum CS value is only one instance of evolution, but the FI 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


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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 | 7,176 | 0.0080 |
| Diamond | 53,337 | 0.13292 | 2.91 | 13 | 761.61 | 9,075 | 0.0143 |
| Tub | 10,696 | 0.02666 | 5.23 | 7 | 746.32 | 6,580 | 0.0698 |
| Beehive 1 | 5,839 | 0.01455 | 6.10 | 9 | 751.77 | 5,677 | 0.1287 |
| Beehive 2 | 5,835 | 0.01454 | 6.10 | 12 | 755.65 | 6,043 | 0.1295 |
| Boat 1 | 5,055 | 0.01260 | 6.31 | 10 | 738.47 | 7,626 | 0.1461 |
| Boat 2 | 5,031 | 0.01254 | 6.32 | 8 | 729.91 | 7,157 | 0.1451 |
| Boat 3 | 5,010 | 0.01249 | 6.32 | 7 | 748.76 | 6,180 | 0.1495 |
| Boat 4 | 4,960 | 0.01236 | 6.34 | 10 | 752.95 | 6,104 | 0.1518 |
| Barge 1 | 4,460 | 0.01111 | 6.49 | 16 | 739.44 | 6,156 | 0.1658 |
| Barge 2 | 4,257 | 0.01061 | 6.56 | 13 | 752.47 | 5,200 | 0.1768 |
| Yacht-1 | 3,480 | 0.00867 | 6.85 | 15 | 757.82 | 5,957 | 0.2178 |
| Yacht-2 | 3,474 | 0.00866 | 6.85 | 19 | 734.44 | 4,779 | 0.2114 |
| Yacht-3 | 3,432 | 0.00855 | 6.87 | 19 | 745.89 | 5,732 | 0.2173 |
| Yacht-4 | 3,425 | 0.00854 | 6.87 | 20 | 768.49 | 4,850 | 0.2244 |
| Loaf 1 | 2,042 | 0.00509 | 7.62 | 11 | 751.93 | 5,757 | 0.3682 |
| Loaf 2 | 2,038 | 0.00508 | 7.62 | 27 | 753.90 | 5,293 | 0.3699 |
| Loaf 3 | 1,979 | 0.00493 | 7.66 | 24 | 755.31 | 6,145 | 0.3817 |
| Loaf 4 | 1,963 | 0.00489 | 7.68 | 9 | 721.81 | 5,885 | 0.3677 |
| Ship 1 | 1,855 | 0.00462 | 7.76 | 18 | 755.12 | 6,218 | 0.4071 |
| Ship 2 | 1,853 | 0.00462 | 7.76 | 15 | 770.63 | 6,157 | 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.


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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.

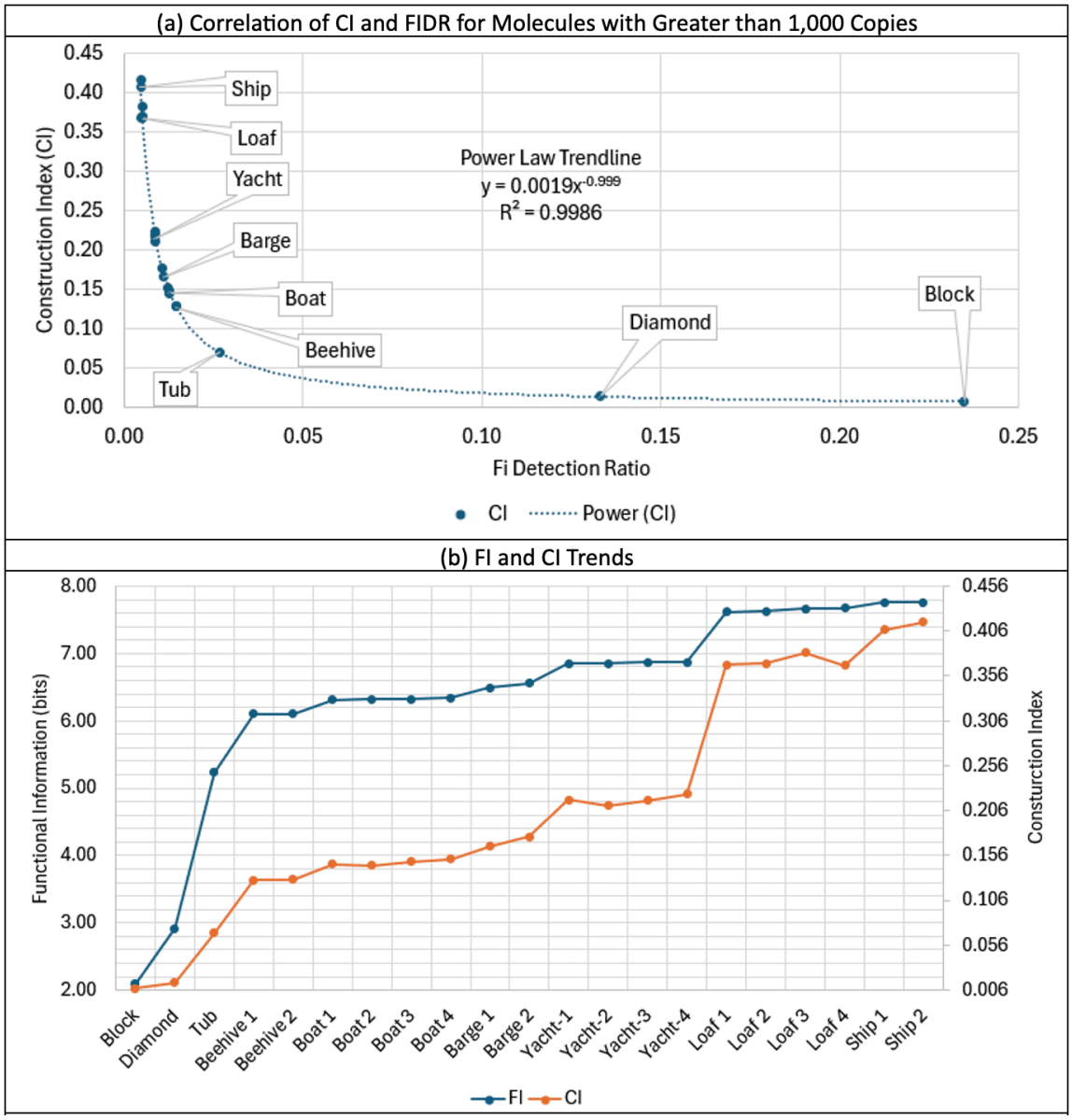


**Figure 12. Construction and Functional Information**. In (a), to eliminate visual clutter, those molecules with multiple orientations only have their most frequent example labeled. (See Appendix A1 regarding the power law trend in (a) that was discussed regarding Figure 2). Based on this correlation, 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.


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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.

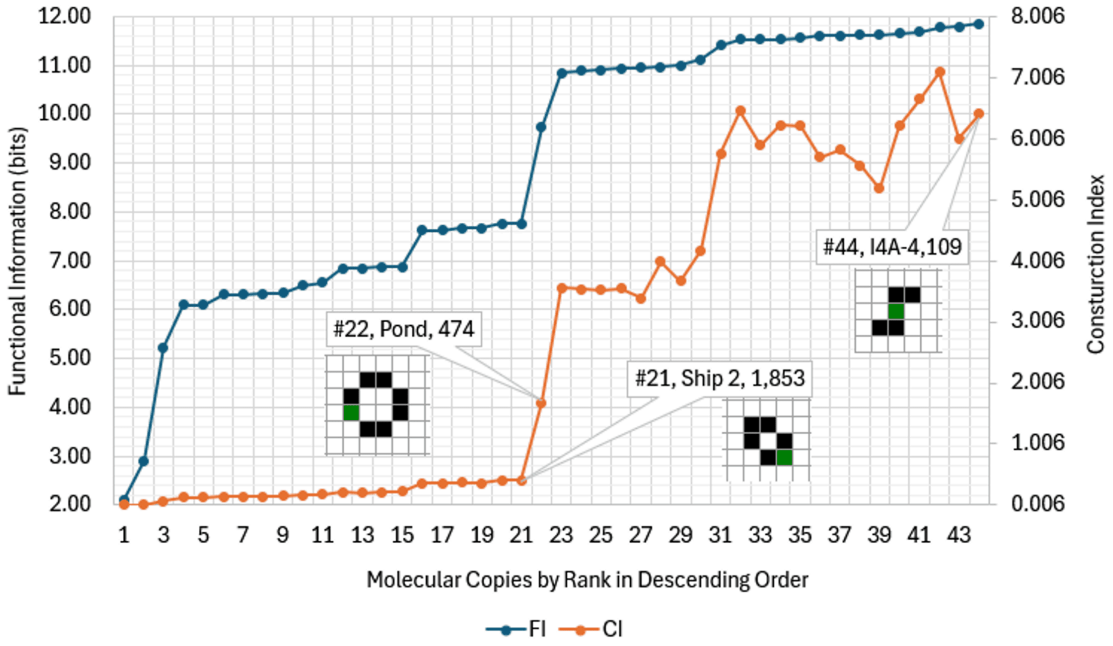


**Figure 13. FI and CI Trends for Molecules with Greater than 100 copies.** The first 21 molecules are those shown in Figure 12 with greater than 1,000 copies where Ship 2 has 1,853 copies. After the molecule numbered by rank as 22, a GoL Pond, with 474 copies, the variability of the CI trend increases. 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.


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| 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 stated 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.


doi.org/10.32388/HX4713.2

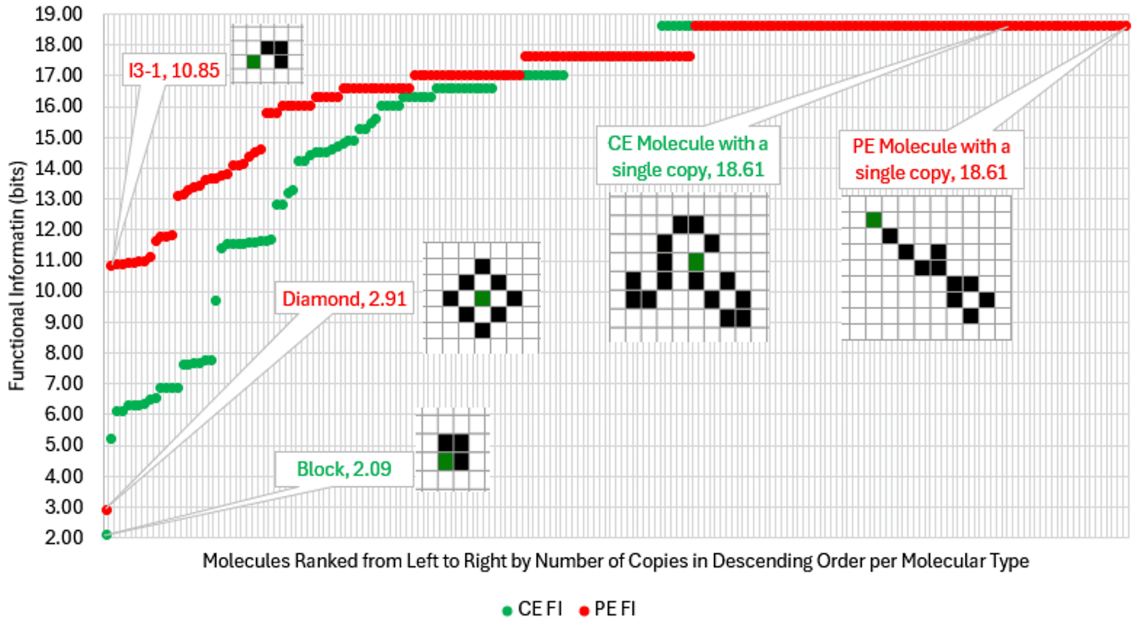
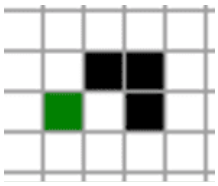
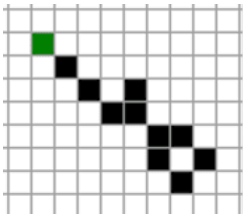
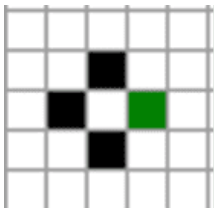
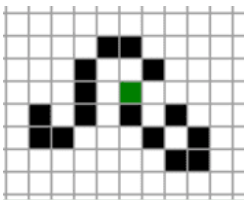
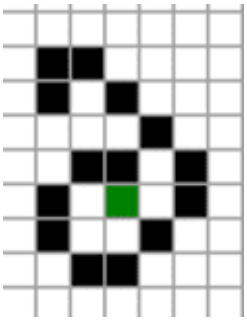
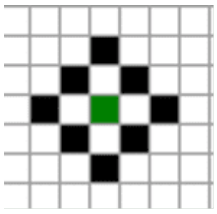
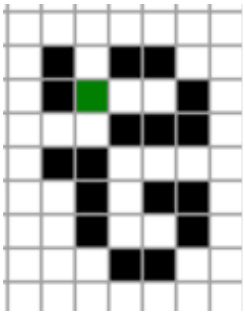



**Figure 14. FI values for CE and PE molecules.** Of the total 351 molecules 165 are CE and 186 PE. Several of these two types of molecules are shown on the graph. The molecule labeled 'I3-1', first encountered in Figure 6 concerning isomers in families, is typical of many forms in several families where 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.


doi.org/10.32388/HX4713.2

| 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 |  |  |


doi.org/10.32388/HX4713.2

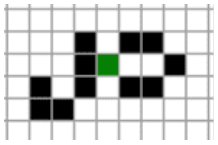
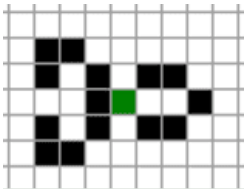
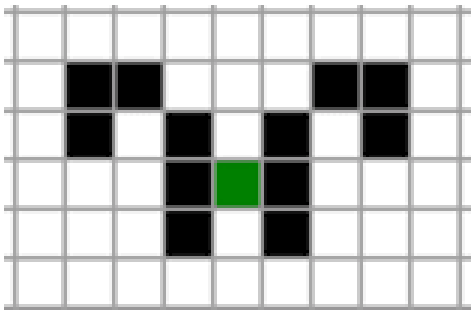
| PE Atom Bonds | Molecule Type | Number of Molecules | Range of FI Values in Bits | Least Complex Example | Most Complex Example |
|---|---|---|---|---|---|
| 5 | PE | 21 | 17.03 to 18.61 |  |  |
| 6 | PE | 1 | 18.61 |  | |

**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. Complexity and Frequency of Occurrence*

As noted in Figure 9, PE created several of the frequently occurring GoL still life with a different rank, i.e., frequency of occurrence, compared with their GoL rank. To apply the GoL's community ranking scheme (LifeWiki) to the PE-generated CE molecules that have several orientations, they must be represented by the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sum of each orientations number of copies. This refactoring results in a different ranking from Figure 9 but allows the top 10 most frequently occurring GoL-created molecules to be compared with the top 10 created in PE as seen in Table 4.

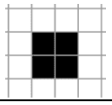
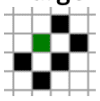
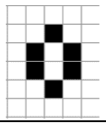
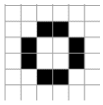
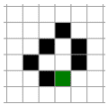
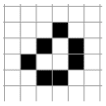
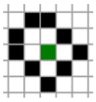
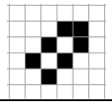
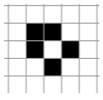
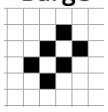
| Top 10 Rank | GoL | PE | GoL Rank | Top 10 Rank | GoL | PE | GoL Rank |
|---|---|---|---|---|---|---|---|
| 1 | Block  | Block  | 1 | 6 | Tub  | Barge  | 10 |
| 2 | Beehive  | Boat  | 4 | 7 | Pond  | Loaf  | 3 |
| 3 | Loaf  | Yacht  | 134 | 8 | Long Boat  | Ship  | 5 |
| 4 | Boat  | Beehive  | 2 | 9 | Ship-tie  | Mango  | 12 |
| 5 | Ship  | Tub  | 6 | 10 | Barge  | Pond  | 7 |

**Table 4. Rank Variations in PE-Generated CE Molecules.** The 'Top 10 Rank' column applies to both the 'GoL' and 'PE' columns while the 'GoL Rank' column governs only the PE-generated molecules, displaying differences with their equivalently ranked GoL-created molecule. The only common rank is for the Block, and the Ship-tie and Long Boat were not among the top 10 for PE that instead included a Yacht and Mango.

The results of metric consolidation for molecules with multiple orientations demonstrate that the correlation between FI and CI is maintained like that previously seen and is presented in Figure 15.


doi.org/10.32388/HX4713.2

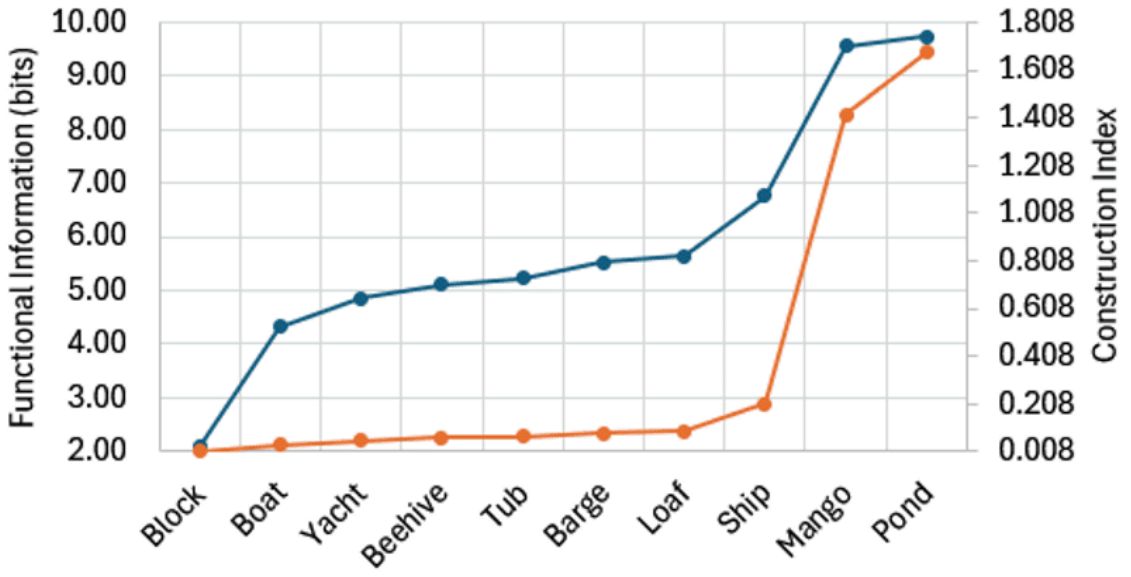



**Figure 15. Top 10 PE-Generated CE Molecules.** Note that the Diamond, a PE molecule, is missing from this graph since it only shows CE molecules. If the Diamond were included, it would be 2nd in rank after the Block. (See Appendix A3 for the metrics that created this graph.)

While the FI/CI correlation of Figure 15 quantifies complexity relative to the computational work done by the STR in bits and the construction steps by the CI metric, it doesn't explain why the PE rank differs from the GoL rank and why the Block is ranked #1 in both lists. The presence of the perennial atom in the PE-generated CE molecules is responsible for these differences, but how does it have this effect? The explanation is given as follows: a CA with deterministic rules but an evolution contingent on the interaction of every cell in the CA universe with each of its eight neighbors at each discrete generation of the evolution demonstrates a particular type of contingent behavior. This contingency is described in the context of paleontological history as "...a thing unto itself, not the titration of determinism by randomness"[29]. In this view of biology, evolution is driven by random genetic mutations with natural selection acting as a *filter* allowing reproductively successful mutations to survive. In the context of a driven CA, the single PE atom also functions as a type of filter by acting as an *attractor*, gathering canonical cells to form stable structures in the region of the CA universe in which it is located. This attraction results in changing the dynamics of construction in the area around the PE atom while the dynamics in the rest of the universe follow the canonical GoL rules as stated in the model definition in Section 2.

An example of this attractive effect of a perennial atom is demonstrated during the construction of the Block, ranked #1 in both the Gol and PE, the least complex according to FI theory at 2.09 bits, and occurring 94,219 times in this project, formed with a minimum of 4 construction steps and a maximum of 7,171 from random

soups. Using a heat map designed for this project's software to track the state transition (active-to-inactive or inactive-to-active) of each cell in the CA universe at each generation of evolution, a measure of the percentage of evolutionary time a cell is active illustrates the attraction as shown in Figure 16.

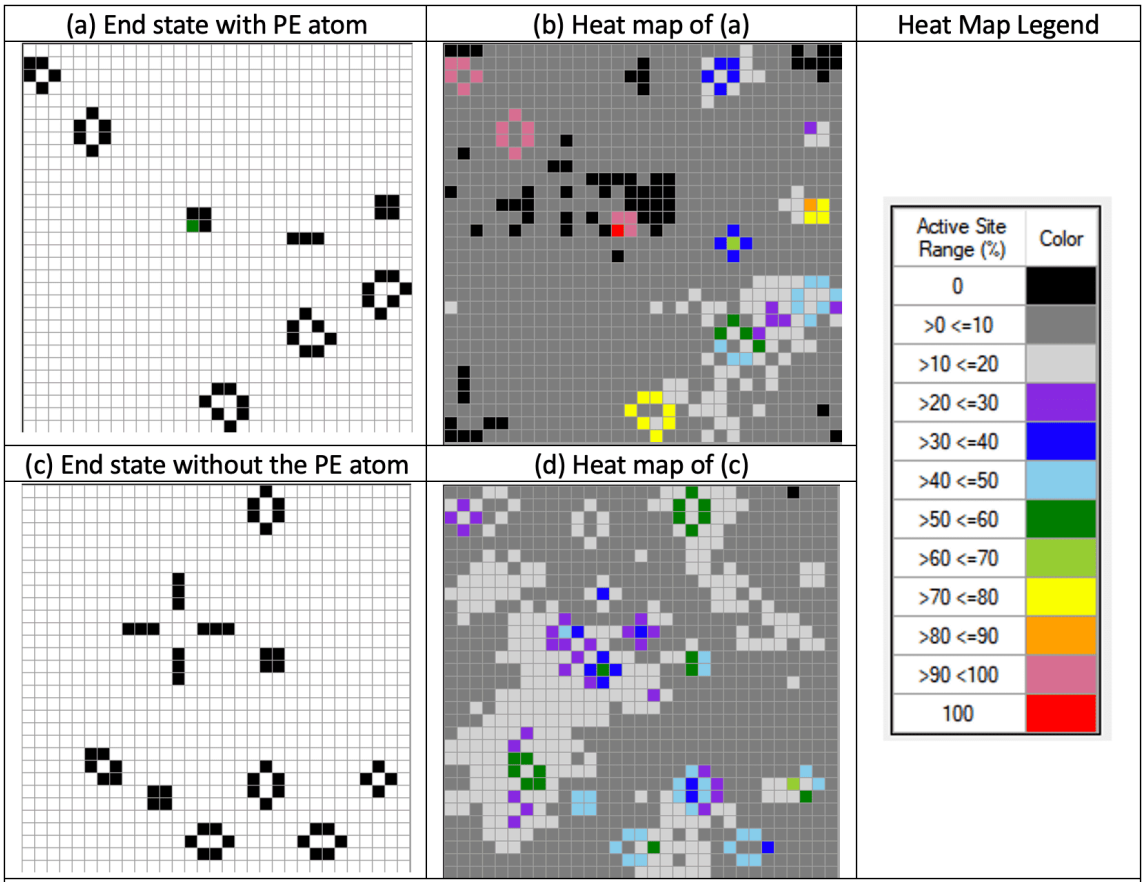



**Figure 16. PE Block's Minimum Construction Steps.** In (a) the Block formed in 4 generations and remained stable until the end state of 200 generations. The PE atom in (a) was active during all generations and thus its activity as measured by the heat map was 100%. The three canonical atoms that are part of the PE Block were also active in the a range of over 90% to slightly less than 100%. The cells black in color near the Block in the heat map are evidence that once the Block formed at generation 4, it was somewhat isolated from the interactions occuring elsewhere in the universe. In (c) the same soup as (a) *without* the PE atom created a different pattern of structures after 350 generations without any cells having activity as high as those in (b).

The next graph, Figure 17, shows the Block being constructed with the maximum number of construction steps.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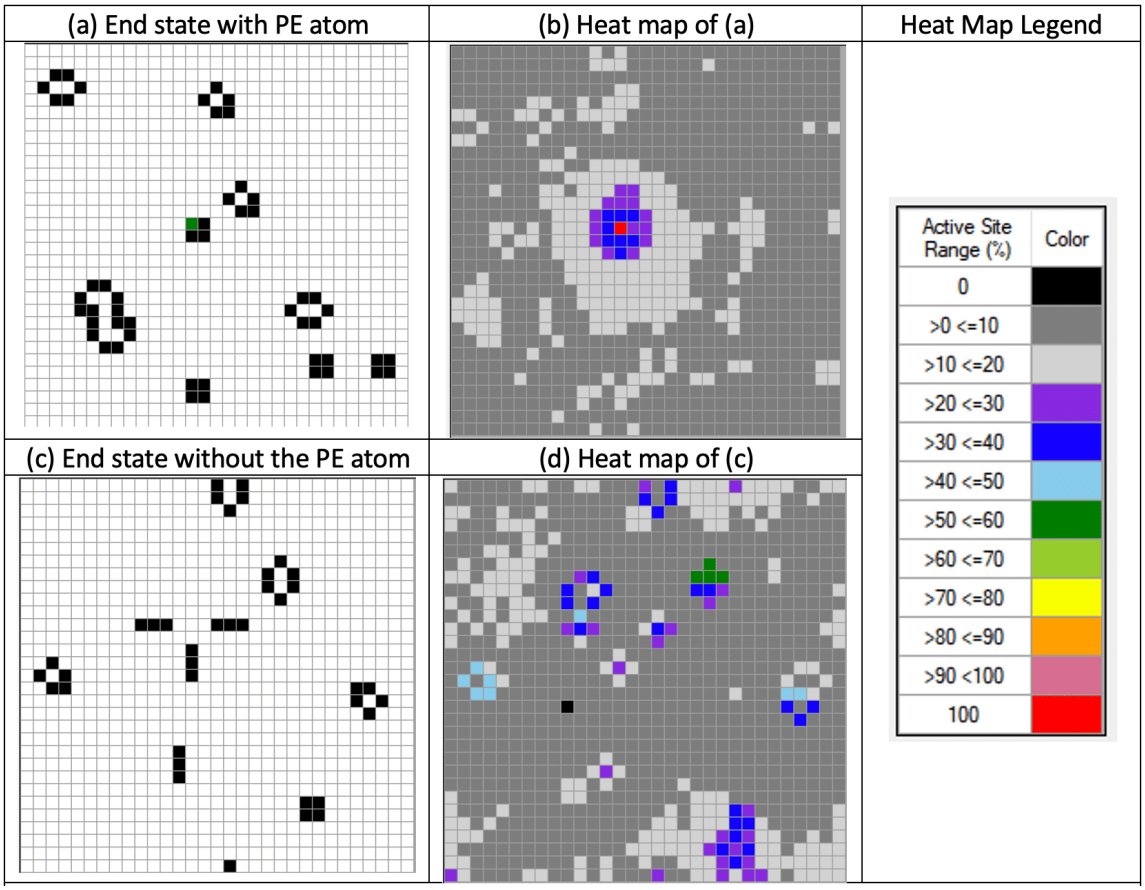


**Figure 17. PE Block's Maximum Construction Steps.** In (a) the end state occurred after 7,171 generations with the the PE atom's attractive effect in (b) more obvious than that shown in Figure 16. In (c) the end state was reached in 450 generations without the PE atom in the soup.

The effect of a single PE atom in Figure 16 & 17 – both its presence and absence – demonstrates that PE contingency is "a thing unto itself" where the end state is unpredictable, but the attractive effect of a PE atom is clear, changing the dynamics of self-organization around the PE atom as compared with the rest of the universe. This change in dynamics is illustrated in the example of the Block forming after 4 generations shown in Figure 16, and the actual dynamic differences are illustrated in Figure 19.


doi.org/10.32388/HX4713.2

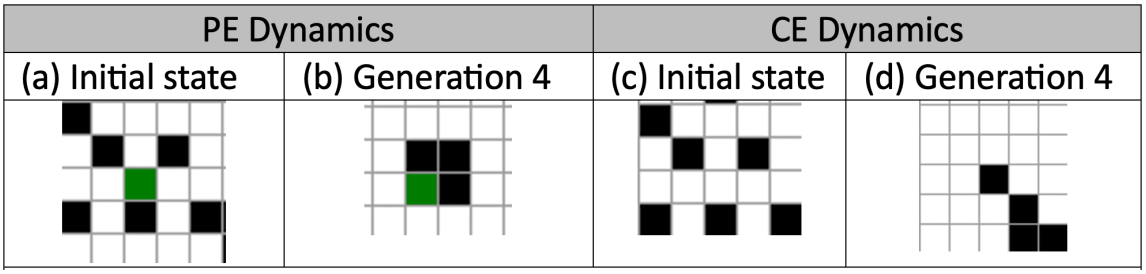


**Figure 19. Block Construction.** In (a) only the region in the soup around the PE atom is shown and the Block is constructed at generation 4 in (b) and remains stable until the end state. The same soup in (c) without the PE atom has a different evolution as seen in the end state shown in Figure 16 (c).

A more explicit example of dynamic differences is given in Figure 20.

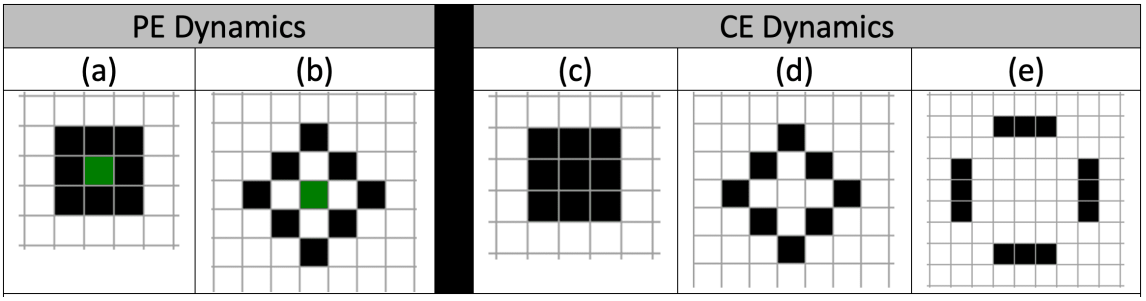


**Figure 20. Construction Dynamics.** A possible initial state around the region of the PE atom in (a) creates a PE Diamond in a single generation of evolution in (b). In (c) a similar initial state as in (a) without the PE atom creates the unstable structure in one generation in (d) that becomes a GoL oscillator in (e) after 5 generations known as a 'Traffic Light'.

The fact that the Block ranks #1 in both the GoL and PE could be stated using Darwinian terminology as 'survival of the least complex' and the other PE-generated CE molecules 'survived' and are ranked according to their complexity. But this explanation is given after the simulations have been performed in the CA since the contingent nature of evolution doesn't permit prediction. Thus, the concept of rank is an *a posteriori* concept like 'fitness' in biological evolution[30] and explaining rank differences beyond the attractive effect of a PE atom will require new insights beyond FI theory to formulate.


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## 5. Discussion and Outlook

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[31] has proven useful in developing metrics that quantify complexity for evolving systems with many interacting components. Perennial evolution is one such system and the analysis presented in this project by functional information theory revealed a correlation between the information-centric work of the STR measured in bits, with the average number of construction steps resulting in a stable molecule's frequency of occurrence. The model created for this project, and the software developed to work with the model, was designed to search for correlations of this type. 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 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 appears 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 and attractive effect of a permanently active cell. This phenomenon could be explored in other models of natural systems and, with the techniques developed in this work, yield insights into their complexity. Consider, for example, the molecules created in this project as primordial minerals: two can interact to create a bonded pair analogous to the way minerals become more complex[24] over long periods of

geological time during which thermodynamic and gravimetric churning introduce phase changes[32]. These phase changes could be represented as the conversion of primordial molecules to a fully perennial form as shown in Figure 21 and allow the molecules to interact *without* any soup of canonical cells, forming new stable structures.

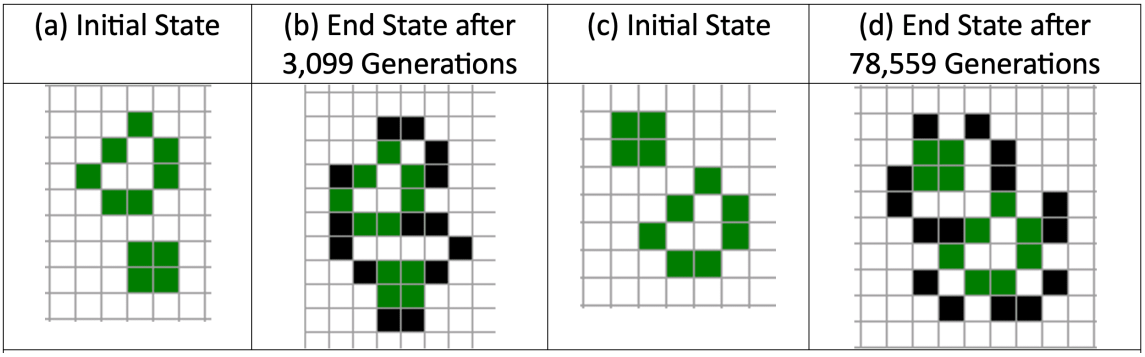


**Figure 21. A Loaf and Block as Interacting Molecules.** The relative location of the two molecules shown in (a) vs (c) results in different end state structures as well as differences in the length of self-organized construction as measured in generations.

This project's model has demonstrated one technique of using cellular automata to quantify complexity, and future possibilities remain to be explored. Good hunting to all those who share in this quest.


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# Appendix

## *A1. Dissipation Factor and Generations*

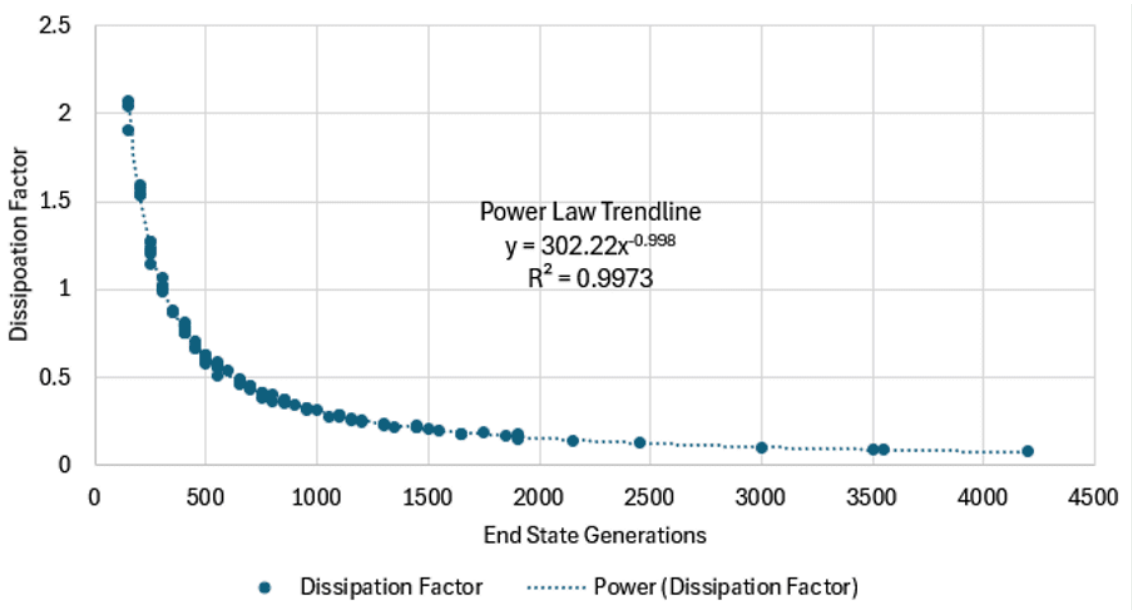


**Figure A1-1. Correlation of Dissipation Factor and Generations.** The data in this graph is from a subset of 100 of the 94,219 soups that created the Block; each soup evolved to its end state.

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[11]; for more details see Appendix A1 in the referenced article.


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*A2. Additional FI/CI Graphs*

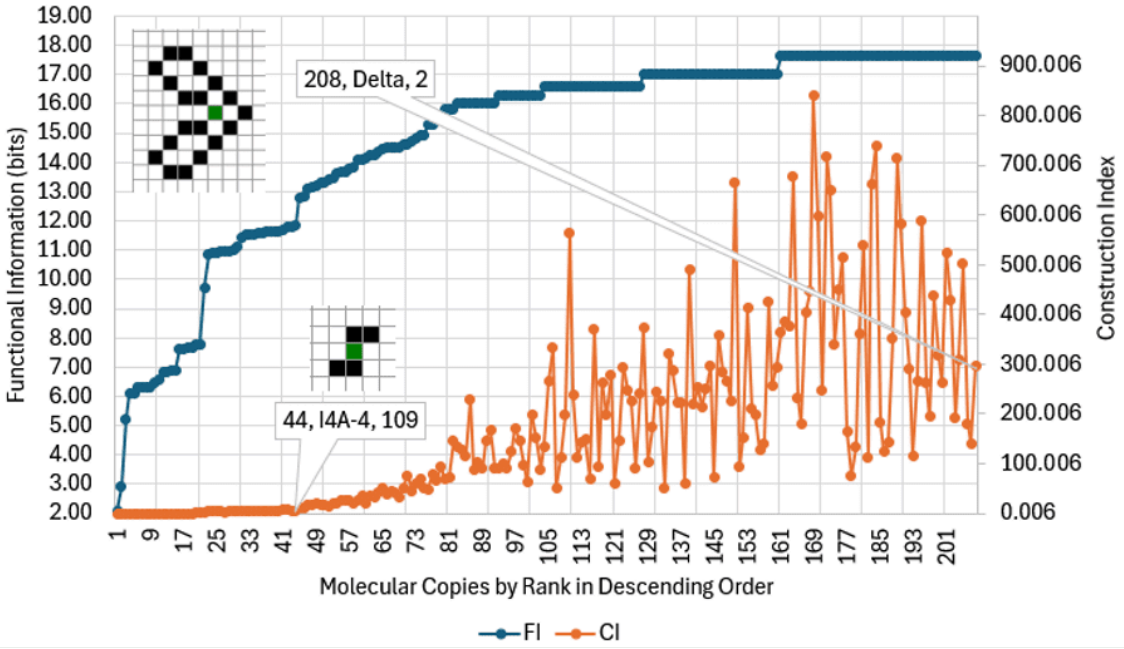


**Figure A2-1. FI and CI Trends for Molecules with Greater than 1 copy.** This graph shows 208 of the 351 molecules. Number 44 was at the end of the graph in Figure 15 in the main text and number 208, the Delta, is the last of those molecules with greater than 1 copy.


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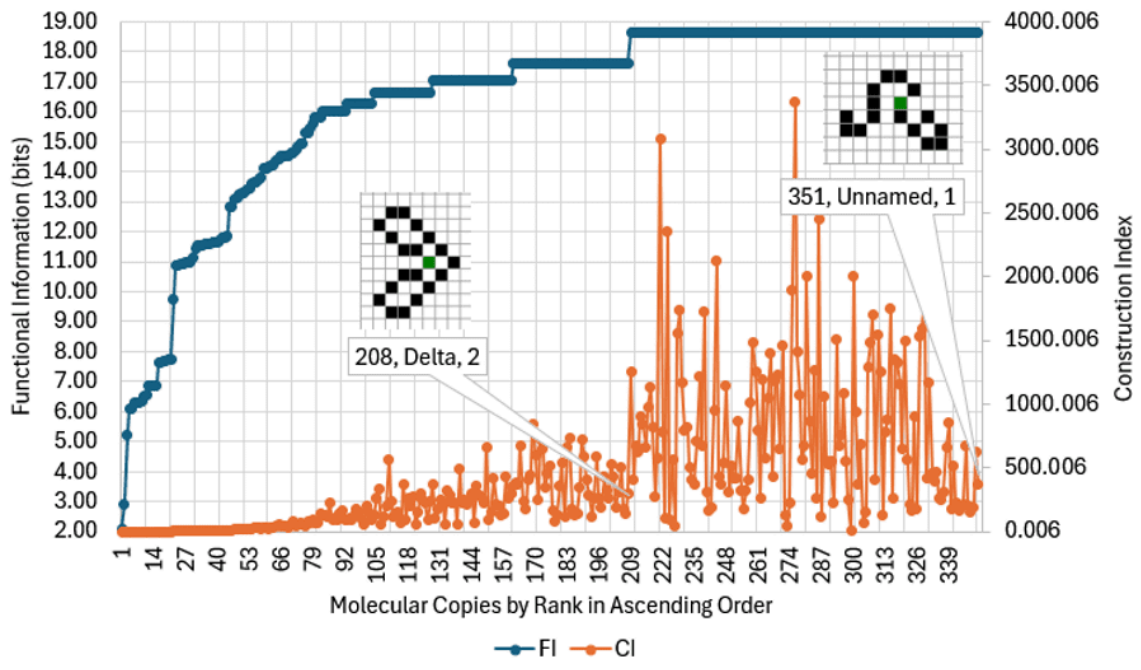


**Figure A2-2. FI and CI Trends for Molecules all 351 Molecules.** The Delta molecule is the last one on the previous graph, A2-1, and the final molecule, number 351, is unnamed and shown above.


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*A3. Metrics for Figure 15 of the Top 10 PE-generated CE Molecules*

| PE Rank | Molecule | Copies | FIDR | FI | Avg CS | CI |
|---|---|---|---|---|---|---|
| 1 | Block | 94,219 | 0.234799 | 2.09 | 749.22 | 0.007952 |
| 2 | Boat | 20,056 | 0.049981 | 4.32 | 742.52 | 0.037022 |
| 3 | Yacht | 13,811 | 0.034418 | 4.86 | 753.51 | 0.054559 |
| 4 | Beehive | 11,674 | 0.029092 | 5.10 | 753.71 | 0.064563 |
| 5 | Tub | 10,696 | 0.026655 | 5.23 | 746.32 | 0.069776 |
| 6 | Barge | 8,717 | 0.021723 | 5.52 | 745.96 | 0.085575 |
| 7 | Loaf | 8,022 | 0.019991 | 5.64 | 745.74 | 0.092962 |
| 8 | Ship | 3,708 | 0.009241 | 6.76 | 762.58 | 0.205658 |
| 9 | Mango | 537 | 0.001338 | 9.55 | 761.91 | 1.418827 |
| 10 | Pond | 474 | 0.001181 | 9.73 | 796.78 | 1.680970 |

**Table A3. Metrics of the Top 10.** Refer to the Supplementary Data for the origin of this data where all 351 molecules created in this project are listed.

## 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.

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**Supplementary data:** available at https://doi.org/10.32388/HX4713.2

## Declarations

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