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Article

Symmetry and Historicity in the Game of Life: Modifying Rules to Simulate Evolutionary Dynamics

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Abstract: The Game of Life (GoL) is a paradigmatic computer simulation that exhibits the emergence of complex properties of the whole from relatively simple sets of heuristic rules operating at lower organizational levels. Therefore, it is widely understood as a valuable tool for investigating global properties of evolutionary processes. Cognizant of refined concepts that emerged in recent debates on the central role of historical contingency (historicity) in evolution, we modify the original GoL rules by introducing an updating feedback loop and a probability factor that reflect the degree of historicity in pattern evolution as both stochastic path dependence and sensitivity to initial conditions. We examine this trait in simulations of the emergence and breaking of bilateral and radial symmetries commonly observed in the evolution of life, most prominently as evolving body plans. We show that the implementation of historicity parameters leads to a more realistic sequential and gradual alternating emergence and the breaking of new symmetries than the original set of rules. Apart from its more realistic representations of evolutionary processes, the new approach allows for easier exploration of the parameter space, demonstrates the sequential and gradual emergence and breaking of symmetries, and provides a publicly available and modular simulation tool. We discuss the exploratory potential of the modified GoL platform we designed as an extended thought experiment to study the parameter space defining the historicity of biological processes.



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Keywords: Game of Life; biological evolution; stochasticity; historical contingency; path dependence; body plans; symmetry

1. Introduction

The original iteration of the Game of Life (GoL) relies on a set of simple deterministic rules that drive the evolution of the system. The simulated evolutionary outcome depends on both the configuration of the initial system and the chosen set of rules. While the GoL is an exemplar of how complex properties can emerge from simple heuristic rules at lower levels of organization, as a simulation, it often exhibits properties that are too coarse-grained to allow it to be used as an analogy to natural systems whose evolutionary principles it purports to reflect. Our hypothesis contends that GoL's potential as a tool for reflecting evolutionary processes has been underestimated, because earlier versions of GoL leave out the most distinctive feature of evolutionary processes—their historicity. To address this, in this paper, we modify the original rules by introducing a feedback loop to the cell updates, thus disrupting the Markov chains in the simulation. Our modification is aligned with the notion of historical contingency as both path dependence and sensitivity to initial conditions introduced and developed in recent conceptual debates on historicity in evolution, which we implement in this study through different structures and degrees of stochasticity in the GoL rules. Given that historicity is one of the central themes of this paper, and considering the ambiguities in the semantic determination of this concept in the

literature, we find it appropriate to define it in the manner that will be used in this paper. If there is a series of causally connected events, $X_0, X_1 \dots X_n$, that occurred at moments $T_0, T_1 \dots T_n$, historicity represents the temporal depth of the causal relationship, which is the number of preceding states connected causally. In the realm of modeling time series in the field of machine learning, historicity would correspond to the concept of a “look-back window”. Essentially, we fine-tune the GoL by introducing parameters that reflect key aspects of historicity in evolutionary processes, such as path dependence, sensitivity to initial conditions, and stochasticity. In this way, we create a simulation tool to explore the evolutionary domain, including parameters’ interactions and the options defined by them.

We developed an independent, publicly available, and modular *brute force* simulation software platform (the platform and the code are publicly available at <https://github.com/jtadic/GOL> (accessed on 10 August 2024) that isolates GoL patterns exhibiting specific properties (e.g., stationarity). Our platform accommodates three GoL simulation regimes:

- (1) Simultaneous cell updates according to the classical rules.
- (2) A historicity-driven feedback loop as a sequential update, where each individual cell is updated based on varying degrees of “visibility” of updated and non-updated cells in the environment.
- (3) Stochastic (probability factor) variation in cell updates.

The Research Questions/Contributions that have been explicitly addressed in this study are as follows:

How does the introduction of historicity and stochasticity into the GoL affect the emergence and breaking of symmetries in the simulated patterns?

Can the modified GoL perhaps provide a more accurate representation of evolutionary processes by incorporating path dependence and sensitivity to initial conditions?

What are the philosophical and theoretical implications of shifting from deterministic to stochastic rules in the context of evolutionary simulations?

How do different degrees and structures of stochasticity influence the behavior and stability of patterns in the GoL?

We philosophically and theoretically propose the introduction of regimes (2) and (3) as closer to evolutionary processes driven by historical contingencies. We analyze the philosophical implications of changing the set of rules (from deterministic to stochastic) in terms of the instances obtained in simulations, the theoretical implications of the observed properties, and the role of historicity and stochasticity in generating and breaking characteristic initial patterns.

Our analysis of the emergence and breaking of symmetries in emerging patterns in the GoL simulations reveals that regime (1) generates various symmetries (bilateral, radial, etc.) commonly found in the evolution of life as body plans or molecular chirality, and eventually stabilizes such symmetric patterns. Those symmetrical stable forms (attractors) can result naturally from both symmetrical and asymmetrical initial patterns in this regime. Yet, symmetry breakings in evolutionary processes are as crucial as the emergence of functional symmetries. In fact, the sequential generating and breaking of symmetries is a key characteristic of longer evolutionary processes. Regimes (2) and (3) reflect both the constructive and the destructive roles of historicity in evolution, as emphasized by biologists [1–3]. Stochastic factors certainly play a role in such sequences, but the question is whether there is a general stochastic mechanism behind them. Regimes (2) and (3) offer simulation options for sequential evolutionary changes in symmetries predicated on the parameter space, as defined in the aforementioned debates.

To systematically explore all these ideas, this paper is structured as follows:

Section 2: Game of Life—provides an overview of the classical Game of Life (GoL), discussing its traditional goals, methods, and how stochasticity can be introduced into the model. It also explores the constraints involved in the discretization of evolution within GoL simulations.

Section 3: GoL, Stochasticity, and Historicity —examines the concept of historicity in evolutionary processes and how it can be incorporated into GoL simulations to model more realistic evolutionary dynamics.

Section 4: A Case Study: Generating and Breaking Symmetries in Living Systems—presents a case study using GoL as a simulation tool to explore how symmetries emerge, evolve, and break within this framework.

Section 5: The Platform—introduces the computational platform used in this study, including the preliminary setup and the brute force pattern search method employed to analyze GoL configurations.

Section 6: Conclusions—concludes the paper by summarizing the key findings and discussing the implications of integrating stochasticity and historicity into GoL.

By following this structure, this paper aims to provide a comprehensive understanding of how modifications to the GoL can serve as a more accurate analog to natural evolutionary processes, emphasizing the critical roles of historicity and stochasticity.

2. Game of Life

2.1. The Goals and Methods of Classical GoL

Cellular automata, such as the GoL, are deterministic dynamic systems capable of generating or exhibiting very complex nonlinear phenomena. The GoL is based on a field of cells resembling a chessboard, where time and space are discrete, and each cell simultaneously undergoes sequential evolutionary transitions depending on its current state and a set of deterministic rules that take into account the state of the eight neighboring fields (known as the Moore environment). In essence, cellular automata provide artificial universes that permit the creation and study of various phenomena, ranging from simulations of the reproductive behavior of theoretical organisms and the evolution of their societies to the molecular logic of living matter [4]. John Conway, a mathematician, constructed the evolutionary rules of the GoL in a manner similar to the way Verhulst [5,6] and Robert May [7] represented population growth in logistic equations and maps, respectively.

The applicability of the GoL to evolution can be broadly understood in two ways. First, it may be reasonable to assume certain living individuals who depend on cooperation or multiplicity have significantly reduced chances of survival in the event of general population thinning or isolation from sexual partners. Second, overpopulation can create excessive pressure on the resources of the ecological niche to which an organism belongs, leading to pollution, degradation of quality of life, and poverty. However, life usually thrives between these two extremes, as represented by the GoL's requirement for a cell or field to have at least three living neighbors to sustain its existence. Through implementing the local evolution rules in each cell in the GoL, the entire field generates global distributive (visualizable) patterns.

There are several variations of the GoL. Some occur along an asynchronous time axis, while others feature continuous time transitions, instead of discrete ones, and extended environments [8,9], or they are autoreproductive loops, such as Langton's loops and "evolops", which demonstrate the mutual relationship between genotype and phenotype [10]. Another model has been developed to mimic the behavior of viruses [11], where certain cells of the GoL can hibernate in an inactive state, awaiting specific external conditions before activation. In the GoL, each set of rules can vary, allowing the simulation to embody a wide range of logics and systems. These rules are uniquely defined and can be articulated using logical or linguistic terms, reflecting our human approach to conceptualizing and narrating complex behaviors.

The classical GoL exhibits the property of *irreversibility*, whereby the system's previous states cannot be uniquely determined from its current state and evolution rules alone [11,12]. This property aligns with the contemporary understanding of evolutionary processes as having multiple pasts when run backward in a thought experiment [13,14].

The GoL also demonstrates the self-organizing properties of statistical stationary states that emerge after any arbitrarily selected cell or field is perturbed. "Statistical stationary

states” refer to stable patterns or configurations that emerge in a system after it has been perturbed, and these states exhibit statistical regularities. In the context of the Game of Life (GoL), when any arbitrarily selected cell or field is perturbed, the system tends to reach certain stable configurations that persist over time. These stationary states are called “statistical” because they are not rigidly fixed but exhibit certain statistical patterns. These stationary states are independent of the initial configuration, and the system generates order from chaos [12]. The “criticality” of such systems is manifested in the appearance of avalanche effects at all spatial scales, whose frequency obeys the so-called “power-law”. As with other critical phenomena, critical properties do not depend on the specific characteristics of the rules themselves but are universal and determine the appearance of patterns without local conservation laws, that is, at all scales [15]. In other words, no rule of the Cellular Automaton holds that would allow us to predict which class of stationary states the system will belong to, or with which it will converge [16]. Bak et al. [17] suggested that the GoL spontaneously evolves into a self-organized critical state [15,17]. More precisely, at all spatial scales, a global order has emerged from the nonlinear interactions of the system’s constituents. Disagreement about whether the GoL leading to critical or slightly subcritical states [18] arises as a result of the interpretation of boundary condition effects in the scaling behavior of the GoL [19]. It has been found that the GoL is quasi-critical; that is, it shows some but not all properties of a critical system. This idea has been confirmed by changes in the fractal dimensionality at different scales [20]. Some suggest that Conway’s GoL is only a special case of cellular automata in which the “dead” phase is slightly supercritical, or the process of nucleation is slightly subcritical for the “live” phase [16]. This debate exceeds the scope of this work.

While pattern evolution is an interesting aspect of the classical GoL, it does not fully capture the unpredictable time-dependent pattern changes seen in biological evolution. The evolution of the GoL should ideally mirror the evolutionary process—a process in which replicator agents exhibit variations, and the most adapted individuals have a higher probability of spreading and achieving dominance in a colony [10]. This is akin to the conceptual treatment of evolutionary processes implemented in Avida-ED, one of the most popular evolutionary simulators [21]. However, the replicators in the GoL, including Langton’s loop, are morphologically and functionally designed by humans. Consequently, their self-replication process does not increase their complexity, nor do they display robust resistance to perturbations or unexpected external interactions [22].

The survival and stability of self-replicators face a significant obstacle since the typical paths of both chaotic and stochastic processes appear to be irregular in time. Conway’s (“classical”) GoL is defined by discrete states at discrete positions in space, with logical rules dictating the dynamics (considered as degenerate Markov chains). Even when the rules of the cellular automaton can be chosen in such a way as to “generate interesting structures that appear from very large sets of possible rules”, in our view, this should not be seen as “finding a way to directed evolution” [22,23]. Stochasticity of some kind is necessary for directed evolution, and we explore how historicity enables this in Section 3. Before doing so, however, we examine the ways stochasticity has been implemented in the GoL.

2.2. Stochasticity in the GoL (An Overview)

GoL patterns do not exhibit non-exponential decay (non-exponential decay refers to a decay process in which the rate of decay does not follow an exponential function) or explosive behavior (become chaotic; “explosive behavior” in the context of complex systems, such as cellular automata like the Game of Life (GoL), refers to a rapid and unbounded amplification of certain characteristics or events within the system that implies a sudden and extreme change or growth in some aspect of the system’s behavior), as the life and death events in the system are highly correlated in both time and space, ultimately leading to a critical or quasi-critical state as suggested by Bak et al. [15]. In the context of complex systems, a “critical state” refers to a point where the system undergoes a phase transition or

a critical transition, leading to a change in its overall behavior. This is often associated with the emergence of self-organized patterns and structures. A “quasi-critical state” is similar but may indicate a state that is close to criticality but not precisely at the critical point. This critical or quasi-critical state is characterized by a balance between order and disorder, where the dynamics of the system become complex and exhibit interesting features. In the context of cellular automata and other complex systems, understanding critical states is crucial for grasping the system’s behavior and its transition between different phases or patterns. Critical states often signify a point of instability and sensitivity to initial conditions, leading to the emergence of intricate and often unpredictable dynamics. Consequently, the classical GoL lacks dynamic randomness over time: its dynamics propagate the initial system configuration, which may eventually become random in its statistical properties with respect to spatial distribution. In contrast, genuinely probabilistic (stochastic) cellular automata generate randomness at each space–time point, producing positive entropy per unit time and volume, as noted by Gaspard and Wang [23].

In the stochastic version of the two-dimensional (2D) GoL, the fate of each field (cell) depends on the eight nearest neighbors, similar to its deterministic counterpart. However, the stochasticity is introduced by two parameters: the probability of survival and the probability of birth [24,25]. While death is still determined by deterministic criteria based on overcrowding and isolation, survival is affected by a probabilistic element. For instance, a cell with two or three living neighbors may survive with a certain probability, p_s , whereas in the classical version, any dead cell would become alive if it had exactly three living neighbors. Another rule introduces probability to the scenario: when there are exactly two living neighbors, a new cell may not necessarily be born, depending on the new condition, the probability p_b . The probability parameters are chosen to ensure that the stochastic GoL converges to Conway’s classical deterministic version when $p_b = 0$ and $p_s = 1$ [24,25].

A one-dimensional (1D) model of the stochastic GoL has three phases: living, extinct, and overcrowded. The term “overcrowded” refers to a state where the cells or sites in the automaton are densely populated, in this case beyond the GoL threshold. The concept of overcrowding implies that there are too many living cells in close proximity, leading to specific dynamics or behaviors in the system. Many critical edges are observed at the irreversible phase transitions between extinction and life and between life and overcrowding [24,25]. The extinct phase remains “frozen” in both the 1D and 2D models, while the overcrowded phase is present only in the 1D model. Specifically, for small values of p_b , while keeping p_s constant at 0.5, all living sites and their descendants eventually die. However, as p_b is increased, the emergence of life is observed in the abrupt increase in the density of living sites ($\rho > 0$). Through varying the parameter space (p_b, p_s) , a set of critical points can be obtained that defines a critical curve, $p_b^c(p_s)$. Within the living phase, aperiodic behavior has also been identified, indicating a divergence of two initially close trajectories [24–26].

Yaroslavsky’s [27,28] modification of the GoL introduces a different set of stochastic rules. For example, the individual cells die with a probability $p_d \leq 1$. In addition, the inclusion of 3×3 weight matrices, denoted as masks, provides non-uniformity of the spatial impact of cells and their immediate eight-member environment. For instance, isotropic masks correct the impact of cells in the environment based on their Euclidean distances from the central cell. The corner cells of the environment are $\sqrt{2}$ times farther from the central cell than those in the middle of the sides of the Moore square, so their impact is normalized using a spatial distance. Yaroslavsky discovered, named, and studied several new phenomena, including the formation of patterns resembling labyrinths as fixed points in the model, “self-controlled growth”, “eternal life in a limited space”, and “coherent compression”. Familiar with the stable and oscillating patterns of the classical GoL, he labeled stable structures “entangled chaos” rather than “frozen”. As soon as the probability of death (p_d) becomes only slightly less than 1, it seems likely that oscillating formation characteristics of non-stochastic or classical GoL models occasionally collapse,

producing chaotic clouds of living and dying cells that collide without any indication that they will ever stabilize [27,28]).

Yaroslavsky observed that the square cells, or the “living space” for the probability of death, p_d , from $0.3 \leq p_d < 1 - \epsilon$ (where ϵ is an arbitrarily small number), are gradually filled with “eternal life”. When $p_d \approx 0.5$, groups of striped patterns of various dimensions and orientations appear. When $p_d < 0.3$, the boundaries of these groups stabilize into square, labyrinthine structures with a seemingly random distribution of orientations (vertical vs. horizontal) [27,28]. It would be interesting to investigate the relationship of this phenomenon with the aperiodic behavior of the so-called living phase described in the Monetti-Albano study [24–26]. In the same study, Yaroslavsky observed the patterns of living cells that emerge stop growing if they do not touch another neighboring “population”. If they touch the neighboring “population”, the groups will join and continue to grow until they take on a similar spatial shape, but with larger dimensions, called the “mature state”. After achieving relative stability, or after a certain number of evolutionary iterations, the communities begin to contract, that is, to recede from their own boundaries and move inward, while maintaining their shape [27,28]. The existence of “static” and “oscillating” life seems to be a byproduct of the deterministic rules applied to a square grid, resulting in phenomena arising from the finiteness and boundedness of the given space. As previously discussed, stochastic models of the GoL “produce chaotic clouds of “live” and “dying” cells that collide with each other and give the impression that they will never stabilize”.

It is noteworthy and pertinent to our investigation that the results mentioned above were obtained through a single modification—the introduction of the probability of death (p_d)—and the use of square 3×3 masks that normalize the impact based on the Euclidean spatial distance.

The stochastic models of the GoL discussed above do not appear to accurately represent any particular living system. Nonetheless, they demonstrate distinct aperiodic and irreversible critical global behaviors that define biological systems [27,28] generated by simple local rules in the simulation. As an illustration of the divergence of two initially similar evolutionary trajectories, it could be argued that by adjusting these probabilities, the dynamic behavior in the simulation can be changed over the long term from one in which all cells are dead to one in which all are thriving [29].

Another way to implement a stochastic model in the GoL is to have individual cell states evolve with a certain probability, rather than applying the rules simultaneously to all cells, thus introducing asynchronous evolution into the model in discrete steps. This can be achieved by either randomly selecting cells that will evolve or refreshing the cell state based on an internal cell clock [30,31]. However, it has been suggested that most cellular automata models, including the GoL, break down under such evolutionary conditions (Peper et al. [8] commenting on Blok & Bergersen [19]).

The first model of this type was proposed by Blok and Bergersen in 1999 [19]. They used an update scheme with $0 < p \leq 1$ and observed that for $p \rightarrow 0$, the model approximates a time-driven method based on a Poisson random process. They found that “the cellular automaton shows a second-order phase transition belonging to the universality class of directed percolation” [19,30].

Lee et al. [31] and Peper et al. [8] improved the classical evolutionary rules and tracked intermediate states in their resulting model, showing another phenomenon of potential interest in the study of evolution; the existence of synchronization waves indicating which cells are correlated during the collision of two gliders. Since there is an evolutionary probability parameter that affects the speed of evolution and the reproducibility of certain states in the GoL, the smaller the probability p , the more steps are needed to achieve the same configuration as in the classical GoL with the same initial configuration, if this can be achieved at all [8]. The authors also observed patterns evolving into alternating strips of live and dead cells, as similarly found in previous studies [19,27,28]. Moreover, varying the parameters of the evolutionary model and the initial patterns led to qualitatively different

stable states, such as dead, frozen (low density and stabilized), and labyrinth phases [30]. The simulation platform we developed implements stochastic rules inspired by Fatès [30].

A recently published, intriguing technique for treating the square lattice asynchronously by exchanging the positions of a randomly selected pair of “to become alive” and “to become dead” cells (in the next time step), regardless of their distance, to satisfy the conservation criterion of mass, requires something to die for something else to be born. The authors call this the “no *ex-nihilo*” rule, and its goal is “to enforce conservation of the number of cells of both types” [29]. This model and its predecessor [32] “changed the nature of the lattice into a small-world network, obtained by replacing nearest-neighbour links with long-range ones”. The authors discovered that “as the [local] density of dead cells increased, [they] identified a discontinuous phase transition between an inactive phase, in which the dynamics freeze after a finite time, and an active phase, in which the dynamics persists indefinitely in the thermodynamic limit” [29]. Importantly for our study, they stated that “although the conservative and random character of the dynamics does not allow for the appearance of oscillatory or spaceship patterns, [they did] observe familiar static patterns when the density of dead cells is large enough” [29].

2.3. Discretization of Evolution in GoL: The Simultaneous Update Approach and Related Constraints

The classical rules of GoL updates are relatively simple [15]. If there are fewer than two or more than three live cells among the eight neighbors of a cell, that cell will die; otherwise, it will remain alive. A new cell will appear in an empty field in the next iteration only if the empty field has exactly three live neighbors.

One of the remarkable features of the original GoL is that the update, or discrete evolutionary transformation of all cells, occurs simultaneously according to the all-cells-at-once approach. This means cells are analyzed to determine which ones need to be updated and then are all updated at the same time, constituting one generation in the simulation—a process that is repeated in subsequent cycles. Although heuristic update rules are applied independently to each cell to determine its fate, the actual change in all cells occurs in a discontinuous manner, in discrete collective evolutionary steps. The system behaves like a vector transformed by a linear algebraic evolutionary operator, i.e., a matrix that moves the system vector through the evolutionary space. Intuitively, the application of evolutionary rules independently for each cell and the transformation of all cells at once create a discrepancy between the temporality of determining the fate of the cell and the actual update.

The all-at-once approach to updating cells in the GoL presents a challenge to the GoL’s representativeness as a paradigmatic analogy for evolutionary features observed in various biological systems. In its original form, the GoL’s evolution depends solely on its rules and current state, not on the history of its environment. Therefore, the evolution of each cell is independent of its past and represents a Markov chain [33]. While this property is not inherently advantageous or disadvantageous, it raises questions about whether biological systems analogous to those simulated in the GoL are essentially Markov chains.

To illustrate our argument, consider a bacterial colony as an example. While sharing some similarities with the Game of Life (GoL)—both involve survival, division, and death of individual elements—there are notable distinctions. In bacterial colonies, unlike the GoL, the fate of individual bacteria is not strictly time-dependent, and changes are not synchronized in time. There is no universal external clock dictating the step structure of the evolutionary process. In other words, the behaviors of individual bacteria are not exclusively determined by specific points in time. Chemical signals dissipate not only spatially but also temporally, extending beyond the immediate neighborhood in both space and time. The persistence of residual signals and non-updated states expands the look-back window, introducing a deeper historicity into the bacterial colony environment. This divergence has significant implications. In an environment where updates do not occur simultaneously, each bacterium partially interacts with a deeper history of its environment, not simply with the state of its neighbors in the immediately preceding moment. We

interpret time in the bacterial colony as discretized, drawing an analogy to the simulation. In reality, introducing a discrete structure to time might be deemed unnecessary. However, for the purpose of facilitating a meaningful comparison between the GoL environment and a bacterial colony, we find it convenient, without adverse effects. *The less probable an update is for an individual bacterium at any given moment in the colony as whole, and the more the simultaneity is violated, the more chance there is for the single bacterium to factor in the deeper history of its environment during its own update.* Thus, the colony evolves while retaining residual memory of its past states, violating the Markov chain. We will demonstrate that an analogous effect can be achieved in the GoL by introducing the probability of update into the set of rules.

As a second example of a natural process that exhibits significant similarities to the GoL but does not maintain strict simultaneity, we mention apoptosis [34,35]. Apoptosis, also known as programmed cell death, is essential in organogenesis, inflammation, and other biological processes. It occurs due to one of three factors: (1) the effect of activating substances, (2) the absence of growth factors necessary for cell survival, or (3) the effect of damaging substances on the cell. Signals are conveyed through two pathways, extrinsic and intrinsic. The rules that initiate apoptosis are generally equivalent, so to speak, to specifically designed or adapted rules of the GoL. Therefore, in principle, apoptosis could be simulated by modifying the GoL's rules. However, because of the absence of the absolute synchronization of metabolic processes in cells and the delay in transmitting apoptotic signals to various spatial distances in tissue (limited by diffusion or other forms of chemical transport), a group of cells exposed to apoptotic signals will not react simultaneously (all at once). In organogenesis, the successfully developed symmetrical body forms or functional organs must be analogs of the GoL in which the simultaneity of updates is disrupted, but the set of rules is such that, despite this disruption, the desired form, shape, or metabolic outcome is ultimately generated.

3. GoL, Stochasticity, and Historicity

3.1. Historicity in Evolution

Over the last several decades, biologists have widely recognized the central role of historicity in biological processes [2,36–38]. In addition to natural selection and various mechanisms at different levels, a third general factor, “historical contingency”, also plays a part in “determining properties of Earth’s biota” [38]. Although it has been acknowledged that chance and initial conditions are key elements of historicity in biology, the details of precisely what constitutes historicity in biology are still debated. The recognition that evolution’s immense diversity of phyla, including various body plans, stems from the accumulation of numerous improbable events [3], was a pivotal insight that underscored the significance of historicity in evolutionary processes. Yet, it has been argued that this does not necessarily point to the central role of history per se, but to the difficulty involved in predicting the trajectories that biological processes take in the longer run. Conway Morris [39] suggests evolutionary outcomes such as *Homo sapiens* are very predictable precisely because they are contingent on myriad turns in evolution. Conway Morris argues that the evolutionary outcomes, including the emergence of *Homo sapiens*, are not random and contingent but, in fact, highly predictable. Conway Morris suggests that, despite the contingent nature of specific events, the overall trajectory of evolution is biased and tends toward certain outcomes. He emphasizes that certain features and body plans have a high likelihood of evolving repeatedly due to the constraints and opportunities presented by the structure of the evolutionary process itself. His views are based on the concept of evolutionary convergence, where similar traits or body plans evolve in unrelated species facing similar environmental challenges. In any case, a stronger claim has been defended: there are multiple possible pasts of each evolutionary stage if the evolutionary processes are run backward as a thought experiment [13].

A comprehensive of the theories of historical contingency is given in Turner and Havstad [40]. Gould’s stance on contingency revolves around the argument that the

shape of life's contingency challenges the notion that natural selection alone can explain macroevolutionary patterns [3,36]. He critiqued the overreach of evolutionary theory, emphasizing natural selection, and advocated for theoretical pluralism. Gould's critique aimed to keep microevolutionary theory in check, asserting that if macroevolution is contingent, natural selection becomes insufficient to explain life's overall shape. His arguments were often presented in non-binary terms, highlighting the relative significance of causal forces. They contend that natural selection can itself be a source of contingency, as evolutionary outcomes depend on initial conditions and exhibit path dependency. Gould's discussion underscores the need to establish that contingent patterns cannot be accounted for by the theory in question, emphasizing the distinction between source-independent and source-dependent accounts of contingency.

Recent work has drawn a few refined distinctions that help clarify the parameter space of historical contingency. Desjardins [41] distinguishes two types of historical contingency in evolutionary processes: *dependence on (sensitivity to) initial conditions* and *path dependence*. Instead of presenting a sharp dichotomy, the two are *on a continuum* and characterize relevant evolutionary processes as a matter of the *degree of stochasticity*. Degrees of path dependence are also context- and instant-relative [41], and this is unavoidable, given the complexity of the environments and targets of natural selection.

Turner [42] and Beatty [13] explore different evolutionary forces categorized under "contingency". Beatty focuses on microevolutionary processes like drift and mutation, questioning the exclusion of drift by Gould. Turner, on the other hand, emphasizes the macroevolutionary process of species sorting. The discussion revolves around whether mutation, drift, or species sorting serves as a source of evolutionary contingency. Mutation is highlighted for its role in providing variation for selection. Drift, a process independent of environmental fit, influences gene frequency changes. Species sorting, akin to macroevolutionary drift, involves the non-directed persistence or extinction of species. Beatty includes mutation as contingent due to its impact on variation, excluding drift. Turner, focusing on macroevolution, distinguishes contingency at the micro- and macro-levels, excluding processes like mutation and drift. The disagreement revolves around whether these processes contribute significantly to specific patterns of evolutionary change. Source-dependency clarifies their differences. It involves identifying a causal process and pattern, discussing their sufficiency in generating that pattern. Mutation, drift, and species sorting can be sources of evolutionary contingency, depending on the pattern of change considered. The key question is whether these sources are responsible for the observed patterns, emphasizing empirical considerations. The paper concludes by highlighting the importance of understanding which sources contribute to the patterns of evolutionary change under consideration.

In a recent study, McConwell and Currie [43] explore the role of source-dependency in understanding Gouldian arguments and contingency. They focus on empirical approaches to test Stephen Jay Gould's claim that macroevolutionary patterns are driven by processes beyond the reach of natural selection. Investigative methods such as models of macroevolutionary processes, lab-based experiments, and natural experiments are discussed. The paper delves into biological convergence, using trichromacy in mammals as an example. The authors argue that the sources of convergence and divergence are crucial for evaluating Gould's thesis. They emphasize that the ubiquity of convergence does not necessarily contradict Gould's view, as the focus should be on the causes of convergence. The paper examines trichromacy in primates and marsupials, highlighting the sensitivity of convergences to various descriptions and the importance of developmental resources in explaining convergent traits. Additionally, the authors discuss a case of evolutionary divergence between cephalopod and vertebrate eyes, emphasizing the role of common history and developmental constraints in shaping traits. The paper concludes by asserting the significance of source-dependent understandings of contingency in testing Gouldian arguments and justifying Gould's position on the insufficiency of microevolutionary theory to account for macroevolutionary patterns.

Building on S. J. Gould's work, McConwell [1] recently argued that the stochastic processes aspect of historicity causes structural diversity across biological levels, including cells, genetic codes, and phyla. Thus, historical contingency as a stochastic process is bound to cause diversity across biological levels [1], and plays both a *constructive and a destructive role*, for example, in the emergence of body plans. McConwell provided various measures and assessments of diversity to demonstrate the validity of this view.

These distinctions provide a parameter space within which to explore their interdependence. Methodologically speaking, however, tracing these parameters is not easy. Desjardins analyzed experiments with bacterial colonies that were prepared and developed under the same conditions and followed their fitness trajectories over time to record the potential exhibition of substantial differences [44]. Experiments are undoubtedly an ideal tool for such purposes, but populations identical in terms of the key parameters are highly unlikely to be found in nature. They are also hard to track in fossil records, while varying relevant parameters in laboratories has serious limitations. Desjardins [41] also points to a lack of realistic complexity in mathematical models and simulations. Another problem we noted earlier is that simulations do not really match the target phenomena; instead, they aim at exploring very general properties that may or may not converge with the parameter space of actual biological processes. And often the more refined the parameter space, the less hope there is for identifying helpful convergence or learning something of biological interest.

Rectifying this limitation in a particular way to make GoL simulations more useful for understanding evolutionary historicity is the basic goal of our work. More realistic simulations can anticipate real phenomena and their properties within the matching parameter space of historicity. Swan [45] suggested using these distinctions and notions to define a parameter space, enabling the exploration of the interdependence of various parameters. Within this framework, extended computer simulations of the Game of Life (GoL) can be conducted as thought experiments to further this investigation.

3.2. Introducing Historicity in GoL Simulations

We consider the lack of stochasticity and the simultaneous change in all cells in GoL to be unrealistic representations of the functioning of evolutionary and biological systems, particularly in the long term. Therefore, we introduce an update protocol that we consider substantially closer to historicity-driven evolutionary mechanisms, including natural selection operating at various levels, and closer to biological mechanisms in general. The underlying idea is that these mechanisms at the individual scale are dependent on the local environment's present state, which is determined by its history.

Our modified version of the GoL implements a feedback loop that performs sequential history-sensitive cell updates. Instead of updating all cells at once (regime (1), discussed below), our approach allows each cell to consider both updated and non-updated cells in its environment (regimes (2) and (3)) when deciding whether and how to update itself. Then, the update process moves on to another cell, factoring in the updates or the lack of updates. Thus, both mapping and updating happen in one step, as each cell is immediately updated without waiting for all the other cells to be updated. Therefore, the update of a cell is determined not just by the states of its neighboring cells, but also by the current state of the selected environment. This environment encompasses both cells that are updated and those that are not, indicating that cell updates are influenced by a broader context than merely the immediate neighborhood. This violates the Markov chain and introduces a representative form of stochastic update as historicity.

First, the user determines the exact nature of the loop itself, i.e., the order of the cells in it and the "visible" environment. Then, depending on the decision on how to loop through the cells, the cell will check out different parts of its environment for updates (or lack of them). Figure 1 illustrates the update regime that includes a particular stochastic component. This update regime is deterministic as far as the update rules go, and it leads to a unique and reproducible outcome in each simulation step. Yet, it differs from the

original GoL simulation in that it is not deterministic in every sense: the arbitrariness and resultant stochasticity arise from the fact that the user pre-selects the update order, and each order implies a different evolutionary pathway. The number of available choices equals the number of permutations of all cells on the board, resulting in a limited and discrete set of possibilities, but this set can be large in practical scenarios (i.e., for n cells, the number of choices is $n!$).

A		B		C				
1	2	3	9	6	3	2	4	7
4	5	6	8	5	2	8	6	1
7	8	9	7	4	1	9	3	5

Figure 1. A visual representation of three alternative cell-updating orders, (A–C), arbitrarily chosen under the modified update regime (regime (2)).

To summarize, the platform offers the user three regimes for the evolution of cells: (1) the classical deterministic GoL rules; (2) historicity—a sequential implementation of the classical rules based on the “visibility” of previous updates for each cell; and (3) cell update depending on the update probability parameter.

In regime (3), cell updates are carried out by generating a random number between 0 and 1 using a flat distribution and comparing the number to a predetermined threshold. If the generated number exceeds the threshold, and the criteria for updating the cell are met, the cell will be updated. Conversely, if the generated number is less than or equal to the threshold, the cell will remain non-updated even if the criteria for state change are met. (We remind readers that this probability factor only applies to the two rules—the birth rule and the death rule—wherein the state of the cell changes. It does not alter the third rule of the classical GoL—the survival rule—as its application does not alter the state of the cell.)

The modifications outlined above have several consequences. Firstly, the environment functions as a combination of immediate and more distant preceding steps, acquiring a partial memory that reflects not only its current state but also its deeper history in previous evolutionary steps. In regime (2), the depth of the environment’s history as part of the update rules can be adjusted by manipulating the probability update parameter, thus implementing the stochastic degree of path dependence. Our update rules amplify the asynchronicity that already reflects path dependence to some extent in any non-classical GoL. In regime (3), updates more akin to endogenous stochasticity, or “mutations”, can affect the evolutionary trajectory. In both regimes, evolutionary trajectories are sensitive to initial conditions manipulated either through historical depth (regime (2)) or through level of endogenous stochastic oscillations (regime (3)). In either case, the implementation of historicity into the evolutionary environment breaks the Markov chain during the simulation by reflecting the non-simultaneity of evolutionary transitions and real biological mechanisms. (Note that we are planning an update of the platform by adding the option of switching between the classical rules (regimes (1) and (2)) based on a probabilistic parameter. The modification would imply that the classical update rules are transformed so that they are applied with a certain probability).

4. A Case Study: Generating and Breaking Symmetries in Living Systems

4.1. Evolving Symmetries

We chose the case of evolving symmetries as a pilot explorative case because it potentially represents functional biological properties, such as symmetries in body plans, that are evolutionarily quite diverse, yet simply definable and easily visualizable. The study of symmetries is invaluable in many areas of biology and evolution, and there is a pressing need for their realistic simulation. Although symmetries that define body plans are the most well-known and apparent [46,47], research also extends to the cellular [48], molecular [49,50], and population levels [51].

Studying their evolution is crucial, as it defines the key morphological and functional constraints, for example, in terms of feeding, movement, and metabolism. The causal, functional, and other roles of various symmetries at the molecular, organismal, population, and biosphere levels have been the subject of philosophical and theoretical studies, and symmetry breaking points in evolution have been understood as crucial features of the inception and evolution of life on Earth [52,53].

4.2. Simulating Symmetries with Classical GoL Rules (Regime 1)

The classical GoL rules are designed to be uniform, symmetrical, and isotropic (i.e., with no preferential treatment of any direction in space). They are applied uniformly to all cells regardless of their location. Due to the uniformity of the update rules, it is intuitively expected that symmetrical initial patterns will produce symmetrical outcomes or have symmetrical evolutionary attractors. However, the situation is somewhat more complicated for asymmetrical patterns, and it is theoretically possible to imagine asymmetrical patterns in which a series of updates leads to the elimination of asymmetrical properties to generate a completely symmetrical form. Figure 2 illustrates such a pattern and its evolutionary trajectory from asymmetrical to symmetrical, as implemented in the platform's classical regime (1).

In this regime, the initial pattern, marked with "1" in Figure 2, does not possess symmetrical properties. In the fourth step of the GoL run on classical deterministic rules, the asymmetric pattern takes on a form characterized by the point symmetry group. The point symmetry group is one where an organism (shape) can be divided into two identical halves by a single plane. Many living organisms belong to this group, including most invertebrates and all vertebrates [54]. Bilateral symmetry is maintained in seven evolutionary steps, after which the pattern transitions to another point symmetry group, radial symmetry. Radial symmetry is defined as one in which an organism (shape) can be divided into two identical halves by two or more planes passing through the center [55]. This type of symmetry is particularly common in sessile organisms (like many plants) or those that move very little (like invertebrates, starfish, sea anemones, jellyfish, etc.). After acquiring radial symmetry, the pattern further evolves without changing the point symmetry group it belongs to, ultimately taking on a stationary form after a total of 21 steps.

It is interesting to note that in the simulation depicted in Figure 2, the point symmetry groups that the patterns take on are the two most dominant forms of symmetry in the living world, and once they are realized, symmetrical forms cannot return to an asymmetrical state. In other words, symmetry appears here as a form of evolutionary attractor that spontaneously follows from the very construction of the classical rules of the GoL.

This seems to straightforwardly reflect the mechanism of emergence and the cause of analogous symmetrical forms of life, given that the classical rules of the GoL were intentionally designed to reflect the global features of natural evolution. However, there is stochasticity and historicity in nature, and the patterns that evolve in a natural environment will eventually evolve into symmetry, *gradually* lose that symmetric feature, and *gradually* acquire another or disappear. The GoL patterns in regime (1), however, take on a form that has a symmetrical attractor, or they are the precursors of symmetrical forms, which then remain permanently trapped in *abruptly* changing rigid symmetric patterns. The key question is to what extent the assumptions about abruptness and rigidity reflect relevant biological and evolutionary processes?

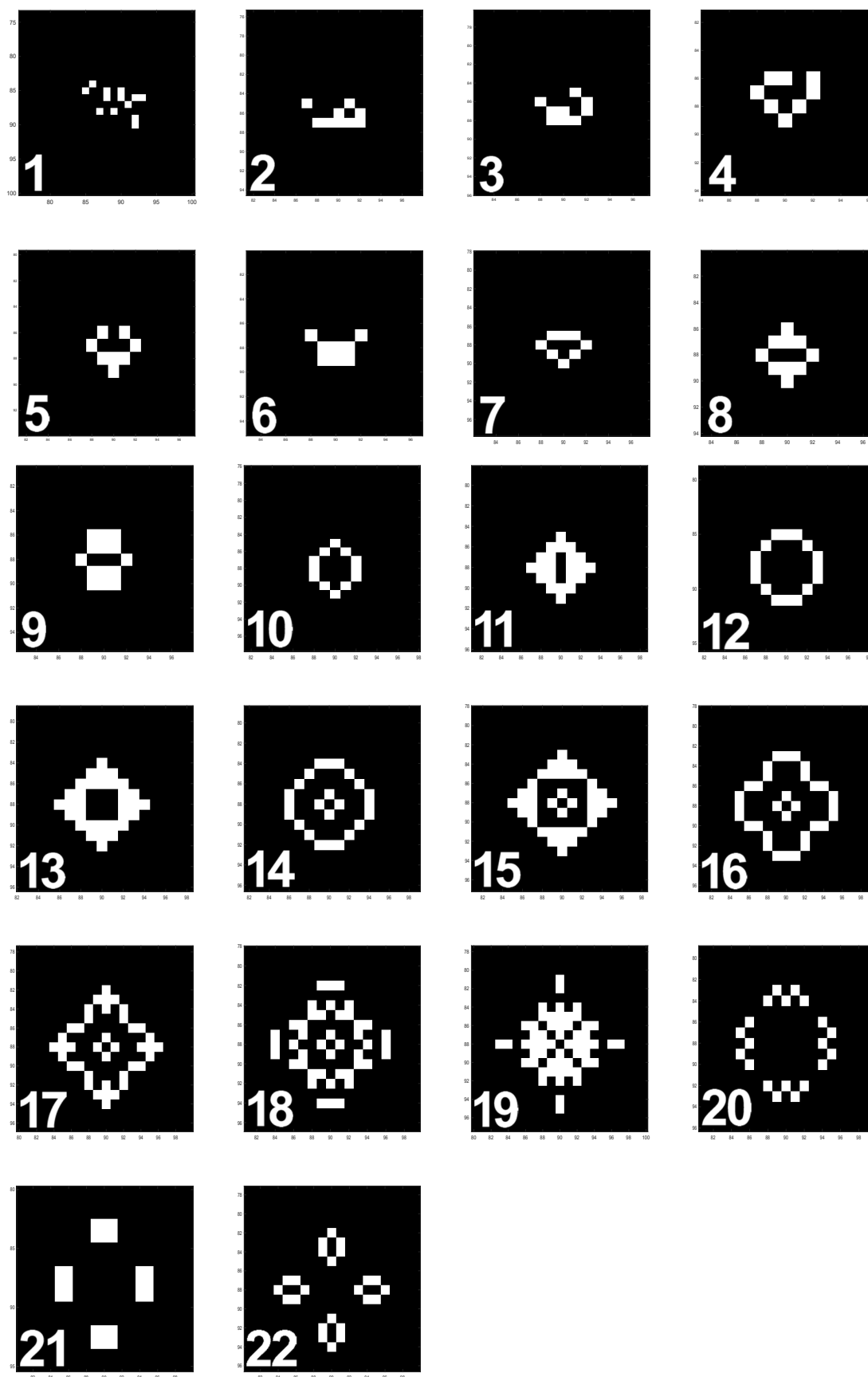


Figure 2. Under classical deterministic regime (1) of the GoL, a paradigmatic evolutionary sequence of 22 states in which the initial pattern undergoes two changes in the point symmetry group it belongs to.

4.3. From Emergence to Breaking of Symmetries and Back: Realistic Evolutionary Trajectories and Historicity in GoL

In assuming the deterministic and stationary nature of the GoL rules in regime (1), both asymmetric and symmetric patterns can settle in symmetrical attractors, while symmetric patterns can only have symmetrical attractors. This leads to a permanent symmetry of life forms regardless of the initial state, for once achieved, they become irrevocable states in the absence of stochasticity in pattern construction.

Although bilateral and radial symmetry are dominant forms of the living world (not to mention biradial and spherical symmetry), there are pervasive deviations from strict symmetry. The Tasmanian giant crab (*Pseudocarcinus gigas*), shown in Figure 3, is an example of bilateral symmetry disrupted by the disproportionately developed claws on the left side. While most crabs have a strictly bilateral body form, a similar deviation is present in a number of other species [56].



Figure 3. In the Tasmanian giant crab (*Pseudocarcinus gigas*), the presence of a larger left claw breaks the bilateral symmetry of the crab's body.

Partial symmetry breaking can also be experimentally identified at the cellular level. For example, during the transmission of neural signals, it has been observed that when the signal (action potential) reaches the presynaptic terminal (axonal ending), the release of neurotransmitters occurs with “probabilities the order of 0.25” (The term “all-or-nothing event” in the context of neurotransmitter release (i.e., exocytosis) implies that, once started, the process completes fully without any partial release. This characteristic is common in many cellular processes, where a stimulus exceeding a specific threshold elicits a complete response. However, the reference to a probability of 0.25 indicates that in the cited experiments, exocytosis happens only one in four times under conditions conducive to its initiation [57].). This represents a deviation from the deterministic nature of the rules in the case of neural signal transmission and could be seen as an analog of the GoL in stochastic regimes.

The strict bilateral body form of the crab can be achieved through deterministic, symmetric, and stationary rules, which, as demonstrated, lead to the permanent trapping of spatial patterns in symmetrical forms. However, the presence of stochasticity via historicity may be crucial for the emergence of deviations from strict symmetry, as seen in numerous similar cases at various levels [58]. A question then arises: How was this strict bilateral body form disrupted? Regime (1) is not able to simulate such evolutionary, organismal, and molecular processes. Introducing the historic–stochastic parameter as one of the update conditions disturbs the strictly deterministic character of the evolutionary rules and allows for the possibility of gradual deviation from rigidly symmetrical forms. This stochasticity in the rules of updating serves as an available source of evolutionary advantage.

Thus, simulation regime (2) can result in transitions between symmetries, but unlike regime (1), it can also knock the pattern from its trajectory of strictly symmetric distributions (Figure 3). This provides much more realistic long-term evolutionary scenarios, as well as a diversity of possible trajectories that lead to sequential symmetry emergence and breaking. For instance, in regime (2), pattern 6 in Figure 2 will be the same if it results from pattern 5 and previous steps. However, the entry from a different updating feedback loop could result in the same pattern, unlike in regime (1), or could skip it entirely. Symmetric patterns can emerge but not necessarily stabilize, or they can eliminate symmetries for longer periods or even entirely.

An intriguing preliminary result in regime (3) is that symmetry breaking occurs only when the emerging pattern is symmetric but unstable when subjected to changes according to the rules of regime (1). The probability factor appears to guarantee that the evolutionary process is never too stable. Thus, the “bare” stochastic factor may serve as a fundamental underlying factor that operates across the individual-environment network, enabling constructive and destructive cycles of, for instance, body plan evolution (see Figure 4).

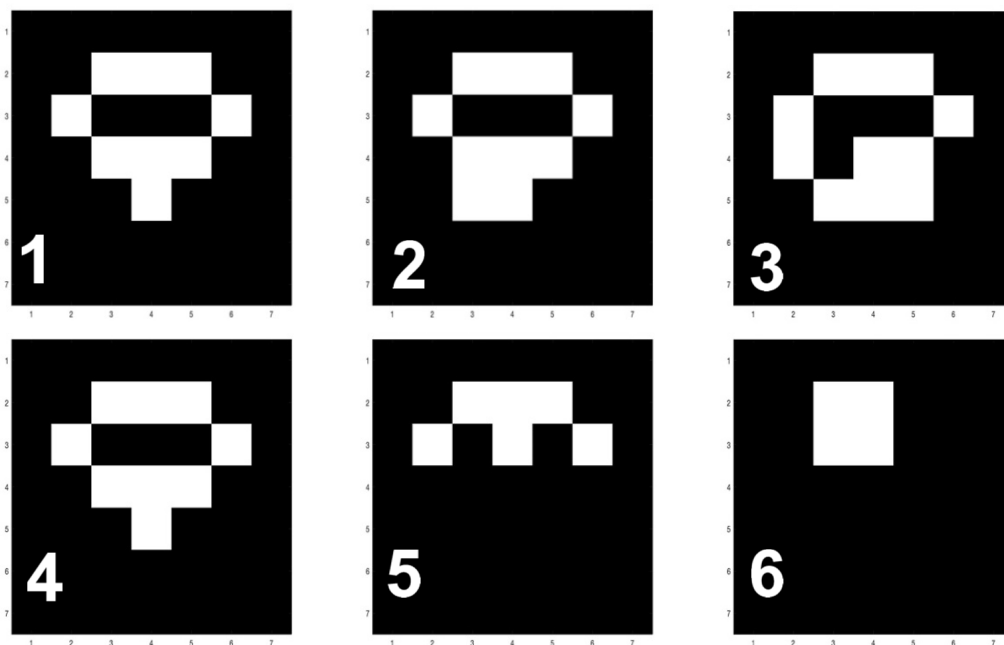


Figure 4. Three characteristic evolutionary steps obtained by simulation in regime (3).

The simulation results obtained in regime (3) illustrate the consequences of the stochastic nature of the underlying rules. Figure 4 portrays the first three evolutionary steps (patterns 1–3), as well as steps 15 (pattern 4), 19 (pattern 5), and 21 (pattern 6). To demonstrate the difference in evolutionary outcomes and trajectories after introducing stochasticity to the original rules, we use the initial pattern 7 from Figure 2 as a starting point, while maintaining an update probability of 0.5 (regime (3)). The symmetry observed in the initial pattern is lost after the first step, but after a series of asymmetric transitional patterns, it reoccurs in the 15th evolutionary step (pattern 4), matching the initial pattern. The symmetry is lost again for 4 steps, before reoccurring in the 19th step (pattern 5). Finally, in the 21st step (pattern 6), the evolution is permanently captured in one of the stable forms/attractors (called “still life” in classical GoL). Regime (3) allows symmetry to appear and disappear, unlike evolution governed by the classical rules, thus suggesting stochasticity plays a significant role in the evolutionary process.

Transitions between symmetries are particularly interesting, and in regime (1), they are abrupt with no visible transitional sequences. For example, the transition from step 11 to step 12 is abrupt (Figure 2). However, the slow differentiation of symmetries and

open trajectories are much more realistic scenarios. For instance, the abiogenetic processes resulting in homochirality, i.e., the breaking of mirror symmetry at the molecular level of homochiral L-amino acids in proteins and D-sugars in all nucleotides composing life, likely emerged from a racemic mixture in a series of steps (plausibly representing families of trajectories) [59]. The partial symmetric outcome in the crabs we described likely belongs to such gradual transitions. Thus, the visible stepwise transitional differentiation of both symmetry emergence and symmetry breaking is the key element of simulation, introduced in regimes (2) and (3) via stochastic historicity. Finally, varied evolutionary processes could accommodate switching between streamlined abrupt transitions and slow differentiation, and another regime could simulate this via stochastic switching between regimes (1) and (2). We introduced this through our platform.

5. The Platform

5.1. Preliminaries

Our study required the development of a simulation platform to test various rules and patterns in the GoL. We developed the platform using the Matlab programming language, version R2019a. The simulation platform is structured modularly to allow for the flexible selection and construction of rules and initial patterns. The size of the simulation field is determined ad hoc using a special argument of the simulation function. The initial simulation pattern is also passed to the simulation function as an argument. To select evolution rules from the current set of three options, the simulation function accepts a numerical notation symbol to select among the current set of rules. This approach allows researchers to easily switch between different rules without altering the underlying code structure. This means that different rules can be tested and compared directly by simply changing the rule parameter. The number of iterations in each simulation is also determined ad hoc, using an argument of the simulation function. After the simulation is over, the simulation function returns the resulting pattern. Throughout the simulation, the platform visualizes the simulation field in real time with a delay of 0.2 s, allowing for the real-time tracking of the simulation flow.

5.2. Brute-Force Pattern Search

As part of the simulation platform, we developed a pattern search tool in addition to simulating the GoL using pre-defined or subsequently adjusted rules of evolution. The evolution of patterns in this game depends on the initial state and the evolution rules, or updates. Given the computational complexity and the large number (theoretically infinite) of patterns and rules that can be constructed, finding patterns with characteristic properties is a demanding and time-consuming process. Automating this process can significantly speed up the search and isolation of characteristic patterns. Examples of characteristic patterns include stationary patterns (which do not change at all—“still life”), oscillators (which periodically return to their initial state after n steps), and mobile patterns (“gliders” and “spaceships”) that move across the simulation field and may have an oscillatory component during their movement. Importantly, the criteria for selecting characteristic properties can be defined in any way. In our case study, we chose symmetrical properties of patterns.

The developed tool searches for a characteristic pattern using a *brute force* approach. Brute-force algorithms exhibit both advantages and disadvantages. Advantages: Brute-force algorithms are straightforward to implement and understand. They do not require complex logic or data structures. Since brute-force methods systematically explore all possible solutions, they are guaranteed to find the correct solution if it exists. Disadvantages: Brute-force search is often inefficient, especially for large problem spaces. It can be very slow because it examines every possible solution, leading to high time complexity. As the size of the problem increases, the time required for brute-force search grows exponentially, making it impractical for large datasets or complex problems. We kept the computational complexity of the problem small enough to allow for brute-force pattern search. It is

implemented as a Matlab function that takes as inputs arguments the size of the simulation field in which it will perform the search and the size of the pattern that will be tracked for changes during evolution. The size of the pattern cannot exceed the size of the simulation field minus one, as evolution does not occur on the edges of the field, in the last row of cells on either side. For a given field size $m \times m$, the search tool generates all possible variations without repetition of three to m^2 living cells in the given field, arranged in every possible unique way, and then simulates the GoL and tracks the outcomes. The initial size of three is chosen because patterns with one and two cells are simple and have been thoroughly explored. Because larger patterns have memory management issues, it is impossible to memorize all possible variations without repetition. Therefore, we developed a pattern generator to pass the search tool one pattern at a time until the entire range of possible patterns has been exhausted. During a simulation, the search tool saves the patterns in a special Matlab data structure that it returns after the simulation.

A step-by-step explanation of the *brute force* pattern search is as follows: (1) initialize parameters (input the size of the simulation field $m \times m$, input the size of the pattern $p \times p$), (2) generate all possible patterns with a size between three and p , (3) iterate over patterns (place the pattern in the simulation field and initialize the GoL simulation with the pattern as the starting state), and (4) simulate the GoL (run the GoL simulation for a predefined number of steps or until a stable pattern emerges and keep recording states of the GoL at predefined checkpoints).

Figure 5 displays the outcome of a search for stationary patterns in the simulation field. We chose a relatively small field to minimize computational demands, as searching for patterns on excessively large fields exerts unnecessary pressure on computational resources and prolongs the simulation. This simple case serves as a demonstration of the search for stationary patterns. Unlike oscillators and mobile structures, stationary structures are insensitive to the introduction of stochasticity into the evolution rules in the implementation described here. Therefore, all three types of rules have common stationary patterns. In future research, it would be interesting to investigate whether certain oscillating or mobile patterns are insensitive to stochasticity, or to investigate those that arise due to stochasticity in the evolution rules and are not present in the original simulation.



Figure 5. Results of *brute-force* search for stationary 4×4 patterns on 5×5 field.

6. Conclusions

In this paper, after reviewing previous studies of the GoL, we discuss relevant philosophical and evolutionary–biological implications of the historicity of evolution and an implementation of the historicity feedback loop of updates in GoL simulation. We developed a simulation platform with conveniently changeable rules and the ability to visualize the evolution of the GoL on a field of arbitrary dimensions and a pattern searcher that meets certain criteria, such as stationarity or oscillating patterns, in a certain period. In the first regime, the initial set of rules that can be selected includes the classical Conway rules. The second regime introduces sequential stochastic evolution that violates Markov chains through historicity (the sequential update of cells based on the “visibility” of the chosen environment, achieved via a feedback loop on already completed updates), and the third regime includes probabilistic factors in updates. We discuss a convenient case of symmetry emergence and breaking in evolution and in the GoL in relation to all three simulation regimes on the platform. It turns out that bilateral and radial symmetry occur as evolutionary by-products in regime (1), the classical GoL regime, but once achieved as stable forms in classical GoL, they cannot be escaped. We argue that introducing stochasticity via historicity (regimes (2) and (3)) leads to more realistic evolutionary and biological scenarios. The introduction of stochasticity and historicity in regimes (2) and (3) allows

for more dynamic and complex evolutionary scenarios. In these regimes, the feedback loop and probabilistic factors disrupt the deterministic nature of the classical GoL rules. This disruption enables the system to explore a broader range of configurations and patterns, including those that break the symmetries observed in the classical regime. By incorporating stochastic elements and historicity, the simulation can exhibit more realistic evolutionary behaviors, including symmetry breaking. Symmetry breaking in this context refers to the process where initially symmetric patterns evolve into configurations that no longer maintain the original symmetry. This phenomenon is more representative of real-world biological and evolutionary processes, where symmetry is not always preserved due to varying environmental conditions and historical influences. The ability to observe symmetry breaking through stochastic and historical updates provides insights into how evolutionary processes might occur in natural systems. It reflects a more nuanced view of evolution, where randomness and historical context play crucial roles in shaping patterns and structures. This approach aligns with biological systems where symmetry is often broken due to adaptive changes, environmental factors, and historical contingencies.

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