Characterizing Open-Ended Evolution Through Undecidability Mechanisms in Random Boolean Networks

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Abstract

Discrete dynamical models underpin systems biology, but we still lack substrate-agnostic diagnostics for when such models can sustain genuinely open-ended evolution (OEE): the continual production of novel phenotypes rather than eventual settling. We introduce a simple, model-independent metric, Ω, that quantifies OEE as the residence-time-weighted contribution of each attractor's cycle length across the sequence of attractors realized over time. Ω is zero for single-attractor dynamics and grows with the number and persistence of distinct cyclic phenotypes, separating enduring innovation from transient noise. Using Random Boolean Networks (RBNs) as a unifying testbed, we compare classical Boolean dynamics with biologically motivated non-classical mechanisms (probabilistic context switching, annealed rule mutation, paraconsistent logic, modal necessary/possible gating, and quantum-inspired superposition/entanglement) under homogeneous and heterogeneous updating schemes. Our results support the view that undecidability-adjacent, state-dependent mechanisms—implemented as contextual switching, conditional necessity/possibility, controlled contradictions, or correlated branching—are enabling conditions for sustained novelty. At the end of our manuscript we outline a practical extension of Ω to continuous/hybrid state spaces, positioning Ω as a portable benchmark for OEE in discrete biological modeling and a guide for engineering evolvable synthetic circuits.

Introduction

Biological evolution has generated a broad diversity of forms and functions across scales, from microbes to large multicellular organisms. As an example, if we focus on microbial species alone, their variety has been estimated to be $\sim 10^{12}$ (Locey and Lennon, 2016), which is approximately the number of galaxies in the observable universe (Conselice et al., 2016). One of the central lessons from Darwin (1859) is that this diversity is not a static catalogue but is dynamically produced by evolution. Even though any real biosphere is finite and the underlying physical and chemical mechanisms have remained largely unchanged for roughly 4 billion years, the biosphere has continued to explore new combinations of forms and functions without any clear sign of saturation. In this practical sense, biological evolution appears *effectively open-ended* on geological timescales (Packard et al., 2019a): the combinatorial space of possible genotypes and phenotypes is so large, and the dynamics of evolution so far from equilibrium, that ongoing novelty can be expected rather than exceptional. In the artificial life literature, this has motivated the study of *open-ended evolution* as the ongoing production of novel, adaptive structures without an intrinsic upper bound on diversity or complexity (Packard et al., 2019b). Since processes having the property of ongoing creative productivity are not necessarily biological, we have generalized this conceptualization to include *open-endedness* in any form (Stanley, 2019).

Despite its ubiquity in the literature, there is no full consensus on how to define open-ended evolution (OEE). Some authors take the continual generation of novelty—the sustained appearance of previously unseen entities or behaviors—to be sufficient for a system to be labeled as *open-ended* (Soros and Stanley, 2014). Others argue that OEE should be reserved for cases in which some notion of system *complexity* can grow without an a priori upper bound, as seems to be suggested by empirical scaling laws across levels of biological organization (Corominas-Murtra et al., 2018). However, this immediately raises the methodological problem of how to define and measure complexity in a way that is both domain-independent and monotonically increasing along evolutionary trajectories. As a result, the literature distinguishes between variety-based and complexity-based conceptions, and more generally between multiple "flavors" of open-endedness (Taylor et al., 2016). For our own purposes, we will operationally define open-endedness as the capability of a system to continually generate novel (without necessarily being increasingly complex) structures or behaviors without settling into fixed or cyclic states. In this way, given a system, we are interested in how to classify its dynamics as open-ended.

So far, two overarching suites of metrics have been proposed to measure OEE. On the one hand, *Evolutionary Activity Statistics* measures the degree of adaptive dynamics within a population by tracking the persistence of specific elements, called "components" (Bedau et al., 1997, 1998).

As a disadvantage of this approach, we should know what the "components" are *ab initio*; these, in fact, are selected arbitrarily. Furthermore, it also fails to take into account that "components" can evolve over time, disregarding their ability to acquire new functions (or become obsolete) through adaptation (Wong et al., 2023). On the other hand, *Measurements of Open-ended Dynamics in Evolving Systems* (MODES) is a toolbox designed to analyze and quantify the dynamics of evolving systems, specifically focusing on identifying features that are indicative of OEE (Dolson et al., 2019). Although MODES is an ambitious proposal, its application is limited to specific systems. In fact, some of its metrics only make sense in AVIDA, an artificial life software platform to study the evolutionary biology of self-replicating and evolving digital organisms (Lenski et al., 2003).

Moreover, classifying a system as open-ended does not help us to understand how this property arose evolutionary speaking. As Stepney and Hickinbotham (2024) have pointed out, the focus should be on scrutinizing the mechanisms underlying open-endedness, not simply trying to quantify it. Of course this requires a thinking shift with respect the current approaches to OEE, suggesting that the capacity for open-endedness arises from evolution itself, rather than being a pre-existing condition of the entire evolutionary system. This perspective, championed by Pattee and Sayama (2019), emphasizes how organisms can create their own mechanisms, such as language, that make late evolution more open-ended. Thus, we must first discern what universal conditions or mechanisms contribute to the emergence of evolutionary open-endedness.

Using a sufficiently general and formal approach to circumscribe any resource-bounded discrete system, Adams et al. (2017) have shown that state-dependence is a universal mechanism to achieve OEE. However, as the authors recognized, they did not explore self-referential mechanisms between organisms and their environment, which they warned could have enriched their experimental findings. As we have shown in previous research using the power and generality of category theory to encompass all kinds of mathematical structures (and formal or computational models), semantic closure—the self-referential mechanism where an organism's own actions and interpretations create the context for future actions—is crucial for robust self-replication, niche construction, and evolved open-endedness in any system (López-Díaz and Gershenson, 2024). CGG: update reference (2026)

In particular, in the case of non-cyclical discrete dynamical systems where there are an infinite number of possible states and each state must contain all the information needed to compute successive states, Hernández-Orozco et al. (2018) have formally proved undecidability to be a requirement for OEE, showing that adaptation itself is a generalization of the halting problem (Turing, 1936). The existence of adapted behaviors whose appearance is formally un-

decidable reframes evolution as not merely a search through a possibility space, but as an ongoing construction of uncomputable futures (Kauffman and Roli, 2021). Therefore, any mechanism associated to the impossibility of constructing a single algorithm that always leads to a correct yes-or-no answer is a potential candidate for promoting open-endedness.

Using Random Boolean Networks (RBNs), we build on earlier work that treated changes in the attractor landscape as a proxy for evolvability. In particular, Torres-Sosa et al. (2012) introduced selection criteria that reward networks which both conserve existing attractors and generate new ones, showing that this conservation-innovation trade-off can drive the evolution of critical dynamics. Here we repurpose this attractor-level perspective as an explicit, substrate agnostic metric of open-endedness that is applicable to any dynamical system with discrete state space. Recognizing that open-endedness is inherently a product of evolutionary processes, we further explore the underlying mechanisms driving this phenomenon. Particularly, we focus our attention on non-classical logics: formal systems that modify, extend, or deviate from the foundational principles of classical logic by rejecting or altering concepts such as the law of excluded middle (a statement is either true or false) or bivalence (only two truth values exist) (Priest, 2008). These alternative frameworks are necessary for modeling situations where classical logic is insufficient, such as dealing with incomplete information, statements that are neither true nor false, paradoxical information, and alternative kinds of knowledge and reasoning. In this way, we investigate the role of undecidability in its different facets to promote open-endedness in a biological model.

In the next section, we detail our methodology, emphasizing the relevance of Random Boolean Networks (RBNs) and non-classical logics in biological modeling, while also introducing our novel open-endedness metric. Afterwards, we proceed to show our results considering both homogeneous and heterogeneous RBNs, exploring whether structural and temporal heterogeneity also serve as key drivers of open-endedness. Subsequently, we discuss the results obtained, revealing strategic insights into how systems can maximize their open-endedness based on their inherent conditions. Finally, we conclude our work by proposing avenues for future research, including a generalization of our metric to encompass systems with continuous state space.

Methods

Random Boolean Networks

A gene regulatory network (GRN) is a collection of genes, RNA, and proteins that control which genes are turned on or off, and how active they are, in a cell (Davidson and Levin, 2005). They act as a cellular control system, determining when and where genes are expressed, which in turn dictates the cell's function and behavior. These net-

works are crucial for fundamental biological processes like cell development (Levine and Davidson, 2005), differentiation (Roy and Kundu, 2014), and responding to environmental changes (Crombach and Hogeweg, 2008). As a way of capturing the complexity of GRNs, Kauffman (1969) first introduced Random Boolean Networks (RBNs): discrete dynamical systems modeled as directed networks, where each node (a gene) has a Boolean value (0 or 1) and is randomly connected to other nodes.

Formally, a directed graph D consists of a set V of elements $a, b, c, \ldots$ called the nodes of D and a set A of ordered pairs of nodes (a, b), (b, c), $\ldots$ called the arcs of D. We use the symbol ab to represent the arc (a, b). If ab is in the arc set A of D, then we say that a is an in-neighbor of b, and also that b is an out-neighbor of a. We say that D is k-in regular ($k \geq 1$) if every node has exactly k in-neighbors. The out-degree of a node a is the number of out-neighbors of a. Let $D = (V, A)$ be a k-in directed graph; a family $(f_a)_{a \in V}$ of functions $f_a : \{0, 1\}^k \longrightarrow \{0, 1\}$ is called a Boolean network on D.

A Boolean network is called random if the assignment $a \mapsto f_a$ is made at random by sampling independently and uniformly from the set of all the 2^{2^K} Boolean functions with K inputs. A function $\phi : V \longrightarrow \{0, 1\}$, $a \mapsto \phi_a$, is called a state of the random Boolean network on D. The value ϕ_a is called the state of a. The updating function $F(\phi)$ of a state ϕ is the function $F : V \longrightarrow \{0, 1\}$, $a \mapsto \phi'_a$, defined as

$$\phi'_a = f_a\left(\phi_{a_1}, \ldots, \phi_{a_k}\right). \tag{1}$$

Given the complexity exhibited by real GRNs, Kauffman assumed the following four conditions in his model (Kauffman, 1969):

1. Each gene is regulated by exactly K other genes.

2. The K genes that regulate each node are chosen randomly using a uniform probability.

3. All genes are updated synchronously, i.e., at the same time step (Gershenson, 2004b).

4. Each gene f_a maps the input $(\phi_{a_1}, \ldots, \phi_{a_k})$ to the 'on' state with probability p and to the 'off' state with probability $1 - p$.

The first two imply *structural* homogeneity, the third *temporal* homogeneity, and the fourth *functional* homogeneity. In this paper, a heterogeneous RBN refers to an architecture with structural and temporal heterogeneity (Sánchez-Puig et al., 2023). Otherwise, a homogeneous RBN refers to an architecture with structural, temporal, and functional homogeneity. Following the methodology proposed by López-Díaz et al. (2023), to implement structural homogeneity (heterogeneity), we use Poisson (Exponential) as the degree distribution. For implementing temporal heterogeneity

we resort to the pre-programmed asynchronous scheme in CUBEWALKERS, an open-source, GPU-based Python tool for simulating Boolean networks (Park et al., 2023). Once we have introduced RBNs, let us discuss the biological role of non-classical logics and how we can implement them using RBNs.

Probabilistic Boolean Network (PBN)

A PBN is a collection of Boolean networks in which a constituent network governs gene activity for a random period of time before another randomly chosen constituent network takes over. Stochastic phenotype switching is a well-established adaptation strategy in fluctuating environments, classically demonstrated in many bacterial systems (Acar et al., 2008). PBNs were introduced precisely to capture rule-based uncertainty and context switching in GRNs, and have since become a standard for modeling, inference, and control of genetic networks (Shmulevich and Dougherty, 2010). This makes PBNs the most direct way to incorporate environmental contingency and regulatory program switching into an otherwise Boolean framework.

Formally, a PBN consists of a sequence $V = \{x_i\}_{i=1}^n$ of n nodes, where $x_i \in \{0, 1\}$, and a sequence $\{\mathbf{f}_l\}_{l=1}^m$ of vector-valued functions, defining constituent networks. Each vector-valued function $\mathbf{f}_l = (f_l^{(1)}, f_l^{(2)}, ..., f_l^{(n)})$ determines a constituent network, or context, of the PBN. The function $f_l^{(i)} : \{0, 1\}^k \to \{0, 1\}$ is a predictor of gene i whenever network l is selected. At each updating epoch a decision is made whether to switch the constituent network. A constituent network is randomly selected from among all constituent networks according to the selection probability distribution $\{c_l\}_{l=1}^m$ such that $\sum_{l=1}^m c_l = 1$. In our code, we generate m pure-Boolean contexts by resampling lookup tables (LUTs) from a base BN and set uniform c_l. We then execute long segments in the current context, updating deterministically within that context and only sampling a new context at segment boundaries. This cleanly reproduces the standard PBN semantics used in the gene-regulation literature (Shmulevich and Dougherty, 2010).

Annealed Rule Mutation (ARM)

GRN logic is not immutable: transcriptional programs can rewire or tune their effective rules across time due to chromatin remodeling (Filtz et al., 2014), TF post-translational modifications (Swift and Coruzzi, 2017), or changing cofactor abundance (Tomljanović et al., 2025). From a modeling standpoint, this is the annealed perspective familiar from RBN theory, where rule tables are treated as stochastic variables across updates, capturing plasticity not represented by fixed ("quenched") rules. Empirically, modern time-resolved genomics underscores that regulatory interactions are dynamic over minutes-hours, supporting annealed or partially annealed abstractions when studying innovation and adaptability (Meeussen and Lenstra, 2024).

The annealed approximation of Derrida and Pomeau (1986) remains a standard conceptual scaffold, and recent reviews emphasize explicitly time-dependent GRN modeling (Marku and Pancaldi, 2023).

Formally, an ARM network is a BN in which each LUT entry $f_i(\cdot)$ is a *mutable rule* with parameter $p_{\mathrm{ARM}} \in [0,1]$. Concretely, for an input key u, the stored value is a record $\theta(u) = \{\text{initial value} \in \{0,1\}, \text{mutation probability} = p_{\mathrm{ARM}}\}$. The evaluator η samples the output each time step by flipping the initial bit with probability p_{ARM} : $\mathrm{Bernoulli}(1 - p) \times \text{initial value} + \mathrm{Bernoulli}(p) \times (1 - \text{initial value})$. Thus, $x_i(t+1) = \eta(\theta(x_i(t)))$. If $p_{\mathrm{ARM}} = 0$, we recover a quenched BN; $p_{\mathrm{ARM}} > 0$ produces an annealed mutation rate in the gate outputs. In our code, we flip the stored bit with probability p_{ARM} each time it is read. In practice, this means our update loop should pass LUT entries before computing the node's next value, thereby sampling an annealed truth-table at run time. This ARM mechanism is distinct from PBNs (which switch entire contexts); here, individual rules mutate locally and continuously, providing a complementary axis of plasticity.

Paraconsistent Logic

Cells frequently face conflicting regulatory cues: the same upstream factor can both promote and inhibit a response depending on context, dosage, or timing (Hart et al., 2012). This is well documented in immune and developmental systems, e.g., IL-2 simultaneously supporting proliferation and death in T cells (Hart and Alon, 2013); such circuits exploit antagonistic arms to achieve robustness, fold-change detection, and pulsatile dynamics, hence called "paradoxical components" (Hart et al., 2014). These phenomena motivate logics that tolerate local contradictions rather than exploding to triviality, which is exactly what paraconsistent formalisms provide (Gershenson, 1999). Using an inconsistency-tolerant semantics at the rule/local-gate level mirrors how GRNs integrate pleiotropic, noisy, or partially contradictory inputs without collapsing function.

Formally, let $V = \{x_i\}_{i=1}^n$ be nodes with Boolean states $x_i \in \{0,1\}$. Each node i has LUTs $f_i : \{0,1,\times\}^k \to \{0,1,\times\}$, where $\times$ denotes an inconsistent output. In our implementation, inconsistency is annotated: some LUT entries are replaced by pairs $(2,b)$ with contradiction probability $\pi \in [0,1]$. At update time, a resolver ρ maps regulator inputs $u \in \{0,1,(2,b)\}^n$ to a determinate value by discarding 2's where possible and returning unanimity if present; otherwise it returns $(2,b^*)$ with b^* the local majority. This the network's global update is $x_i(t+1) = \rho(f_i(x_i(t)))$, which preserves non-explosive behavior under local contradictions. In our code, each LUT entry is independently replaced by a pair as described above with certain probability π, such that contradictions can persist and propagate until later steps resolve them via majority among incoming signals, closely matching a three-valued, inconsistency-tolerant gate seman-

tics; echoing how paradoxical circuits stabilize responses in biology.

Modal Logic

Many regulatory claims in biology are modal: a factor may be necessary (must be present) or merely possible/sufficient (can enable) for an outcome, and these claims are inherently contextual (cell type, chromatin state, signaling milieu) (Monteiro et al., 2008). The systems biology community routinely encodes such "must/possibly" properties with temporal/modal logics and verifies them on GRN models via model checking, e.g., verifying that "eventually gene A activates B and always C stays off" in stress-response or cell-cycle networks (Monteiro et al., 2014). This makes modal operators a natural abstraction layer for contextual constraints in GRN dynamics. Representative overviews and applications include model checking for logical regulatory networks and temporal-logic pattern mining in cellular models (Giacobbe et al., 2015).

Formally, a modalized RBN augments a standard RBN with a Kripke frame $\mathcal{K} = (V, R)$, where V is the set of nodes and $R \subseteq V \times V$ encodes *accessibility* among nodes. Each LUT entry for node i may take values in $\{0, 1, \text{possible}, (\text{necessary}, v)\}$. At time t, let $A_i(t) = \{j \in V | (i,j) \in R\}$ be i's accesible set and let $\mathbf{x}_{A_i}(t)$ be their current states. The evaluation map μ is: $\mu(\text{possible}) = 1$ iff $\exists j \in A_i(t) : x_j(t) = 1$; $\mu((\text{necessary}, v)) = v$ iff $\forall j \in A_i(t) : x_j(t) = 1$, else 0; and $\mu(b) = b$ for $b \in \{0,1\}$. The network update is $x_i(t+1) = \mu(f_i(x_i(t)))$. In our code, we build a Kripke frame as described above and sample an accessibility degree d, wiring each node to up to d accessible nodes. It then rewrites LUT outputs by flipping entries to the literal tokens *possible* or *necessary* (the latter carrying a concrete bit) with probabilities p_{possible} and $p_{\text{necessary}}$. This cleanly imports necessity/possibility semantics into our RBN while keeping the base state space Boolean.

Quantum Logic

While canonical GRNs are classical, quantum-inspired rules can model contextuality and "superposition-like" uncertainty during decision points (e.g., fate priming) (Cao et al., 2020). Moreover, quantum coherence and related effects have been directly observed in biological light-harvesting complexes (e.g., the Fenna-Matthews-Olson bacteriochlorophyll complex), suggesting that non-classical information processing can appear in biology under some conditions—even if not in gene regulation *per se* (Engel et al., 2007; Panitchayangkoon et al., 2010). The point here is not that GRNs are quantum, but that quantum-style operators offer a principled way to represent context-dependent mixture/branching and long-range correlations that classical gates do not capture natively (Franco et al., 2021).

In our work, we extend BN with (i) a *superposition* token and (ii) an *entanglement* pairing $E \subseteq V \times V$. LUT entries

then take values in $\{0, 1, \text{superposed}\}$. At each update, the evaluator κ maps the superposed state to a Bernoulli$(1/2)$ collapse in $\{0, 1\}$. If i is entangled with j, then $x_i(t + 1) = x_j(t)$ (a classical proxy for instantaneous correlation). Formally, $x_i(t + 1) = \kappa\left(f_i\left(x_i(t)\right)\right)$ if $(i, j) \notin E$; otherwise, $x_i(t + 1) = x_j(t)$. In our code, we uniformly assign a value (0 or 1) to the superposed state and, for entangled nodes, we simply copy the partner's current bit. This mirrors the behavioral signatures emphasized by Franco et al. (2021), i.e., superposition-like sampling and long-range correlations without changing the underlying Boolean state space. Now we can proceed to introduce our open-endedness metric.

A Novel Metric for Quantifying Open-Endedness in Any Discrete State Space

In the deterministic case, regardless of their initial configuration, all Boolean networks fall into an attractor (Gershenson, 2004a). Attractors are stable sets of states that represent the long-term behavior of the network. Once a Boolean network reaches an attractor, it will remain within that set of states indefinitely unless perturbed. Attractors can be single states (point attractors) or cycles of multiple states (cycle attractors) and are often linked to biological phenotypes, such as cell types in GRNs (Kauffman, 1969). For any attractor in a Boolean network, we can calculate the number of unique states the network cycles through repeatedly (cycle-length) and the number of time steps the network remains trapped within the attractor (residence-time). In this way, given a RBN with N nodes where m different attractors appear during T time steps, we define open-endedness as

$$\Omega = \lim_{T \to \infty} \frac{1}{T^2} \sum_{j=1}^{m} d_j \, k_j \, , \qquad (2)$$

where k_j and d_j are respectively the cycle-length and residence-time of the attractor A_j discovered within T time-steps. In layman's terms, open-endedness is the residence-time-weighted temporal average of the individual cycle-lengths for each attractor discovered in the current dynamics, as the number of time steps tends to infinity. In the deterministic case, when $m = 1$, we have a single attractor of length $k_1 \in \{1, 2, \ldots, 2^N\}$. If we enter this attractor at time step t_0, then

$$\Omega = \lim_{T \to \infty} \frac{1}{T^2} d_1 \, k_1 = \lim_{T \to \infty} \frac{1}{T^2} \left(T - t_0\right) k_1 = 0. \qquad (3)$$

Thus, according to Ω, a system with a single attractor has always null open-endedness. This is totally coherent to what we have defined as open-endedness: having a single attractor implies that the system, regardless of its initial state (within a certain basin of attraction), will eventually settle into a specific, predictable long-term behavior represented by that single attractor. It is also instructive to consider the opposite

extreme: a maximally random process with lots of novelty but minimal dwell time. Suppose that at each time step the network jumps independently to a randomly chosen configuration in $\{0, 1\}^N$. We may treat each visited configuration as a point attractor with $k_j = d_j = 1$. After T steps we have $m(T) = T$ such "attractors", so

$$\Omega = \lim_{T \to \infty} \frac{1}{T^2} \sum_{j=1}^{T} 1 \cdot 1 = \lim_{T \to \infty} \frac{T}{T^2} = \lim_{T \to \infty} \frac{1}{T} = 0 \quad (4)$$

In other words, a process that constantly produces new states but never dwells on any of them is classified as non-open-ended by our metric: its novelty is pure noise. The same conclusion holds for a "slow" or delayed random walk on a finite state space that includes self-loops, as long as the expected residence-time in any configuration remains bounded while T grows. In that case, the numerator $\sum_j d_j k_j$ can grow at most linearly with T, so $\Omega(T) = \mathcal{O}(1/T)$ and still vanishes in the limit. Non-zero Ω therefore requires not only the continual appearance of distinct attractors, but also that the total time spent in structured, recurrent dynamical patterns grows faster than linearly with T. Now let us assume that the dynamics are no longer deterministic or completely random. By construction, there exist an ordered sequence of time steps, $\{t_1^i, t_1^f, t_2^i, t_2^f, \ldots, t_m^i, t_m^f\}$, such that A_j appears in $[t_j^i, t_j^f] \quad \forall j \in \{1, \ldots, m\}$. This implies the following chain of equalities and inequalities:

$$\Omega = \lim_{T \to \infty} \frac{1}{T^2} \sum_{j=1}^{m} d_j \, k_j$$

$$= \lim_{T \to \infty} \frac{1}{T^2} \sum_{j=1}^{m} (t_j^f - t_j^i) k_j$$

$$\leq \lim_{T \to \infty} \frac{1}{T^2} \left[\sum_{j=1}^{m} (t_j^f - t_j^i) k_j \right]^2$$

$$\leq \lim_{T \to \infty} \frac{1}{T^2} \left[\sum_{j=1}^{m} (t_j^f - t_j^i)^2 \right] \left[\sum_{j=1}^{m} k_j^2 \right]$$

$$\leq \lim_{T \to \infty} \frac{1}{T^2} \left[\sum_{j=1}^{m} (t_j^f - t_j^i) \right]^2 \left[\sum_{j=1}^{m} \left(2^N\right)^2 \right]$$

$$\leq \lim_{T \to \infty} \frac{1}{T^2} \left[T\right]^2 \left[m \, 2^{2N}\right]$$

$$\leq m \, 2^{2N}.$$

The first inequality is due to $\sum_{j=1}^{m}(t_j^f - t_j^i)k_j > 1$, the second due to the Cauchy-Schwarz inequality, the third due to $t_j^f - t_j^i > 0$ and $k_j \in \{1, 2, \ldots, 2^N\}$, and the fourth because $\sum_{j=1}^{m}(t_j^f - t_j^i) \leq T$. Therefore, $\Omega \leq m \, 2^{2N}$, where

N is the number of nodes in the network and m the number of attractors reached during the dynamics. Observe that, as $m \to \infty$, $\Omega \to \infty$. This is again coherent with our conception of open-endedness, as generating an unbounded number of potential phenotypes is translated as being open-ended. Later in the Discussion section, we will situate our metric with respect to prior definitions and measurement programs in the OEE literature.

Results

We evaluated open-endedness (Ω) across classical Random Boolean Networks (RBNs) and four non-Boolean extensions (Paraconsistent, Modal, Quantum-inspired, and Annealed Rule Mutation (ARM)) together with Probabilistic Boolean Networks (PBNs). The analysis pipeline proceeded as follows.

1. First, for each average connectivity K on a fixed grid ($K \in [1.1, 4.5]$ in steps of 0.2), we generated $1,000$ independent RBNs of $N = 100$ nodes with random initial states and simulated each network for $T = 10^6$ time steps. The full parameter sweeps used to select the settings reported below, as well as sensitivity checks, are provided in the Supplementary Material.

2. Second, for each base RBN we produced transformed variants by applying the alternative mechanisms to the same structure (see Methods). We then proceeded to run these transformed RBNs under the same conditions.

3. Third, within each logic we scanned a discrete parameter grid and, for each parameter combination, computed the curve $K \mapsto \Omega(K)$ by averaging Ω over the $1,000$ networks.

4. Fourth, to summarize a logic's overall performance we used the *area under the Ω-K curve* (numerical trapezoidal rule) as a scalar objective and selected, per logic, the parameter combination that maximized this area.

5. Finally, to compare logics concisely in the main text we plot only these *best* curves for the homogeneous and heterogeneous cases, respectively; all intermediate sweeps and additional diagnostics appear in the Supplementary Material.

We distinguish two architectural regimes. In the *homogeneous* case, networks have structural, temporal, and functional homogeneity; in practice we use a Poisson in-degree distribution (fixed mean K), synchronous updating, and a constant bias of 0.5. In the *heterogeneous* case, we introduce structural and temporal heterogeneity; in practice we use an Exponential in-degree distribution (same mean K) and a non-deterministic asynchronous update scheme. In both regimes, the classical baseline is a deterministic

BN; PBNs add context switching across deterministic constituents; ARM flips LUT outputs at read-time with probability μ; Paraconsistent logic injects locally contradictory table entries with probability c; Modal logic rewrites entries to modal tokens according to (a, p_p, p_n) (accessibility degree and the probabilities of possible/necessary); and Quantum-inspired logic introduces superposed outputs with probability sp and pairs up to e entangled nodes (see Methods).

Figures 1 and 2 report, for each regime, the single best curve per logic under the selection rule above. Legends list the winning parameter settings for each mechanism; for consistency we abbreviate parameters as: "ctx" = number of PBN contexts, σ = PBN switching probability per epoch, μ = ARM mutation probability, c = paraconsistent contradiction probability, a = modal accessibility degree, p_p/p_n = modal probabilities of writing possible/necessary, sp = superposition probability, and e = number of entangled pairs. Axes are shared across panels: the horizontal axis is average connectivity K; the vertical axis is our open-endedness score Ω (see Methods). Because our goal in this section is to document the outputs and the evaluation process, we defer interpretation to the Discussion section, where we will start by exploring how our metric is related to previous approaches, showing how it is a complementary measure of novelty.

Discussion

Our starting point is the formal program that sought system-independent definitions of "unbounded evolution" (UE) and "innovation" in discrete dynamical systems (Adams et al., 2017). That work emphasizes unboundedness and genuinely novel state production as the core signatures of OEE, abstracted away from any particular substrate or encoding. Our metric takes that spirit and turns it into a computable diagnostic that is applicable to any discrete state space: by counting distinct phenotypic outcomes (attractors or coarse-grained phenotypes) produced across a sliding temporal window, it operationalizes "ongoing innovation" without assuming access to asymptotic time. In particular, once the number m of distinct attractors encountered by the dynamics diverges, our open-endedness score Ω diverges as well, matching the intuition that an unbounded supply of phenotypes corresponds to open-endedness, while remaining usable at finite horizons. This finite-horizon property complements Adams et al. (2017) asymptotic criteria for UE/innovation and allows us to probe parameter regimes where novelty generation accelerates before any formal proof of unboundedness is in sight.

Compared to the *Evolutionary Activity Statistics* (EAS) tradition and the Bedau-Packard classification of long-term dynamics (Bedau et al., 1997, 1998), our approach dispenses with component-level activity counters and the accompanying choices of neutral baselines. The Bedau program classifies systems via diversity and activity time series, a lens
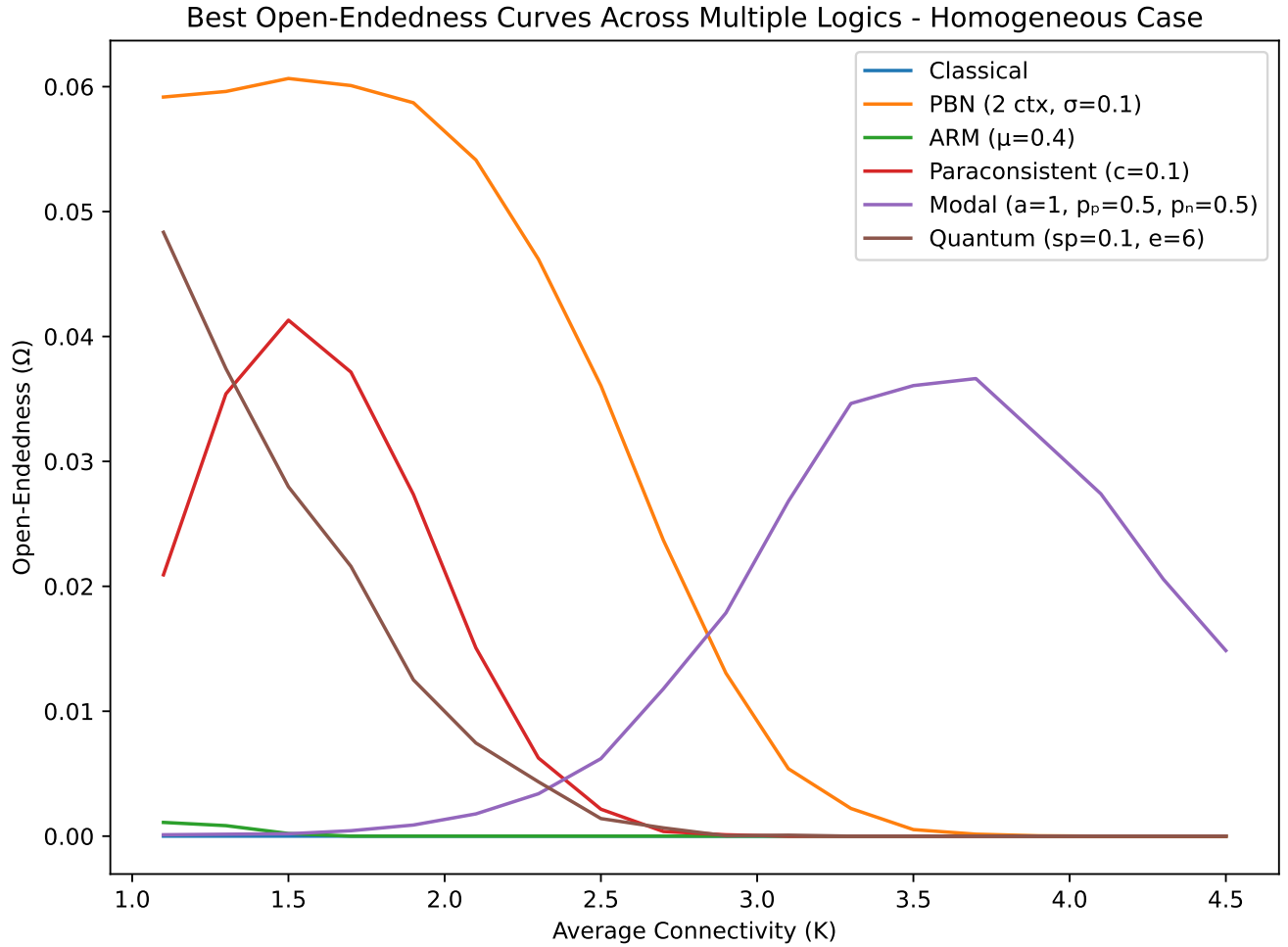
Figure 1: **Best open-endedness curves across logics - Homogeneous Case.** Each curve reports the across-network mean $\Omega(K)$ for the parameter combination within a logic that maximized the area under the curve (AUC) on the K grid (1.1 to 4.5 in steps of 0.2). Homogeneity comprises Poisson in-degree, asynchronous updates, and fixed bias (0.5). For every K, we averaged over $1,000$ independently generated networks of $N = 100$ nodes; each simulation ran for $T = 10^6$ time steps from a random initial state. The legend shows the selected (AUC-maximizing) parameters: *Classical* (deterministic baseline); *PBN* "(2 ctx, $\sigma = 0.1$)" indicates two deterministic contexts with switching probability $\sigma = 0.1$ per epoch; *ARM* "($\mu = 0.4$)" flips each LUT output with probability 0.4 when read; *Paraconsistent* "($c = 0.1$)" replaces LUT entries by contradictory tokens with probability 0.1; *Modal* "($a = 1, p_p = 0.5, p_n = 0.5$)" uses accessibility degree $a = 1$, with probabilities $p_p = 0.5$ and $p_n = 0.5$ of writing `possible` and `necessary`, respectively; *Quantum* "($sp = 0.1, e = 6$)" writes `superposed` with probability $sp = 0.1$ and entangles $e = 6$ node pairs. Note that the *Classical* curve collapses to zero, so it is not visible in the plot. Shaded confidence bands are omitted here to emphasize the comparative shapes; full parameter sweeps are provided in the Supplementary Material.

that has been productively used but depends on how components and activity are defined and normalized across domains. Our metric instead interrogates the reachable state space itself—counting distinct phenotypic outcomes realized within a moving window—and therefore avoids reliance on a priori component partitions or domain-specific neutral models while still distinguishing regimes with sustained novelty from those that saturate. In this way it is

compatible with, but orthogonal to, EAS-style summaries.

The MODES toolbox reframed measurement around four high-level "hallmarks" (change, novelty, complexity, and ecological potential) offering portable algorithms and inviting lower-level mechanistic metrics to complement them (Dolson et al., 2019). Our metric precisely fills that niche: it is a low-level, substrate-agnostic counter of realized phenotypic novelty that can be dropped into any discrete-
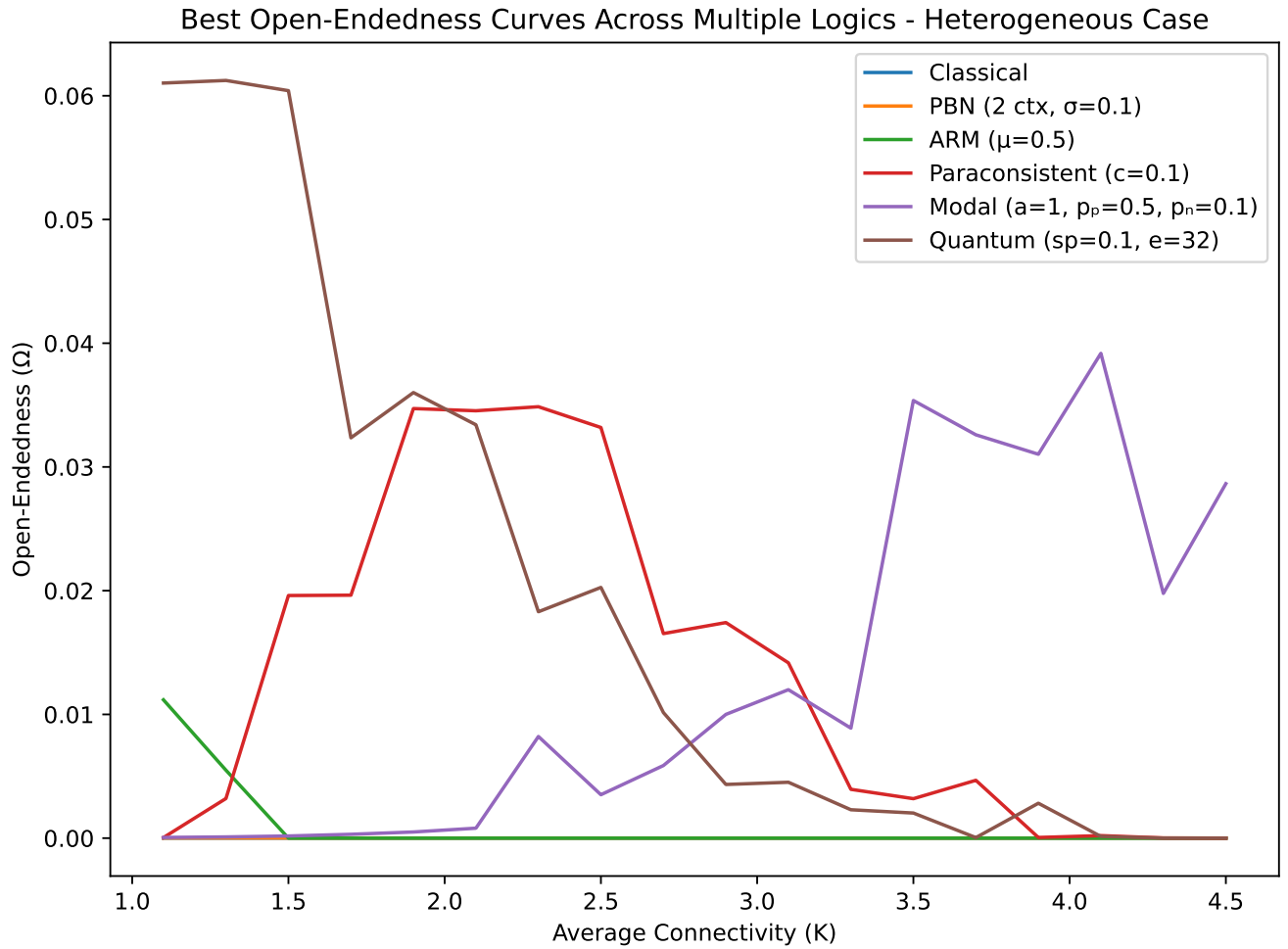
Figure 2: **Best open-endedness curves across logics - Heterogeneous Case.** Same plotting and selection protocol as Fig. 1, but for structurally and temporally heterogeneous networks (Exponential in-degree; stochastic asynchronous updates). For each K, results average $1,000$ networks of $N = 100$ nodes simulated for $T = 10^6$ steps. The AUC-maximizing parameter sets (legend) are: *Classical* (deterministic baseline); *PBN* "(2 ctx, $\sigma = 0.1$)"; *ARM* "($\mu = 0.4$)"; *Paraconsistent* "($c = 0.1$)"; *Modal* "($a = 1, p_p = 0.5, p_n = 0.1$)"; and *Quantum* "($sp = 0.1, e = 32$)". As in Fig. 1, Ω values are residence-time weighted cycle-lengths normalized by T^2 (see Methods). Note that both *Classical* and *PBN* curves collapse to zero, so they are not visible in the plot. All intermediate sweeps, robustness checks (e.g., alternative K grids and T values), and per-logic ablation plots appear in the Supplementary Material.

state model (including RBN variants) and read alongside MODES' hallmarks. In particular, MODES highlights continual novelty as a central hallmark; our sliding-window Ω makes this hallmark numerically explicit in systems where "phenotype" is tied to attractors or coarse-grained dynamical outcomes, and it can be summarized jointly with MODES' other hallmarks to separate sustained novelty from transient bursts.

Our emphasis on ongoing novelty also dovetails with the algorithmic-information view that relates strong forms of OEE to undecidability. Hernández-Orozco et al. (2018) showed that, for a broad class of sophistication-like com-

plexity measures, decidability imposes absolute limits on stable complexity growth and that strong OEE entails undecidability/irreducibility of adapted states. While our Ω deliberately does not attempt to estimate sophistication (Kolmogorov, 1965) or logical depth (Bennett, 1988), it is consistent with that result: in regimes where undecidable structure drives unbounded production of phenotypic outcomes, Ω will continue to rise with the number of distinct attractors realized; in decidable regimes, Ω saturates. Thus, our metric provides a computable proxy for detecting the phenomenology that undecidability results lead us to expect, without invoking heavy algorithmic-complexity estimators

whose incapability of distinguishing novelty from noise has been shown (Posobin and Shen, 2018).

Furthermore, our metric is squarely aimed at the York workshop's category of "ongoing generation of adaptive novelty" (Taylor et al., 2016). It implements exactly what that category asks us to detect: sustained production of new (and potentially adaptive) phenotypes over time, operationalized in finite windows and applicable across substrates. We explicitly do not promote York's second category ("ongoing growth of complexity") as a necessary lens on OEE. Beyond long-standing conceptual worries about what counts as "complexity," there is little biological support for the claim that natural selection relentlessly drives increases in organismal complexity; recent arguments review both theory and evidence indicating that complexity increases are contingent, often nonadaptive, and concentrated in a few lineages, with many trends pointing in the opposite direction (Lynch, 2025). Our focus on novelty avoids conflating open-endedness with monotone complexity growth, in line with these cautions.

Updating York's OEE classification, a group in Tokyo refined such a taxonomy (Packard et al., 2019b). Our metric most directly instantiates Tokyo Type 1 OEE (ongoing generation of interesting new kinds of entities/interactions) when the phenotype map treats attractors or coarse-grained behaviors as entities; it can also serve as an indicator for the evolution of evolvability (Tokyo Type 2 OEE) when the rate of novelty production increases across windows or under meta-evolution of the genotype-phenotype map. Where a system undergoes coarse-graining shifts that produce qualitatively new levels of organization (major transitions; Tokyo Type 3 OEE), the resulting explosion of new attractor classes will register as marked increases in Ω. By construction, our metric remains agnostic about meaning; to speak to Tokyo Type 4 OEE (semantic evolution) requires an explicit interpretation function from system states to task- or environment-defined semantics, at which point one can track whether the new phenotypes also carry new semantic roles. In short, Ω equips us with a portable finite-time detector for the axis of "ongoing generation" that both the York and Tokyo taxonomies place at the center of OEE. Now, let us go back and interpret the results we obtained.

In homogeneous networks, the PBN transformation achieves the largest Ω at low-medium connectivities, whereas Modal logic dominates at high connectivities (Fig. 1). The PBN outcome is consistent with the mechanism: piecewise deterministic motion inside a context, punctuated by rare switches, tends to string together long residence times in distinct attractor families, inflating the residence-time-weighted cycle contribution in Ω. Biologically, this mirrors bet-hedging via phenotype switching under resource-scarce conditions: exactly where sparse coupling (low K) limits within-context exploration, so context changes do the heavy lifting (Acar et al., 2008).

By contrast, when coupling is dense (large K), Modal gating becomes advantageous. "Necessary" constraints act as context-dependent canalizing conditions that suppress runaway sensitivity, while "possible" gates open alternative routes when local context permits; together they tame chaotic overshoot and create metastable corridors that repeatedly access distinct limit cycles. As a practical rule: in synchronous, homogeneous systems with limited connectivity, stochastic program switching (PBN) yields the highest open-endedness; as connectivity grows, context-dependent gating (Modal) overtakes by structuring exploration without freezing it.

Moving to heterogeneous networks, the picture changes qualitatively (Fig. 2). The PBN curve collapses toward zero over the entire K range, while Modal again excels at higher K, and Paraconsistent and Quantum-inspired mechanisms show localized gains at low-intermediate K. This collapse is not due to a change in the *number* of point attractors, those are determined by the rule tables and are independent of the updating scheme (Gershenson, 2004b), but rather to how our stochastic asynchronous updates interact with structural heterogeneity. In our simulations we use CUBEWALKERS' `asynchronous_set` update scheme, which randomly selects a set of nodes to be updated at each time step, so that the dynamics along a single trajectory are effectively noisy and long synchronous cycles are rarely realized. Combined with an Exponential in-degree distribution, this drives most initial conditions quickly into small recurrent classes (often fixed points or very short cycles) that have large basins of attraction.

Within each PBN context, trajectories therefore spend almost all their time in short attractors with cycle lengths k_j of order one; context switches mostly move the system between the basins of these same few attractors, rather than uncovering new long cycles. As a result, the summed residence-cycle contribution $\sum_j d_j k_j$ grows at most linearly with T, so $\Omega \to 0$ despite ongoing context changes. Modal logic is the exception because its necessity/possibility tests provide conditional activation that intermittently re-opens pathways even under asynchronous settling; hence its large spikes at high K. Paraconsistent logic yields a broad shoulder around $K \approx 2.3$: introducing controlled local contradictions near the order-critical boundary sustains exploratory dynamics without exploding to noise, in line with the known criticality-extending effects of heterogeneity (Sánchez-Puig et al., 2023; López-Díaz et al., 2023). Quantum-inspired rules perform best at very low K: superposition tokens plus a few long-range entanglements furnish correlated branching when wiring is sparse, boosting early-time exploration before asynchronous contraction dominates. The strategy that follows is therefore different from the homogeneous case: under heterogeneity/asynchrony, prefer Modal gating at high connectivity and use Paraconsistent or Quantum-inspired rules to lift Ω in sparse networks.

Some patterns are trivial yet worth stating explicitly. In both regimes, the Classical curve sinks over the entire K range because a deterministic network visiting a single attractor contributes $\Omega \to 0$ for large enough values of T (see Supplementary Material); Ω rewards persistent traversal of multiple cyclic phenotypes, not mere residence in one. The consistently poor performance of ARM is also instructive: per-read truth-table mutation anneals away stable local structure, pushing dynamics toward effectively memoryless transitions; this drives down the product of cycle length and dwell time and is qualitatively consistent with the classic annealed-approximation intuition that high flip rates erase organized attractor geometry (Derrida and Pomeau, 1986). In short, ARM provides plasticity but not the kind of structured, state-dependent plasticity that Ω rewards.

Conclusion

Our results allow us to propose the following actionable design principles for maximizing open-endedness:

1. In homogeneous networks with synchronous updates and low connectivity K, our simulations show that temporal heterogeneity is the main lever for raising open-endedness. When context switches are rare, each context relaxes into a long-lived attractor, and the occasional switch effectively concatenates long-residence segments from different attractor families along a single trajectory, yielding large values of Ω. In this regime both the wiring and the rule distribution are homogeneous; the only source of heterogeneity is the stochastic context schedule. When we later introduce structural heterogeneity (Fig. 2), the same context-switching protocol no longer boosts Ω in the same way, indicating that structural and temporal heterogeneity interact non-trivially rather than one simply dominating the other.

2. Dense high-K networks in the homogeneous, synchronously updated ensembles show their strongest open-endedness under Modal logic. Here, context-dependent necessity/possibility acts as a filter that prunes most chaotic branches while still keeping alternative pathways available, so trajectories remain in long, structured attractors rather than collapsing immediately to fixed points. When we later introduce structural heterogeneity and non-deterministic asynchronous updates (Fig. 2), the same qualitative advantage of Modal logic at high K persists, but the overall magnitude of Ω is reduced by the rapid contraction induced by asynchronous settling.

3. For heterogeneous/asynchronous systems: Modal at high K and Paraconsistent or Quantum-inspired logic at low-intermediate K maximize open-endedness.

4. Avoid high mutation rates when the goal is sustained novelty: ARM's indiscriminate flips wash out the attractor geometry that Ω detects.

We note two cross-checks that bolster these interpretations. First, the high-Ω zones for Paraconsistent and Modal variants align with regions where heterogeneity is known to extend or reshape the critical regime in Boolean networks (López-Díaz et al., 2023). Second, the PBN advantage under homogeneity but not heterogeneity is consistent with the literature on update schemes: when all nodes are updated synchronously, the dynamics follow a fixed deterministic map that can sustain rich cyclic structure, whereas *stochastic* asynchronous updates tend to break long cycles and contract dynamics into small recurrent classes (Gershenson, 2004b). In our heterogeneous simulations we combine an Exponential in-degree distribution with CUBEWALK-ERS' non-deterministic `asynchronous_set` scheme, so it is this added randomness in the update order, rather than asynchronicity *per se*, that erodes the attractor geometry that Ω rewards. Deterministic asynchronous schemes with fixed node orderings can, by contrast, preserve or even lengthen cycles, so our claim is restricted to the non-deterministic case we study here.

In the aggregate, Figures 1-2 suggest that state-dependence is necessary but not sufficient; how it is introduced—via context switching, conditional gating, controlled contradictions, or correlated branching—interacts strongly with architectural conditions (connectivity and update heterogeneity) to determine whether open-ended dynamics flourish or fade. This points towards a design principle for engineering OEE: choose the mechanism whose *mode of uncertainty* (what is randomized, when, and where) best complements the system's wiring and timing. In this sense, our results are analogous to the design of *the right amount* of antifragility in Boolean networks—Pineda et al. (2019) showed that the benefit a system derives from perturbations depends on how the level and pattern of external noise are matched to the underlying dynamics, and identified regimes where perturbations improve a satisfaction functional rather than merely degrading performance. Here we obtain a complementary view: instead of tuning environmental noise for a fixed network, we tune the internal realization of uncertainty for a given architecture, and assess its effect on the long-term production of novel attractors via Ω. Still, our approach has focused specifically on discrete state spaces, leaving aside systems with continuous (or hybrid) state spaces. In the following, we sketch a principled extension of our metric that preserves its core properties while making it applicable beyond purely discrete models.

Let (X, d) be a compact metric space and Φ_t a measurable flow (or map) on X. Choose (i) a finite measurable partition $\Pi = \{C_1, \ldots, C_Q\}$ of X that represents the phenotypic coarse-graining of interest and (ii) a tolerance $\varepsilon > 0$ that encodes measurement noise or resolution. Given a trajectory $x(t)$, form the symbolic stream $s(t) \in \{1, \ldots, Q\}$ by setting $s(t) = q$ whenever $x(t) \in C_q$. We say that the dynamics enters an (ε, Π)-*attractor episode* $A_j^{\varepsilon, \Pi}$ at time t_j^{in}

if thereafter the orbit remains in a trapping region $\mathcal{T} \subseteq X$ and returns within distance ε of some previously visited state in $\mathcal{T}$ before time t_j^{out}; the *residence time* is $d_j^{\varepsilon,\Pi} = t_j^{\text{out}} - t_j^{\text{in}}$. For that episode define the *symbolic cycle-length*

$$K_j^{\varepsilon,\Pi} \ = \ \big| \{ \, s(t) \, : \, t \in [t_j^{\text{in}}, \, t_j^{\text{out}}) \, \} \big|, \qquad (5)$$

i.e., the number of distinct partition elements visited before the ε-return (this coincides with the usual cycle-length in a discrete BN when Π separates individual states and $\varepsilon \to 0$). Denoting by $m(T)$ the number of such episodes discovered up to time T, we set

$$\Omega_{\varepsilon,\Pi}(T) \ = \ \frac{1}{T^2} \sum_{j=1}^{m(T)} d_j^{\varepsilon,\Pi} K_j^{\varepsilon,\Pi}, \qquad (6)$$

defining open-endedness for continuous state spaces as

$$\Omega_{\varepsilon,\Pi} \ = \ \limsup_{T \to \infty} \Omega_{\varepsilon,\Pi}(T). \qquad (7)$$

This extension preserves the key behavior of our discrete metric: (i) if the system converges to a single fixed point or limit cycle contained within one recurrent class of Π, then $\Omega_{\varepsilon,\Pi} = 0$ because there is only one episode and $d_1^{\varepsilon,\Pi} = O(T)$ while $K_1^{\varepsilon,\Pi}$ is $O(1)$; (ii) if the number of distinct (ε, Π)-attractor episodes diverges, then $\Omega_{\varepsilon,\Pi}$ diverges as well. Moreover, by the same Cauchy-Schwarz argument used in the discrete case we obtain a resolution-dependent upper bound

$$\Omega_{\varepsilon,\Pi} \ \le \ \limsup_{T \to \infty} \frac{1}{T^2} \Big(\sum_{j=1}^{m(T)} d_j^{\varepsilon,\Pi} K_j^{\varepsilon,\Pi} \Big)^2 \ \le \ m(\varepsilon, \Pi) \, |\Pi|^2,$$

$$(8)$$

since $\sum_j d_j^{\varepsilon,\Pi} \le T$ and $(K_j^{\varepsilon,\Pi})^2 \le |\Pi|^2$. Thus the *same monotone relationship with the number of recurrent phenotypes* holds as before, and when Π refines to singletons and $\varepsilon \to 0$, (7) recovers our original definition. Importantly, eq. (7) lets us assess open-endedness in any continuous (or hybrid) state space system by working with a biologically meaningful coarse-graining Π (e.g., thresholds on gene expression) and a resolution ε reflecting experimental noise.

Two challenges naturally follow. First, Π can be fixed from prior biological semantics (cell fates, pathway activities) or learned as a Markov partition-like discretization that preserves long-time statistics. In continuous systems, exact revisits of a microstate have probability zero, so all recurrences are defined relative to a finite resolution ε and partition Π. For a given (ε, Π) it may happen that no coarse-grained state is ever revisited along a finite trajectory, in which case $\Omega_{\varepsilon,\Pi} = 0$: at that scale the dynamics look like pure exploration with no recurrent patterns. This does not preclude open-endedness at finer or more structured resolutions. As we refine the partition or decrease ε, the same trajectory can reveal recurrent structure (e.g., visits to a fractal

subset within each cell), and by construction $\Omega_{\varepsilon',\Pi'} \ge \Omega_{\varepsilon,\Pi}$ for $\varepsilon' \le \varepsilon$ and $\Pi' \succ \Pi$. A principled program is therefore to study $\Omega_{\varepsilon,\Pi}$ under partition refinement, reporting curves of $\Omega_{\varepsilon,\Pi}$ against $|\Pi|$ and ε, looking for regimes where $\Omega_{\varepsilon,\Pi}$ grows and then stabilizes. This multi-scale analysis plays a role analogous to box-counting methods for fractal dimension, and avoids committing to a single "correct" coarse-graining: overly coarse partitions indeed wash out novelty, whereas overly fine ones see only noise.

Second, for long trajectories, exact recurrence detection is costly. In continuous state spaces many trajectories will cross separatrices, escape to infinity, or otherwise hit "points of no return", so exact state revisits are not expected globally. In practice, we would first identify *coarse-grained recurrent classes* (quasi-attractors) by looking for approximate returns to the same cell of a finite-resolution partition. Our GPU streaming/extractor could be extended to use fast ε-recurrence queries (e.g., locality-sensitive hashing of Poincaré samples or recurrence-plot-based triggers), guaranteeing $O(1)$ amortized checks per step. Trajectories that never return to a cell at the chosen resolution simply do not generate a recurrent class there, and thus contribute $\Omega_{\varepsilon,\Pi} = 0$ at that scale. Once such coarse-grained recurrent classes have been detected, their residence times $d_j^{\varepsilon,\Pi}$ become random variables. We then estimate $\Omega_{\varepsilon,\Pi}$ by ergodic averages over long runs, relating it to return-time statistics *within* each coarse-grained recurrent class (i.e., quasi-attractor), rather than assuming global recurrence of the full system.

Our work then suggests several concrete future research threads. It is possible to explore other mechanisms that promote open-endedness, including the composition of the multiple non-Boolean logics we study here. Our code already supports composition mechanisms, so the next step would be to optimize logic parameters (and their schedules) to maximize Ω subject to resource constraints, turning our pipeline into an automatic "OEE controller" for synthetic circuits. Additionally, because Ω is intentionally agnostic to meaning, we can pair it with a task- or fitness-based functional to separate "mere novelty" from *adaptive* novelty, retaining the York/Tokyo emphasis on ongoing generation while remaining system-independent. To our knowledge, no measure of semantic open-endedness has been explored in the literature, so generalizing the metric proposed here in that direction would be a valuable contribution.

Since we just came up with a continuous generalization of our metric, we could apply it to continuous GRN models (such as Hill-function ODEs (Ehsan Elahi and Hasan, 2018), piecewise-linear Glass systems (Edwards et al., 2007), random fuzzy networks (Zapata et al., 2020), etc.) using phenotype-aware partitions and compare with the discrete-RBN results to test which undecidability-adjacent mechanisms (modal gating, controlled contradictions, context switching) remain most effective in the continuous limit.

Moreover, we could relate $\Omega_{\varepsilon,\Pi}$ to invariants such as topological entropy (Adler et al., 1965) or return-time spectra in chaotic attractors (Boev et al., 2014) and determine the conditions under which $\lim_{\varepsilon\to 0}\lim_{\Pi\to\text{refined}}\Omega_{\varepsilon,\Pi}$ exists and is equal to the discrete-state Ω for Boolean embeddings. This opens a path to compare, on equal footing, discrete and continuous regulatory schemes across modeling paradigms, and to design interventions that promote sustained novelty under real biophysical constraints.

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Data Accessibility

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