

Towards Artificial Open-Ended Evolution within Lenia

Abstract

From the formation of snowflakes to the evolution of diverse life forms, emergence is ubiquitous in our universe. In the quest to understand how complexity can arise from simple rules, abstract computational models, such as cellular automata, have been developed to study self-organization. However, the discovery of self-organizing patterns in artificial systems is challenging and has largely relied on manual or semi-automatic search in the past. In this paper, we show that Quality-Diversity, a family of Evolutionary Algorithms, is an effective framework for the automatic discovery of *diverse* self-organizing patterns in complex systems. Quality-Diversity algorithms aim to evolve a large population of diverse individuals, each adapted to its ecological niche. Combined with Lenia, a continuous cellular automaton, we demonstrate that our method is able to evolve a diverse population of lifelike self-organizing autonomous patterns. Our framework, called Leniabreeder, can leverage both manually defined diversity criteria to guide the search towards interesting areas, as well as unsupervised measures of diversity to broaden the scope of discoverable patterns. We demonstrate both qualitatively and quantitatively that Leniabreeder offers a powerful solution for discovering self-organizing patterns. The effectiveness of unsupervised Quality-Diversity methods combined with the rich landscape of Lenia exhibits a sustained generation of diversity and complexity characteristic of biological evolution. We provide empirical evidence that suggests unbounded diversity and argue that Leniabreeder is a step towards replicating open-ended evolution in silico.

Introduction

Over four billion years, evolution on Earth has showcased a captivating trend of continuous innovation and increasing biological complexity. This phenomenon has intrigued scientists and sparked the fundamental question of how inanimate matter can spontaneously organize into a diversity of life forms. To understand how complex wholes can emerge from simple parts, researchers have turned to computational models.

Pioneered by John von Neumann and others, particularly through groundbreaking work on self-replicating machines (Neumann and Burks, 1966), Cellular Automata (CA) have become a fundamental framework for studying emergence and complexity. CA are capable of generating complex patterns that emerge solely from the local interactions of their

components, following simple, deterministic rules. Conway’s Game of Life (Gardener, 1970) is a prominent example among CA. Despite its underlying simplicity — defined by a set of four basic rules governing the birth, survival, and death of cells on a grid — Conway’s Game of Life has given rise to a surprisingly vast array of self-organizing structures (e.g., stable forms, oscillators, spaceships, etc.). Later on, it was proved to be Turing complete, a property meaning it can simulate any Turing machine.

Continuous CA, such as Lenia (Chan, 2019) and Smooth-Life (Rafler, 2011), marked a significant advancement by bridging the gap between the discrete nature of Conway’s Game of Life and the continuous dynamics characteristic of the real world. Interactive evolutionary computation methods revealed that Lenia can support a diversity of lifelike, self-organizing autonomous patterns. It led to the identification and classification of hundreds of artificial species, uncovering emergent behaviors such as locomotion, differentiation, reproduction, and emission (Chan, 2019, 2020). Consequently, Lenia stands as a fertile ground for exploring the underlying mechanisms of artificial evolution within a controlled computational environment and serves as an ideal testbed for examining the emergence of diverse artificial life. However, self-organizing patterns have mostly been discovered through manual or semi-automatic search algorithms (Chan, 2019), limiting our ability to fully explore this vast potential.

Mirroring biological evolution, Quality-Diversity (Pugh et al., 2016; Cully and Demiris, 2018) is a family of Evolutionary Algorithms that aims to discover a diverse population of individuals, each adapted to its ecological niche. In contrast with traditional optimization methods, the goal of Quality-Diversity algorithms is to find a large collection of different, high-performing solutions. Consequently, these methods hold the promise to realize Lenia’s full potential and illuminate an ecosystem of diverse artificial species. Objective-based optimization methods are prone to get stuck in local optima, whereas keeping a repertoire of diverse solutions can help to find stepping stones that lead to globally better solutions (Mouret and Clune, 2015; Faldor et al., 2023a,b), mimicking evolution in nature.

In this work, we show that Quality-Diversity algorithms are an effective solution to the problem of automatic discovery of *diverse* self-organizing patterns in high-dimensional complex systems (Reinke et al., 2020; Etcheverry et al., 2021). In particular, we demonstrate that Quality-Diversity has the capacity to unleash the untapped potential of Lenia’s rich landscape. To that end, we leverage both supervised and unsupervised Quality-Diversity methods. The supervised approach, MAP-Elites (Mouret and Clune, 2015), utilizes manually defined diversity metrics to guide the exploration towards specific characteristics of interest, facilitating the identification of patterns with unique properties such as color or motion. However, the necessity to manually specify diversity criteria inherently restricts the breadth of discoverable self-organizing patterns. To address this limitation, we employ an unsupervised approach, AURORA (Grillotti and Cully, 2022), that automatically learns a measure of diversity, significantly broadening the scope of discoverable patterns without the need for predefined diversity criteria.

However, this unsupervised method comes with its own set of challenges. Indeed, the Lenia search space is vast, and this artificial evolution process will likely lead to diverse patterns that explode or evaporate quickly. Although some of these individuals present intriguing similarities to Turing patterns (Turing, 1952), in this paper, we focus the search towards *localized* and *autonomous* self-organizing patterns, called *solitons* (Chan, 2019). To that end, we introduce a set of both manually defined and unsupervised fitness functions, that capture basic characteristics of life, such as agency or homeostasis (Bartlett and Wong, 2020). These fitness functions encode simple heuristics that guide the search towards meaningful expressions of artificial life.

We introduce Leniabreeder, a framework designed to automate the discovery of *diverse* self-organizing patterns in complex systems. Our contributions are as follows:

- We show that Quality-Diversity is an effective approach for the automatic discovery of diverse artificial species within Lenia. Those methods are generally applicable to other artificial life systems.
- We introduce a set of manually defined and unsupervised fitness and descriptor functions, tailored to guide the search towards meaningful expressions of artificial life.
- We provide evidence that our method demonstrates some characteristics of artificial open-ended evolution, exhibiting a sustained generation of diversity and mirroring the continuous innovation observed in nature.

We report quantitative and qualitative results, underscoring the potential of our framework to unlock new frontiers in artificial life research. Through the convergence of Lenia and Quality-Diversity, we explore open-ended evolution within computational systems.

Background

Lenia

Lenia is a cellular automaton that generalizes Conway’s Game of Life to continuous space-time-state, generalized local rule as well as higher dimensions, multiple kernels, and multiple channels (Chan, 2020). Interactive evolutionary computation methods have revealed that Lenia supports a diversity of lifelike self-organizing autonomous patterns (Chan, 2019), making it a fertile ground for the study of artificial open-ended evolution (Chan, 2023).

In Lenia, the world starts in an initial configuration \mathbf{A}^0 , defined as a d -dimensional lattice with c channels of real values between 0 and 1. In this work, we use the generalized rule with multiple kernels \mathbf{K}_k and growth mappings G_k (Chan, 2020). The update is calculated as an average of the results for each kernel, weighted by factors h_k/h . The state of the world is updated according to the formula:

$$\mathbf{A}_j^{t+\Delta t} = [\mathbf{A}_j^t + \Delta t \sum_{i,k} \frac{h_k}{h} G_k(\mathbf{K}_k * \mathbf{A}_i^t)]_0^1$$

Each kernel has a relative radius $r_k R$, a parameter $\beta_k \in [0, 1]^B$ and a growth mapping with parameters μ_k and σ_k . In this paper, a growth mapping is a function $G_k : [0, 1] \rightarrow [-1, 1]$ such that $G_k(u) = 2 \exp(-\frac{1}{2}(\frac{u-\mu_k}{\sigma_k})^2) - 1$ and a kernel \mathbf{K}_k is constructed by combining an exponential kernel core and a kernel shell with parameter β_k , as defined by Chan (2019). To summarize, each kernel is defined by a set of parameters $(r_k R, \beta_k, \mu_k, \sigma_k, h_k)$.

Quality-Diversity

Evolution in nature has the remarkable capacity to produce a rich diversity of species, each exquisitely adapted to its local environmental niche. Inspired by this idea, Quality-Diversity approaches, such as novelty search with local competition (Lehman and Stanley, 2011) or MAP-Elites (Mouret and Clune, 2015), are a family of evolutionary algorithms that aim to return a collection of different niches, as well as the best individual living in each niche (Pugh et al., 2016). In contrast with traditional evolutionary algorithms that focus solely on finding the optimal solution, Quality-Diversity methods generate large populations of simultaneously high-fitness and different individuals (Cully and Demiris, 2018).

In addition to the fitness $F(\mathbf{x})$ that determines the quality of a solution \mathbf{x} in the search space \mathcal{X} , Quality-Diversity optimization also considers the descriptor $D(\mathbf{x})$, that is generally manually defined and characterizes the solution \mathbf{x} for the type of diversity desired. The descriptor space $\mathcal{D} = D(\mathcal{X})$ together with the Euclidean distance define a metric space that enables the computation of distances between individuals or to measure the novelty of a new solution. The objective of QD algorithms is to find the highest fitness solution at each point of the descriptor space.

MAP-Elites MAP-Elites (Mouret and Clune, 2015) is a simple but efficient Quality-Diversity method. The algorithm discretizes the descriptor space into a multi-dimensional grid of cells and searches for the best solution in each cell. MAP-Elites starts by initializing the grid with random solutions. Then, the algorithm iteratively executes the following steps until a predefined budget of evaluation is reached: (1) a batch of parent solutions is uniformly selected from the grid, (2) a batch of offspring solutions is generated from the parents through a variation operator, (3) for each offspring solution, both its fitness and descriptor are evaluated, and (4) offspring solutions are added to the grid. A solution is added to its corresponding cell in the grid if and only if the cell is empty or the solution has a higher fitness than the current solution occupying that cell, in which case the current solution is replaced by the new one.

AURORA AURORA (Cully, 2019; Grillotti and Cully, 2022) is a Quality-Diversity algorithm that automatically defines the descriptor function via unsupervised learning. Contrary to MAP-Elites that necessitates the user to manually define diversity criteria, AURORA leverages dimensionality reduction techniques (e.g., autoencoders) to learn the descriptor function D_θ . The algorithm maintains an unstructured repertoire (Cully and Demiris, 2018) of diverse and high-fitness individuals that are evolved through a traditional QD loop. During the evaluation step, the descriptors are determined based on the current descriptor function D_θ . In turn, the data generated is used to train the autoencoder via unsupervised learning. This *dynamic* interaction between individuals and their niche definitions propels a continuous cycle of discovery, where the emergence of new individuals encourages the realignment of niche boundaries. This mechanism allows AURORA to adaptively define niches based on the evolving landscape of the population itself.

Open-Ended Evolution

Understanding the open-ended innovation and diversity characteristic of biological evolution is one of the long-standing problems in evolutionary biology (Packard et al., 2019) and emulating such a process represents one of the greatest challenges in artificial life research. Exploring open-ended evolution extends beyond understanding biology or generating captivating simulations. It raises fundamental questions about the nature of creativity, the emergence of complexity, and how innovative solutions can arise in artificial systems (Soros et al., 2017).

Despite significant efforts, achieving genuine open-ended evolution in silico has proven challenging. A key obstacle is the development of formal and objective definitions, despite some advancements in this area (Maley, 1999; Adams et al., 2017; Taylor, 2015; Soros and Stanley, 2014). Additionally, the concept of truly unbounded evolution is questioned by the eventual fate of our universe: the theoretical heat

death suggests that even nature’s seemingly infinite well-spring of novelty and creativity is ultimately finite (Pattee and Sayama, 2019). Given these considerations, our work does not claim to present an algorithm that achieves theoretical open-endedness. Instead, we offer it as a step toward understanding and mimicking the essence of open-ended evolution.

Nature encompasses numerous niches, and a species dominating a niche does not preclude a different species from being successful in another. For instance, the agility of cheetahs in hunting does not prevent orcas from thriving underwater. Quality-Diversity algorithms have been designed to mimic the creativity and innovation observed in nature, by prioritizing the generation of diverse solutions rather than performance on a specific task. However, MAP-Elites does not allow the addition of new cells over time that did not exist in the original descriptor space, and as a result, cannot exhibit true open-ended evolution (Mouret and Clune, 2015). AURORA moves closer to open-ended evolution by dynamically adapting the criteria through which diversity is assessed, thereby changing the landscape of possible solutions as the system learns. This method allows the algorithm to continuously uncover new niches without being constrained by a predefined descriptor space. As a result, AURORA can foster a more genuinely open-ended process of discovery, akin to the way biological evolution continuously explores new forms of life and strategies for survival. By leveraging unsupervised learning capabilities, we eschew the limitations of manually defined diversity and complexity metrics that have historically constrained open-ended evolution models (Hintze, 2019).

Related Work

Automatic Discovery of Self-Organizing Patterns

Computational models have been widely used to explore artificial self-organizing patterns (Neumann and Burks, 1966; Turing, 1952). Cellular Automata are a prominent example, where interesting rules or patterns have mostly been discovered manually, assisted with computer simulations (Wolfram, 2002). In some cases, more refined methods, such as evolutionary algorithms, have been employed to search for specific rules or patterns (Sapin et al., 2003; Mitchell et al., 2000). Diversity-driven approaches, such as IMGEP, have been applied to the discovery of patterns within Lenia (Etcheverry et al., 2021; Reinke et al., 2020). Our method diverges from IMGEP-based approaches in several key aspects. We adopt a methodology that is not goal-directed, making it inherently closer to the nature of biological evolution. Additionally, we compute fitness and descriptor functions based on multiple timesteps and not only on the final state of the system. This approach aligns more intimately with the dynamics of biological evolution, where the entire developmental process influences adaptability and innovation.

Morphogenesis research has seen significant contributions from various computational models aimed at automating the discovery of lifelike behaviors and complex systems. Notably, Neural Cellular Automata have emerged as a powerful tool for studying regeneration and pattern formation in synthetic organisms (Mordvintsev et al., 2020). This approach, leveraging the principles of cellular automata with the adaptability of neural networks, has provided insights into the self-organizing capabilities of biological and artificial systems (Mordvintsev et al., 2020; Palm et al., 2021). In contrast with our approach, these systems aim to grow target patterns rather than discover an endless diversity of self-organizing structures.

Open-Ended Evolution

Open-ended evolution research focuses on the mechanisms and conditions that allow for the perpetual emergence of novelty, characteristic of biological evolution (Packard et al., 2019). Open-ended evolution is a variegated concept (Packard et al., 2019) and many definitions and necessary conditions have been proposed in the past (Packard et al., 2019; Adams et al., 2017; Taylor, 2015; Maley, 1999; Hintze, 2019; Soros and Stanley, 2014; Pattee and Sayama, 2019). Several artificial life systems have demonstrated the potential for open-endedness (Soros and Stanley, 2014; Standish, 2002; Hintze, 2019), although measuring it is still a challenge (Packard et al., 2019; Dolson et al., 2019).

Recent investigations of open-endedness within Lenia have been conducted. Plantec et al. (2023) introduced a mass-conservative extension of Lenia, diverging from our method by modifying Lenia’s rules. Chan (2023) explored open-endedness through large-scale simulations, a different angle compared to our focus on the intrinsic dynamics of evolution without scaling the system’s size.

Methods

We introduce Leniabreeder, a framework designed to automate the discovery of diverse patterns in complex systems. While we showcase its effectiveness in the context of Lenia, the methodology is generally applicable to other artificial life systems. We formalize the discovery of diverse artificial species as an evolutionary algorithm, specifically a Quality-Diversity optimization problem. We employ two approaches: MAP-Elites (Mouret and Clune, 2015), using manually defined diversity criteria to steer the search towards areas of interest, and AURORA (Grillotti and Cully, 2022), using unsupervised descriptor and fitness functions circumventing the need for predefined diversity criteria and broadening the range of possible discoveries. Both methods follow a traditional QD loop of selection, variation, evaluation and addition. In this section, we detail the search space, the variation operator, as well as additional design choices to direct the search towards self-organizing, autonomous patterns.

Search Space

In this work, we restrict the world configuration to a 2-dimensional 128×128 array with 3 channels as well as the space resolution to $R = 12$ and the time resolution to $T = 2$. We also restrict the number of self-interacting kernels per channel to 3, and the number of cross-channel kernels per pair of distinct channels to 1, adding up to a total of 15 kernels. The search space corresponds to all possible *genotypes*. The genotypes consist of two parts: the *seed* and the *rule parameters*.

The seed corresponds to the initial configuration of an array composed of $32 \times 32 \times 3 = 3,072$ sites. The rule parameters per kernel that are part of the genotype are (μ_k, σ_k, h_k) , see Background section. The parameters $(r_k R, \beta_k)$ are left out of the genotypes and shared across all individuals. The rule parameters contain $15 \times 3 = 45$ parameters. Thus, the search space spans a total of $3,072 + 45 = 3,117$ dimensions. The genes of an individual are expressed by initializing a world configuration \mathbf{A}^0 to a zero array, apart from the center which is initialized with the seed stored in the genotype. Then, the world is updated according to the genotype’s rule parameters for N steps, resulting in a sequence $(\mathbf{A}^0, \dots, \mathbf{A}^{N\Delta t})$.

Variation Operator

Our methods are genetic algorithms that employ a specialized variation operator known as iso+LineDD (Vassiliades and Mouret, 2018). This operator is designed to efficiently navigate the genotype space by introducing variations that are informed by both isotropic and directional perturbations. The isotropic variation introduces small, random changes to a solution, ensuring a thorough exploration of the search space around the current solution. In contrast, the directional variation generates new candidate solutions by exploring along the line defined by two existing solutions in the population. Given two existing solutions \mathbf{x}_1 and \mathbf{x}_2 from the population, an offspring solution \mathbf{x} is generated as follows:

$$\mathbf{x} = \mathbf{x}_1 + \sigma_1 \mathcal{N}(\mathbf{0}, \mathbf{I}) + \sigma_2 (\mathbf{x}_2 - \mathbf{x}_1) \mathcal{N}(0, 1)$$

Soliton

For a given individual, we can decode its genotype into a seed and rule parameters. Its genes are expressed through Lenia simulation: the seed undergoes a developmental process driven by the rule parameters. This developmental process can potentially culminate in the emergence of a distinct, autonomous, self-organizing phenotype, known as a *soliton*. Our focus is on discovering and identifying such solitons that maintain their structure and coherence over time, in contrast with transient, ephemeral or spatially diffused patterns. In this section, we will delve into statistical measures that aid in quantifying the characteristics of patterns and potentially assess their stability and agency.

Statistical Measures We draw inspiration from the original Lenia paper (Chan, 2019) where statistical measures are introduced to characterize phenotypes. These measures can be used to design fitness functions and descriptor functions.

A genotype gives rise to the evolution of a phenotype through time, given by the sequence $(\mathbf{A}^0, \dots, \mathbf{A}^{N\Delta t})$. At each timestep, several statistical measures, such as mass, velocity or color can be computed. A non-exhaustive list is included in Table 1. For example, the statistical measure “color” is a 3-dimensional vector of real values between 0 and 1, representing the average RGB value of the phenotype. This statistical measure also gives information about the mass, because a RGB value of $[1, 1, 1]$ implies a maximum mass while a RGB value of $[0, 0, 0]$ implies a mass of zero.

Statistical measure	Formula
Mass	$m = \sum_{x \in \mathcal{L}} \sum_i \mathbf{A}_i(x)$
Center of mass	$\bar{x} = \frac{1}{m} \sum_{x \in \mathcal{L}} x \sum_i \mathbf{A}_i(x)$
Velocity	$v = \Delta \bar{x} / \Delta t$
Angle	$\alpha = \arg(v)$
Linear velocity	$V = v $
Angular velocity	$\omega = \Delta \alpha / \Delta t$
Color	$C = \frac{1}{ \mathcal{L} } \sum_{x \in \mathcal{L}} \mathbf{A}(x)$

Table 1: Examples of statistical measures used to characterize phenotypes. $|\mathcal{L}|$ represents the size of the lattice \mathcal{L} , in other words, the number of sites in the world.

From the sequence $(\mathbf{A}^0, \dots, \mathbf{A}^{N\Delta t})$, we can calculate time-series of statistical measures, denoted $(\mathbf{a}_0, \dots, \mathbf{a}_N)$. In this paper, the first n steps are considered to be the developmental process of the seed. After n steps, we consider that the pattern has stabilized and the sequence $(\mathbf{a}_{n+1}, \dots, \mathbf{a}_N)$ is used to characterize the phenotype. In particular, the sequence can be aggregated into summary statistics (e.g., mean, median, variance, minimum, maximum, etc.). For instance, the sequence of velocity (v_{n+1}, \dots, v_N) can be aggregated into an average speed. These summary statistics can form fitness and descriptor functions used in MAP-Elites or AURORA. Combined with expert knowledge, these manually defined statistical measures enable to search for solitons with specific characteristics, such as a certain mass, speed or color.

Unsupervised Statistical Measures Unsupervised representation learning techniques, such as autoencoders, enable to automatically discover statistical measures without requiring labeled data. In our approach, we use a Variational AutoEncoder (VAE) (Kingma and Welling, 2014) to compress high-dimensional phenotypes into lower-dimensional latent representations. These representations are essentially statistical measures that can be used to define fitnesses and descriptors. The VAE architecture comprises two main components: an encoder and a decoder that facilitate the learning of latent representations. The input to the VAE is a $32 \times 32 \times 3$ crop

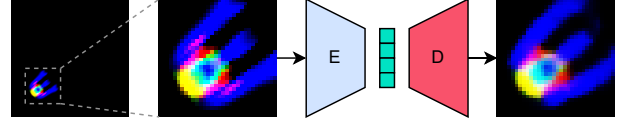


Figure 1: The world configuration \mathbf{A} is cropped around the center of mass of the phenotype to form the $32 \times 32 \times 3$ input to the encoder (blue). Then, the encoder compresses the high-dimensional input into a low-dimensional latent vector \mathbf{z} (green). During training, the decoder (red) transforms the latent vector back to the original input to compute the loss, that is optimized via gradient descent.

of the configuration \mathbf{A} , centered around the center of mass of the phenotype. The encoder transforms the high-dimensional input into a 8-dimensional latent vector \mathbf{z} and the decoder recreates the input from the encoded representation, see Figure 1. AURORA utilizes data generated during the evaluation step of the QD loop to train the VAE.

An individual induces a sequence of configuration $(\mathbf{A}^{(n+1)\Delta t}, \dots, \mathbf{A}^{N\Delta t})$ that can be encoded into a latent space trajectory $(\mathbf{z}_{n+1}, \dots, \mathbf{z}_N)$ with the encoder. This trajectory within the latent space can be considered as a sequence of statistical measures and can be aggregated into descriptors and fitnesses as outlined in the previous section. In this work, to characterize individuals, we take the average latent representation of the phenotype. Thus, we define the descriptor as the mean vector of the latent trajectory, $D_\theta(\mathbf{x}) = \frac{1}{N-n} \sum_{i=n+1}^N \mathbf{z}_i$. The average latent representation provides a succinct and informative summary of a phenotype’s essential characteristics.

This descriptor function can be combined with any manually defined fitness functions, see previous section. Furthermore, we can leverage the latent trajectory to design a fitness function that captures basic characteristics of life. To encourage agency, self-organization and stability, a pattern should exhibit minimal variance in its latent representation. Thus, we define the fitness as the negative average Euclidean distance between the latent vectors and the mean vector of the trajectory, $F_\theta(\mathbf{x}) = -\frac{1}{N-n} \sum_{i=n+1}^N \|\mathbf{z}_i - D_\theta(\mathbf{x})\|_2$, see Figure 2 for a visual representation. This fitness measures the spread or dispersion of the latent vectors relative to their mean in a multidimensional space. This approach is grounded in the principle that “what persists, exists” and is related to homeostasis, one of the pillars of life (Bartlett and Wong, 2020).

These unsupervised descriptor and fitness functions are appealing, because their computation within a latent space makes them domain-agnostic. However, this fitness function is only partially unsupervised as we decided to bias its definition to capture the spread of the latent trajectory. Moreover, this definition of self-organization and stability has limitations, as it tends to penalize individuals exhibiting periodic stability or engaging in chaotic movements.

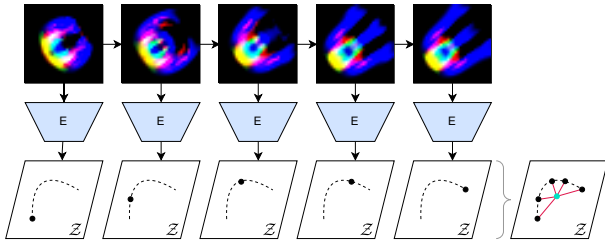


Figure 2: The phenotype at different timesteps forms a trajectory in the latent space \mathcal{Z} . The green dot represents the mean vector of the latent trajectory, i.e., the descriptor of the individual. The red segments represent the Euclidean distance between the latent vectors and the descriptor, used to compute the fitness of the individual.

Constraints on Growth To direct the search towards stable patterns, we enforce three constraints on the phenotypes. The objective of these constraints is to ensure that phenotypes do not exhibit positive or negative infinite growth (Chan, 2019). Explosion or evaporation happens when the mass expands to very large values or shrinks to zero. We discard any individuals inducing a sequence $(\mathbf{A}^{(n+1)\Delta t}, \dots, \mathbf{A}^{N\Delta t})$, where at least one phenotype has evaporated, exploded or is too spread. These constraints are controlled through three hyperparameters: A minimum and maximum mass threshold m_{\min} , m_{\max} and a mass spread σ_m .

Experiments

The objective of our experiments is threefold. First, we assess the capability of Leniabreeder to evolve a population of individuals with a diversity manually directed towards specific characteristics of interest. Second, we evaluate the ability of Leniabreeder to evolve an unsupervised diversity of individuals, illuminating Lenia’s vast landscape. Third, we explore Leniabreeder’s potential to exhibit characteristics of open-ended evolution, such as unbounded diversity.

We conduct a series of experiments using the framework QDax and a GPU-accelerated implementation of Lenia using JAX. The full source code will be made available upon acceptance, in a containerized environment in which all experiments and figures can be reproduced. Each experiment is replicated 10 times with random seeds. For the quantitative results, we report p -values based on the Wilcoxon–Mann–Whitney U test with Holm–Bonferroni correction. Videos are available at leniabreeder.com.

MAP-Elites

We report five experiments using different combinations of descriptors and fitnesses, summarized in Table 2. MAP-Elites requires to choose reasonable bounds for each statistical measure. In this study, the color is in $[0, 1]^3$, the mass is in $[0, 16]$, the velocity is in $[0, 0.5]$ and the angle is in $[-\pi, \pi]$. For comparison purposes, the famous soliton named Aquarium

(pattern id 5N7KKM), discovered by Chan (2020), has a mass of roughly 2.42 units and a velocity of 0.12 units. To evaluate MAP-Elites, we consider two metrics. The *coverage* corresponds to the proportion of filled cells in the grid of solutions and the *max fitness* corresponds to the fitness of the best solution in the grid.

Fitness	Descriptor	Coverage	Max fitness
velocity	[color]	38.5%	1.01
mass	[color]	39.8%	97.5
mass var	[color]	39.0%	1,525
neg angle var	[mass, velocity]	52.2%	-1.31×10^{-7}
neg mass var	[angle, velocity]	42.7%	-2.00×10^{-7}

Table 2: **MAP-Elites** Median coverage and max fitness for different combinations of fitness and descriptor functions. Each experiment is replicated 10 times with random seeds.

The experimental results reported in Table 2 show that MAP-Elites is capable of generating populations of diverse individuals with specific characteristics of interests. For instance, MAP-Elites is able to find solitons with a wide range of colors ($\approx 39\%$ out of the space of all possible colors) combined with three different fitness functions. Notice that some colors are impossible, for example “black” solitons with color close to $[0, 0, 0]$ correspond to patterns that have evaporated, while “white” solitons with color close to $[1, 1, 1]$ correspond to heavy patterns that have exploded. Consequently, those pattern are discarded and those cells are impossible to fill. The qualitative results in Figure 3 confirm that MAP-Elites is able to find patterns with all combination of colors.

MAP-Elites is also able to find solitons with different locomotion characteristics. For instance, the experimental results in Table 2 show that this method is able to evolve a population of species with a wide range of masses, different velocities and different orientations. The fitnesses negative angle variance and negative mass variance are properly optimized as shown by the maximum fitness values being very close to zero. The qualitative results in Figure 3 demonstrate that this approach is able to find patterns with a wide range of mass, as well as different locomotion angles and angular velocities.

AURORA

We report five experiments combining the unsupervised descriptor with different fitnesses: velocity, negative mass, negative angle variance, negative mass variance and unsupervised. The qualitative results in Figure 4 demonstrate that AURORA can evolve a vast diversity of solitons. Unlike MAP-Elites, which targets specific traits, AURORA fosters an unrestricted diversity of shapes, colors, sizes, and locomotion properties, offering a richer and more varied ecosystem.

To evaluate AURORA’s ability to exhibit characteristics of open-ended evolution, we consider three metrics. The

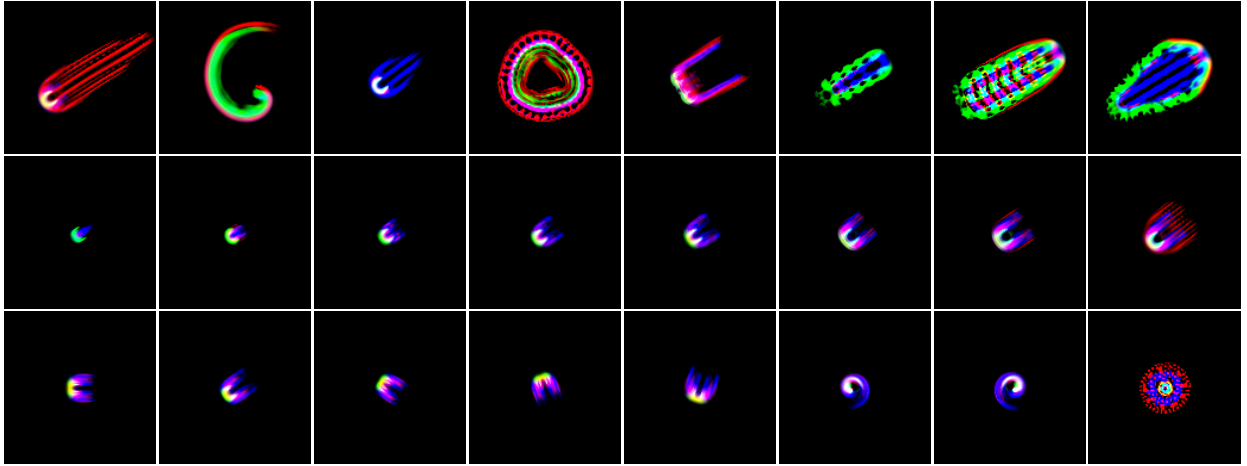


Figure 3: **MAP-Elites** Each row corresponds to a single, independent run, and each image is $128 \times 128 \times 3$. **Row 1** Fitness is the *velocity*, and descriptor is the *color*. From left to right, individuals with descriptor closest to $[1, 0, 0]$ (red), $[0, 1, 0]$ (green), $[0, 0, 1]$ (blue), $[1, 1, 0]$ (red-green), $[1, 0, 1]$ (red-blue), $[0, 1, 1]$ (blue-green), $[1, 1, 1]$ (red-green-blue) and $[0.01, 0.6, 0.5]$ (random). **Row 2** Fitness is the *negative angle variance*, and descriptor is the *mass* and *velocity*. From left to right, increasing mass and constant velocity. **Row 3** Fitness is the *negative mass variance* and descriptor is the *velocity* and *angle*. From left to right, different angles, clockwise and counterclockwise rotations and no rotation.

entropy corresponds to an estimation of the population’s entropy given by the VAE. This metric is related to the notion of *ecology* from Dolson et al. (2019), a measure of information in the population. From the point of view of probabilistic modeling, a VAE models the likelihood $p_\theta(x|\mathbf{z})$ and posterior $p_\theta(\mathbf{z}|x)$. These distributions can be used to compute an estimation of the entropy of the population $p_\theta(x)$ by sampling \mathbf{z} from its prior distribution. The *variance* of the population corresponds to the average pixel-wise variance of the individuals in the repertoire. This measure is a raw estimate of the diversity present in the population. Finally, the *cumulative elites* metric represents the cumulative sum of offspring solutions added to the repertoire during the run.

In Figure 5, we can see that the entropy of the population is settling at the beginning, because the autoencoder is trained from scratch and starts from random weights. After a few generations and for the rest of the run, the entropy of the population is increasing steadily, indicating that the amount of information in the population is increasing, as new and more diverse species are discovered. This result is confirmed by the steadily increasing variance of the population, that indicates that the phenotypes are becoming more and more diverse pixel-wise. This is due to new solitons with different colors and shapes being discovered and stored in the population. Interestingly, the runs with unsupervised fitness are demonstrating higher variance ($p < 0.005$) than the other runs with manually defined fitnesses. Finally, we can see that the the cumulative sum of elites added to the repertoire is steadily increasing, even after one million evaluations, indicating a constant flow of new offspring solitons replacing old

ones. This constant flow shows that the dynamic interactions between the population and the niche boundaries fostered by AURORA is effective in promoting a diverse and ever-evolving ecosystem. The increasing trend in the population’s entropy and variance, along with the continuous addition of new elites, underscores AURORA’s potential for driving open-ended evolution. This evidence suggests that AURORA, with its unsupervised approach, facilitates the emergence of a rich array of solitons, expanding the boundaries of diversity and complexity within artificial life systems.

Conclusion

We show that Quality-Diversity is an effective framework for the automatic discovery of *diverse* self-organizing patterns in high-dimensional complex systems. Our findings not only showcase the breadth of artificial life within Lenia but also underscore the relevance of Quality-Diversity algorithms in evolving diverse patterns and illuminating an ecosystem of artificial species. Combined with Lenia, the process exhibits a sustained generation of diversity that is characteristic of biological evolution.

At the core of Leniabreeder lies the utilization of a novel unsupervised fitness function. Yet, it relies on simple heuristics that only mimics homeostasis. We posit that enhancing this fitness function would enable to discover even more meaningful expressions of artificial life. Furthermore, the current autoencoder architecture is not invariant to rotation or scaling. We believe that improving the autoencoder architecture could also benefit the framework to capture a more refined notion of diversity.

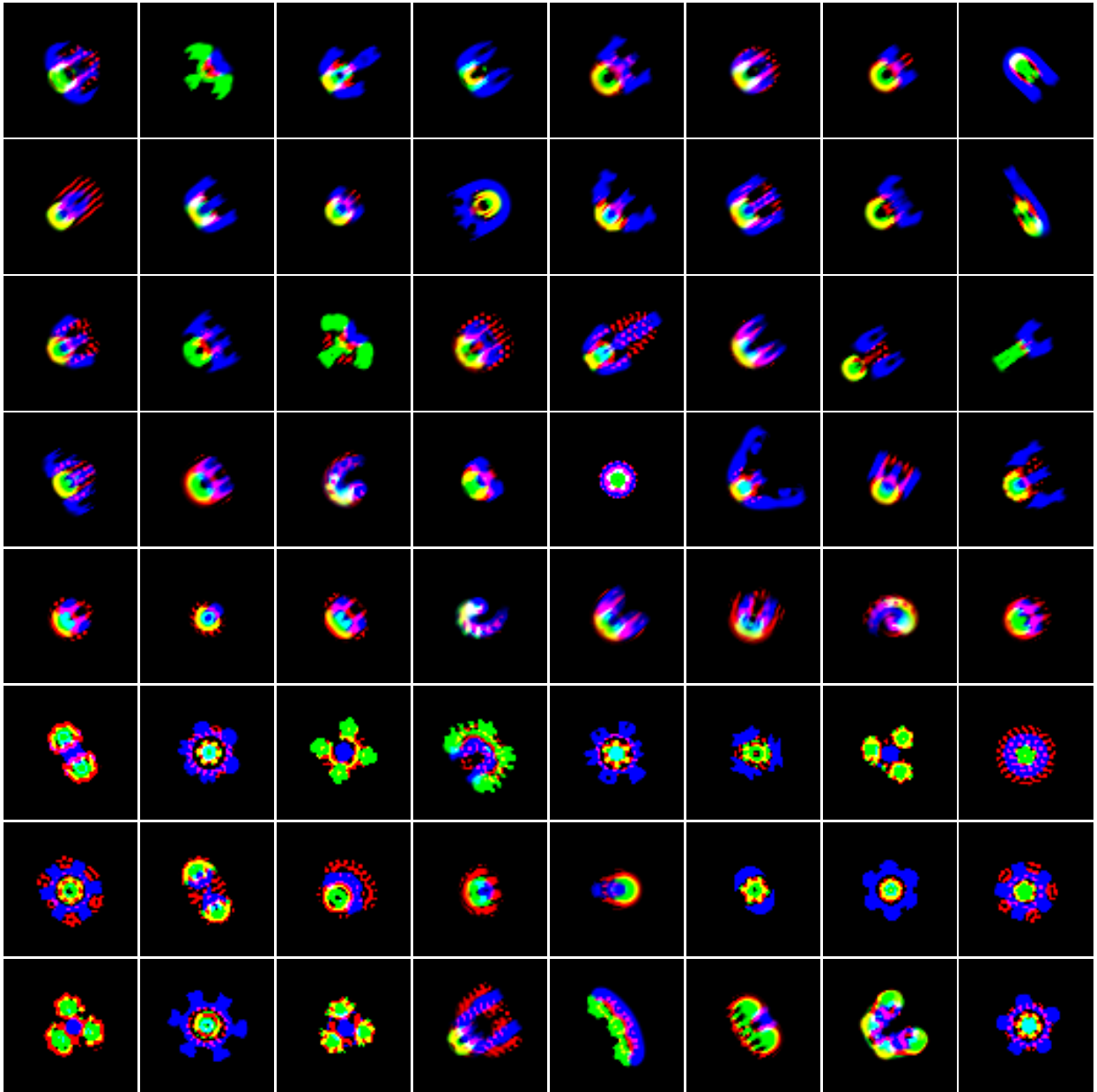


Figure 4: **AURORA** Each image is a $64 \times 64 \times 3$. **Row 1-3** Fitness is the *negative angle variance*. **Row 4-5** Fitness is the *negative mass variance*. **Row 6-8** Fitness is *unsupervised*.

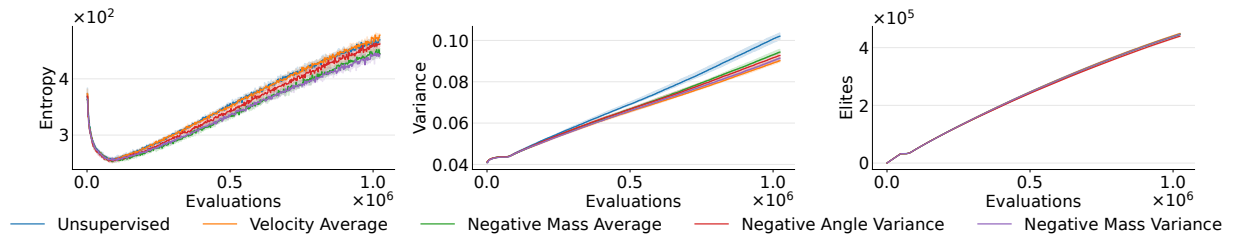


Figure 5: **AURORA** Entropy, Variance and Elites added to the repertoire with different fitness functions. Each experiment is replicated 10 times with random seeds. The solid line is the median and the shaded area represents the first and third quartiles.

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