

Introducing asymptotics to the state-updating rule in Lenia

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Introduction

Lenia (Chan, 2019) is an extension of Game of Life (GoL) with continuous space/time/state and generalized local rules. It can generate various fascinating “lifeforms” which bear a resemblance to real-world microscopic organisms. Chan identified more than 400 “species” and discussed the evolved ecosystem in terms of taxonomy, ecology, morphology, behavior, and physiology (Chan, 2020). He also successfully showed the emergence of essential biological phenomena, including individuality, growth, and self-replication in Lenia and its extended models. We propose a variant of Lenia, in which asymptotic updating by a target function is used in place of the growth mapping function (Kawaguchi et al., 2021). After presenting the new model, we search for organisms and clarify the effects of the introduction of asymptotics by observing the differences between the organisms we found and those in the original Lenia. We also investigate the increase in the viability of organisms by exploring the parameter regions where they exist in the parameter space.

Model

Lenia generalizes GoL to continuous space implemented by using long-distance neighborhoods for high resolution, continuous time implemented with small incremental updates, and continuous state expressed as a continuous value in the unit range. The significant difference with other successor models of GoL, e.g. Larger-than-Life (Evans, 2001), Reallife (Pivato, 2007), and SmoothLife (Rafler, 2011), is that we can arbitrarily change the weight of the neighborhood. The update flow of the original Lenia (**Lenia-0**) is as follows (Fig. 1). Each cell state is updated by repeating 2)-5) in every transition step.

- 1) Initialize the value of each cell in the 2-dimensional cell set \mathbf{A} with a continuous value from 0 to 1, which is \mathbf{A}^0 .
- 2) Calculate convolution with \mathbf{A} using kernel \mathbf{K} , which is a predefined weight array.
- 3) Apply a growth mapping function G $[0, 1] \rightarrow [-1, 1]$, which is unimodal, to $\mathbf{K} * \mathbf{A}$.
- 4) Add a small fraction dt of the growth to the array \mathbf{A} .
- 5) Clip the states of \mathbf{A} to the unit range $[0, 1]$.

This updating is summarized as the equation Eq. 1.

$$\mathbf{A}^{t+dt} = [\mathbf{A}^t + dt G(\mathbf{K} * \mathbf{A}^t)]_0^1 \quad (1)$$

We then explain the proposed asymptotic model (**Lenia-1**) by considering how GoL was extended in the above 2) - 5). Step

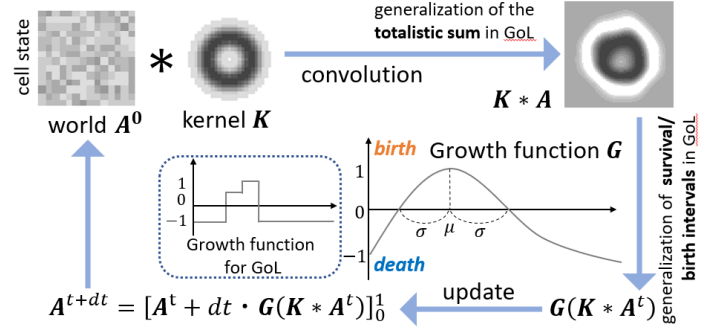


Figure 1: Overview of Lenia.

2 is a generalization of the totalistic sum in GoL. Step 3 is also a generalization of the survival/birth intervals in GoL, where the values of G : positive, near zeros, and negative values correspond to the birth, survival, and death intervals, respectively. In Step 4, the small fraction of the value calculated in Step 3 is added to the current state value of each cell. The proposed model uses a target function T in place of the growth function G , in which T is defined as $(G + 1) / 2$ so that the states stay within the unit range $[0, 1]$. Each state value is increased or decreased to reduce the distance from the target value in the next step. If we take the totalistic sum in GoL as not growth ability but survivability of the cell, we can consider this replacement more closely follows the idea of GoL as this model interprets the calculated convolution value as not an increase in the current state value but a target value. Our modification can be summarized as follows (Step 5 is no longer necessary as the values stay within $[0, 1]$):

- 3') Apply a target unimodal function $T: [0, 1] \rightarrow [0, 1]$ to $\mathbf{K} * \mathbf{A}$. Here, T can be defined as $T = (G + 1) / 2$.

- 4') Add a small fraction of the difference between the target and \mathbf{A} to \mathbf{A} .

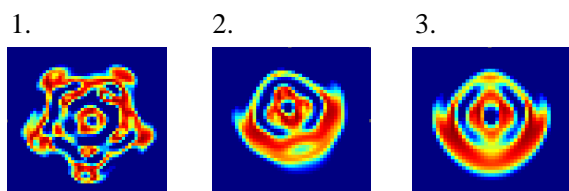
The new model is expressed as Eq. 2 or differential Eq. 3.

$$\mathbf{A}^{t+dt} = \mathbf{A}^t + dt (T(\mathbf{K} * \mathbf{A}^t) - \mathbf{A}^t) \quad (2)$$

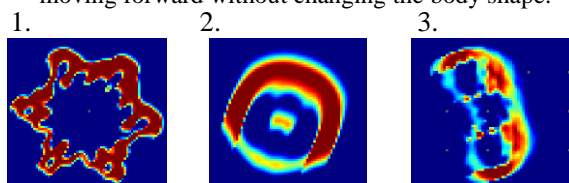
$$\partial_t \mathbf{A} = T(\mathbf{K} * \mathbf{A}) - \mathbf{A} \quad (3)$$

Search for Organisms

We adopted all of the parameter sets (i.e., kernel and growth mapping settings) that were reported to generate organisms in **Lenia-0** (about 500 species) (Chan, 2019) in order to search for organisms in **Lenia-1**. We performed 50 trials for each



Lenia-1. L1-1: moving in meandering trajectories; L1-2: moving the body in waves like a jellyfish; and L1-3: moving forward without changing the body shape.



Lenia-0. L0-1: *Hexastrium*; and L0-2: *Kronium solidus*; L0-3: *Trigeminium arcus natans*.

Figure 2: Organisms found in the proposed model (L1) and the original Lenia (L0). Organisms with the same number in their IDs have the same parameter values.

parameter set with a random initial configuration A^0 . We found just three organisms, each of which belongs to a new species in the sense that they have not been reported as species in **Lenia-0**. Fig. 2 shows these organisms (L1-1, 2, 3) with existing organisms already discovered with the same parameter sets in **Lenia-0** (L0-1, 2, 3), respectively. They tend to move more smoothly than the organisms in **Lenia-0**. Also, the new organisms L1-1&2 have more complex internal structures than L0-1&2, respectively.

We then turned our attention to the parameter regions in which the organisms exist. **Lenia-0** organisms are known to exist in a limited region of μ - σ parameter space. Parameters μ and σ are the position of the peak of the target (growth) function and the width of the peak, respectively. We explored the μ - σ space using all the parameter sets reported to generate organisms in **Lenia-0**. It turned out that of the 155 parameter sets (keeping μ and σ unchanged) organisms were also found in **Lenia-1** when using 154 sets. Fig. 3 shows μ - σ maps of L1-1, L0-1, and L0-4. L0-4 is the organism in **Lenia-0**, which is similar to L1-1 both in structure and behavior. Comparing L1-1 and L0-4, correspondingly, we see a clear difference in their distributions when compared to the distributions between L0-1 and L1-1. These might imply that the distributions of organisms in the μ - σ space are highly dependent on the parameter sets beyond the model difference. Furthermore, we found, as a

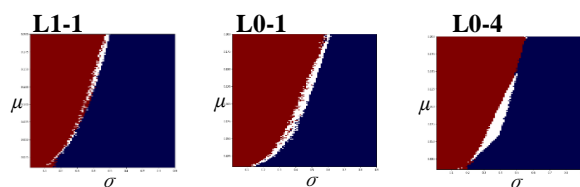


Figure 3: The μ - σ maps of L1-1, L0-1, and L0-4. Blue produces no global or local pattern at all. Red produces a chaotic, aperiodic global filament pattern. White generates organisms.

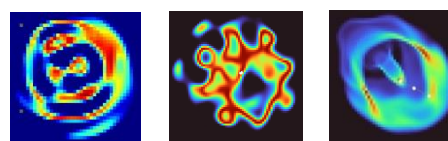


Figure 4: Examples of asymmetrical organisms.

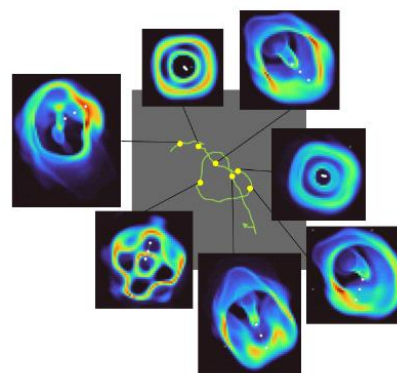


Figure 5: Trajectory of the third organism in Fig. 4.

general tendency with the cases having reduced existence areas (which happened in 143 parameter sets out of 155), that new organisms tend to shake their bodies in non-monotonous rhythms. By contrast, the organisms tend to have monotonous or no rhythms in the cases having enlarged existence areas. It suggests that organisms with simpler behaviors and forms may be more likely to survive in an environment where the boundary between chaos (blue) and sky (red) is ambiguous.

During the search, we found many notable organisms with asymmetric body structure or behavior (Fig. 4). The organism on the left has a round shape, but it shows irregular movements with irregular changes in its internal structure. The middle organism pulsates as a whole, changing its shape and asymmetrical internal structure moment by moment. The right organism has two states, pulsating in place and moving, but in both states the structure and movement continue to change irregularly (Fig. 5). We believe that asymptotics in the state-updating rule increases the effects of continuous space/time/state in the GoL and thus creating smoother lifeforms.

Conclusion

We proposed a model that introduces asymptotics to the state-updating rule in Lenia. We found three organisms with the same parameter sets as those in Lenia. We then focused on the regions for the existence of organisms and explored them in the parameter space. We found that the new organisms tend to move more smoothly than the organisms in Lenia and typically have either more complex internal structures or simpler behaviors. We observed a similarity in the distributions of organisms sharing parameters in the parameter space beyond the model difference. We believe that the proposed model can be another target of ALife research in the sense that not only new species can be found, but also it can create opportunities for investigating biological phenomena using hybrid models.

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