

TRANSLATING THE CONWAY'S GAME OF LIFE AS A DISCRETE LOGISTIC CELLULAR AUTOMATA MODEL WITH DENSITY EFFECTS

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ABSTRACT. *John H. Conway (1937-2020) has introduced a series of cellular automata (CA) models to demonstrate that simple rules can lead to very complex phenomena. Game of Life (GoL) is one of the most renowned CA models invented by Conway in 1970's. In fact, GoL is a 'game' without players, by which the spread of artificial life on 2-dimensional plane under periodic boundary conditions is progressively simulated. The present study shows that GoL can be remodeled as a parameter-adjustable CA-based logistic model applicable for simulating the population dynamics of organisms, by emphasizing the intrinsic modes of density effects found in original GoL which are equivalent to the logistic and Allee effects observed in population dynamics in living organisms. The strategy taken was to design a novel Hill-type density-responsive algorithm functioning behind the actions of the logistic CA model extended from GoL. Lastly, the growth curves simulated by the modified GoL and logistic model were compared to clarify that the growth patterns in GoL obey the logistic growth prediction under strong influence of carrying capacity, but the harm by low density could be overcome by local configuration of live cells.*

Keywords: Allee effect, Cellular automata, Game of Life, Hill equation, Logistic model

1. Introduction. In April, 2020, John H. Conway (1937-2020), a British mathematician known for his active works in the theory of finite groups, knot theory, number theory, combinatorial game theory and coding theory, has passed away due to complications from novel corona virus [1]. In 1970's, Conway introduced a model of cellular automata (CA) to demonstrate that simple rules can lead to a series of very complex behaviors [2,3]. Amongst his works on CA, Game of Life (GoL) became the most renowned and the most studied automaton [4-7]. From the early days, GoL has attracted the attention of ecologists [8], biologists [9], physicists [7,10] and information scientists [11]. To date, a number of works have been dedicated to linking the phenomena in biological system such as population dynamics with CA models including GoL [12].

The group of the author has previously demonstrated that the behaviors of living plants and microorganisms in response to external stimuli can be expressed as the modes of automata by defining the states and the transition functions within these natural automata

[13-15]. Briefly, some paramecium species [14,15], living plants and plant cells [13], or plant-derived molecules [13,16,17] capable of environmental sensing were analyzed and classified as natural sequential machines (such as Mealy and Moore machines) or finite state automata, based on the assumption that the chemical and biological basis could be the key component of natural computing approaches. By observing these living organisms (as natural automata), after defining the modes of actions, the similarity between the computational data processing and the biological decision-making processes without the need for brains could be elucidated. Since the behavior of living organisms can be expressed as automata, CA models such as GoL might be naturally applied for simulating the population dynamics of living organisms.

In fact, every algorithm in CA must be backed by mathematical structure(s), and the mathematical model applied in the recently performed work by Ibrahimi et al. [7], focusing on the GoL's nature as CA, was the logistic map model which was developed and popularized since the work of May [18] based on the discrete-time demographic model highly analogous to the classical logistic equation [19,20]. Generally, the logistic map can be expressed by Equation (1).

$$x_{n+1} = rx_n(1 - x_n) \quad (1)$$

where the parameter r (representing the rate of intrinsic increase) discretely determines the state of x_n which ranges between 0 and 1 representing the ratio of existing population to the maximum possible population [18]. As inspired by the above-mentioned work by Ibrahimi et al. [7] rebuilding the GoL as a logistic map-based CA model, here the author attempted to review and remodel the GoL as the parameter-adjustable logistic model applicable for simulating the ecological population dynamics for living organisms which are continuously challenged by the high- and low-density pressures, known to involve two distinct parameters, carrying capacity (K) and Allee threshold (A), respectively.

2. Theoretical Background and Methods.

2.1. Design of the study. This section for theoretical background and methods consists of three topics. Firstly, defined modes and mathematical features of original GoL are described (see Section 2.2). As the second topic, the author describes the mathematical background of the logistic equations and Hill's equation, which are basis for ecological population dynamics and biochemical kinetics, respectively (see Section 2.3). In the description of the logistic models, strong emphasis was made for comparison of density effects in GoL and logistic population dynamics, by focusing on two parameters, namely Allee threshold (A) determining the low-density effect (known as Allee effect) and high-density limit known as carrying capacity (K) lowering the rate growth as organism approaches the upper-density limit. By aiming to confer the density-responsive behaviors to GoL, a novel Hill-type density-responsive function was chosen for substituting the logistic core algorithm behind the actions of our logistic CA model extended from GoL.

In the last sub-section (see Section 2.4), an attempt for simulating the consequence of modified GoL equipped with Hill-type CA invoking the altered A and K for decision-making is described.

2.2. Cellular automata (CA) and Game of Life (GoL). The automata theory is the mathematical study of abstract machines which is commonly handled in the theoretical computer science and in a wide-variety of interdisciplinary fields combining the natural sciences and the theoretical computer science [13].

In CA models, two types of neighborhood are known. The von Neumann neighborhood is composed of a central cell and its four adjacent cells on a two-dimensional (2D) square lattice [21]. The Moore neighborhood series form a group of neighborhoods with distinct

shapes (square or cube), dimensionality (D), and radius (φ) [22]. The most common example is composed of a central cell and its eight surrounding cells ($D = 2, \varphi = 1$) while its expansion with larger neighborhoods (e.g., $D = 2, \varphi = 2, 3$, and so on) could be defined if required [7].

According to definition, GoL invokes an outer totalistic model with simple rules [17,23], in each cell on the 2D square grids designed to stay in either of two states, dead or alive [7]. In fact, GoL is the “game” progressively simulating the spread of live cell population with time. The extent of live cell occupancy within the neighboring blocks locally determines the thriving behavior of artificial life in a discrete black-and-white (all-or-nothing) manner.

At each generation (time step) in the system, the states of all the cells are synchronously updated according to the rules (1) to (4) defined as below (as summarized in Figure 1) [7].

Rule (1): Any live cell with fewer than two in its Moore neighborhood will die (decay, as shown in Figure 2, case 1).

Rule (2): Any central live cell with more than three live surrounding cells in its Moore neighborhood will decay in the upcoming generation.

Rule (3): A dead cell needs exactly three living neighbors to re-grow in the next generation.

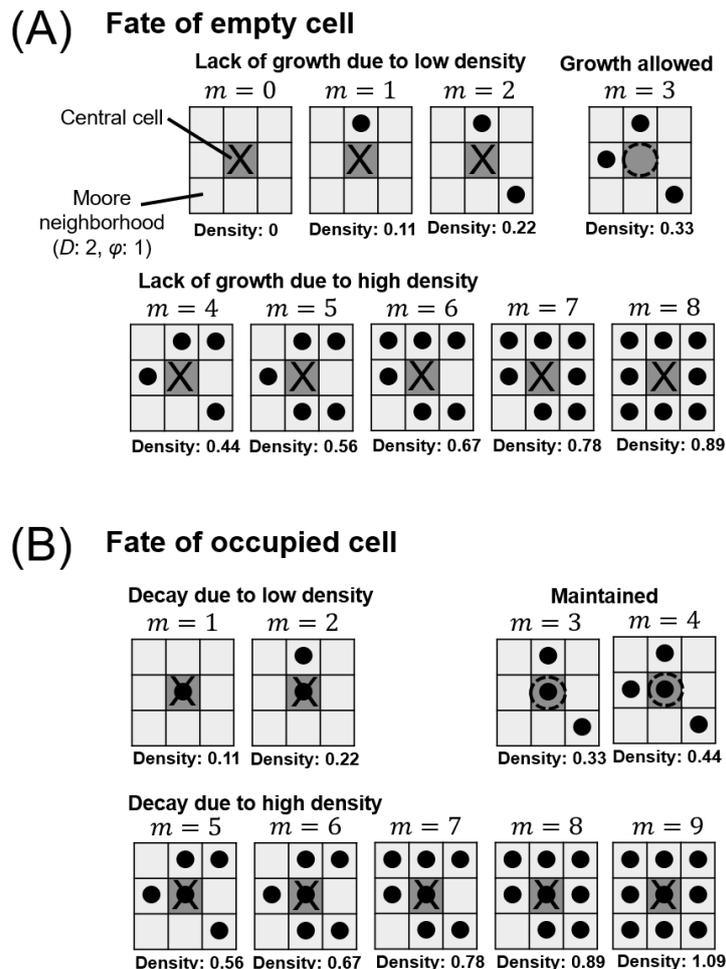


FIGURE 1. Simple rules in GoL determining the fate of cells according to the state of cellular occupancy: (A) the rule for empty cells; (B) the rule for occupied cells

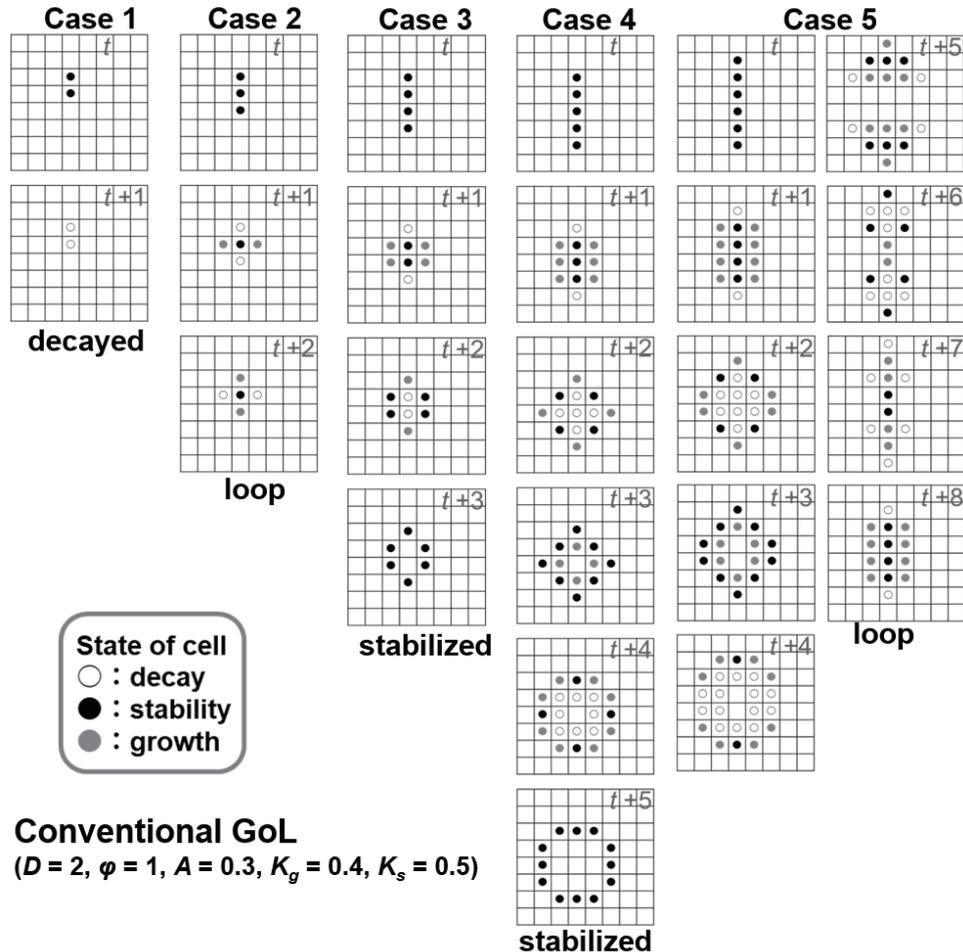


FIGURE 2. Typical growth patterns in GoL affected by initial arrangements of live cells. Here, the behavior of CA on a 2D 8×8 square lattice under periodic boundary conditions is simulated.

Rule (4): The live cells will remain alive (stabilized) in the upcoming generation only if they have two or three living neighbors.

Figure 2 catalogues the typical growth patterns initiated by different sets of cellular allocation on the 8×8 2D plane under the periodic boundary conditions. In the case 1, the live cell population (initially consisted with only 2 live cells) is exposed to immediate decay; the case 2 was shown to be trapped in the loop endlessly repeating two alternating states; in the cases 3 and 4, the games were arrested at stabilized states only after 3 and 5 generations, respectively; in the case 5, the population was again arrested at a stabilized state within 8 generations.

It seems that the growth of cells in original GoL is strongly suppressed under kind of high and low-density effects (as designed to allow no explosive growth). Therefore, some modifications in algorithm are required to allow the microbial explosive growth through the mode of growth which is basically insensitive to the harm by low density condition unless genetically modified [24,25]. In fact, the aim of the present study is to develop a GoL-extended growth-simulating model showing enhanced growth, which is compatible with the growth-simulating logistic mathematical models.

Recently, Ibrahim et al. [7] have demonstrated a deterministic phase transition and self-organization in Conway's GoL expressed as a logistic CA in which a single parameter tunes the dynamics of CA, consequently expanding their discrete state space into a Cantor

set. Their attempt may provide a potent platform for further studies on various emergent phenomena such as deterministic phase transitions, pattern formation, autocatalysis, and self-organization.

2.3. Mathematical background for combining the logistic equations and Hill's equation. Nowadays, logistic models are applied to a wide variety of cases in interdisciplinary fields, chiefly statistics, ecology, demography, and biological mathematics all focusing on the population dynamics [19], as the original studies emerged out through the data-based microbiological [26] and demographical [27] studies. In ecology and population biology, logistic equation and its derivatives are widely applied for simulating the population size or density [25] and the individual size [20] of living organisms.

After formalization of logistic equation by pioneering scholars [28,29], the rate of intrinsic increase (r) and the carrying capacity (K) were defined as key factors determining the growth of population size (N), as shown in Equation (2).

$$\frac{dN}{dt} = rN \left(\frac{K - N}{K} \right) \quad (2)$$

In addition to the upper limit of population growth defined by K , it is assumed that there must be the lower threshold of population density, defined as Allee threshold (A). These two distinct modes of population density effects under K and A , known as logistic effect and Allee effect, respectively, have been observed in a large biological spectrum covering most organisms with minor exceptions such as the lack of A in plants and bacterial species [24,25,30,31].

By combining the above-mentioned pair of distinct density effects, some different variations of mathematical expressions (Equations (3)-(7)) have been proposed as listed below [25,32-34].

$$\frac{dN}{dt} = rN \left(\frac{K - N}{K} \right) \left(\frac{N - A}{A} \right) \quad (3) \text{ [33, etc.]}$$

$$\frac{dN}{dt} = rN \left(\frac{K - N}{K} \right) \left(\frac{N - A}{K} \right) \quad (4) \text{ [32, etc.]}$$

In these equations, the extent of Allee effect largely differs, for instance, Equations (3) and (4) are known to express 'strong' and 'weak and/or flexible' Allee effects, respectively. Interestingly, an equation capable of expressing the Allee effects without setting the threshold (A) can be derived (Equation (5)), by completely shrinking the size of A in the flexible equation (Equation (4)) down to $A = 0$.

$$\frac{dN}{dt} = \frac{rN^2}{K^2} (K - N) \quad (5) \text{ [32, etc.]}$$

Recently, the author made further arrangements of the Allee effect model lacking A value [25]. In order to invoke higher generality to the model, the exponent in Equation (5) (fixed as 2) was replaced with the flexible exponent α (to be either an integer or a non-integer) (Equation (6)).

$$\frac{dN}{dt} = \frac{rN^\alpha}{K^\alpha} (K - N) \quad (6) \text{ [25]}$$

The resultant Equation (6) allows us to perform expanded application of the Allee-type of density effect without defining Allee threshold as similarly to Equation (5). In addition, Equation (6) enables the attenuation of the extent of Allee effect from weak to strong by freely altering the size of the exponent. By fixing the exponent at 1, this equation becomes identical to Equation (2), consequently losing the room for Allee effect.

Finally, further generality was conferred to the model by reintroducing the room for given A (Equation (7)). By freely modulating the size of r , K , α and A in Equation (7), any growth pattern can be effectively reproduced. Recently, the usefulness of Equation (7) was demonstrated by simulating the population dynamics in some density-sensitively growing photosynthetic organisms (*Paramecium bursaria* and *Synechocystis* spp. PCC 6803) [25].

$$\frac{dN}{dt} = \frac{rN^\alpha}{K^{\alpha+1}}(K - N)(N - A) \quad (7) [25]$$

These logistic models powerfully simulate the growth of organisms in a macroscopic manner by assuming that the whole microbial population senses and responds to its own size state (density). In contrast, each microbial cell composing the population may sense the local density in a microscopic manner through interactions with neighboring cells. Therefore, it is natural to infer that the series of decisions made at individual cellular level orchestrate the growing patterns in the whole population. From this point of view, we need to choose a simple and proper mathematical algorithm to be introduced into CA in the modified GoL, which must be practically equivalent to the logistic Allee models.

One of the candidate equations to be applied is Hill's equation (Equation (8)) which highly resembles the Michaelis-Menten equation (Equation (9)), one of the most renowned biochemical formulae expressing the velocity (V) of enzyme reaction as a function of substrate concentration ($[S]$) with a pair of regulatory parameter and constant, namely, V_{\max} , the maximal rate of reaction and Michaelis constant (K_m), the constant for $[S]$ at which a half maximal velocity can be manifested. Previously, the author performed a historical review tracing the origins of, and developments of Hill's equation and Michaelis-Menten equation applied in various areas [19].

In 1910, three years prior to the proposal of Michaelis-Menten equation, Hill's equation was originally proposed by A. V. Hill in order to describe the equilibrium relationship between O_2 tension and the saturation of hemoglobin [19]. Independently, in 1913, Michaelis-Menten equation was proposed specifically for enzyme reaction. Hill's equation can be generalized as the output y as a function of x (Equation (8)) [19], where y_{\max} , c and α stand for maximal output, the constant allowing $1/2 y_{\max}$, and Hill's coefficient determining the steepness of the curve, respectively.

Obviously, Michaelis-Menten equation (Equation (9)) can be considered to be a specific derivative of Hill's equation (Equation (8)) where the flexible exponent known as Hill's coefficient α is fixed to be 1 (thus, omitted).

$$y = \frac{y_{\max}x^\alpha}{c^\alpha + x^\alpha} \quad (8)$$

$$V = \frac{V_{\max}[S]}{K_m + [S]} \quad (9)$$

Today, Hill's equation is widely applied not only to bio-medical and pharmacological studies, but also in a variety of basic and applied eco-physiological fields covering photosynthesis [35] and microbial viability [19]; and even in a field of informatics, especially for probabilistic estimation and calculation of Shannon's entropy [36].

It has been previously demonstrated that the time-dependent growth curves simulated by conventional logistic equation (Equation (2)) for given microorganisms such as paramecia, can be mimicked or reproduced by a Hill-type equation expressed as a function of time as in Equation (10) [19].

$$y = \frac{y_{\max}t^\alpha}{c^\alpha + t^\alpha} \quad (10) [19]$$

In fact, Equation (10) can be expressed for a wide-variety of biological phenomena of interest (y) as the function of time (t) under the controls by the constant (c) equivalent to Michaelis constant modulating the timing of reaction attaining $1/2 y_{\max}$, and the exponent α modifying the steepness of the progress.

Here, a novel set of Hill's derivatives designed to reproduce the density-sensitive behavior of CA in GoL is newly proposed, by introducing the values equivalent to A and K (Equation (11)).

$$G = \frac{d^\alpha}{A^\alpha + d^\alpha} - \frac{d^\alpha}{K^\alpha + d^\alpha} \tag{11}$$

where growth decision (G) by CA can be expressed as a combined function of the live cell density (d) in the neighboring blocks (Moore neighborhood), under the influence of two types of density thresholds (A and K) and Hill's coefficient (α).

2.4. Intrinsic density effects programmed in GoL. As shown in Figure 3(A), the lower and upper thresholds equivalent to A and K corresponding to the lower and higher density effects can be found in conventional GoL. Note that GoL apparently employed two distinct K equivalents, designated as K_g and K_s , corresponding to the upper density limits in the neighborhood for newly inducing the growth in unoccupied cell (K_g) and for conferring the stability (or maintenance) to the occupied cells (K_s), respectively. In the

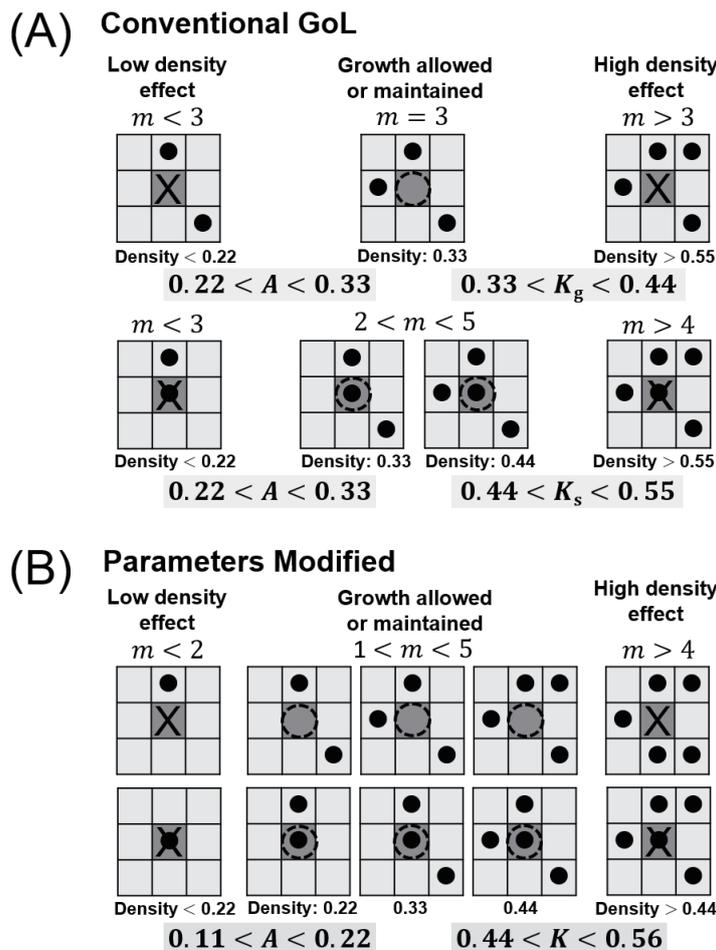
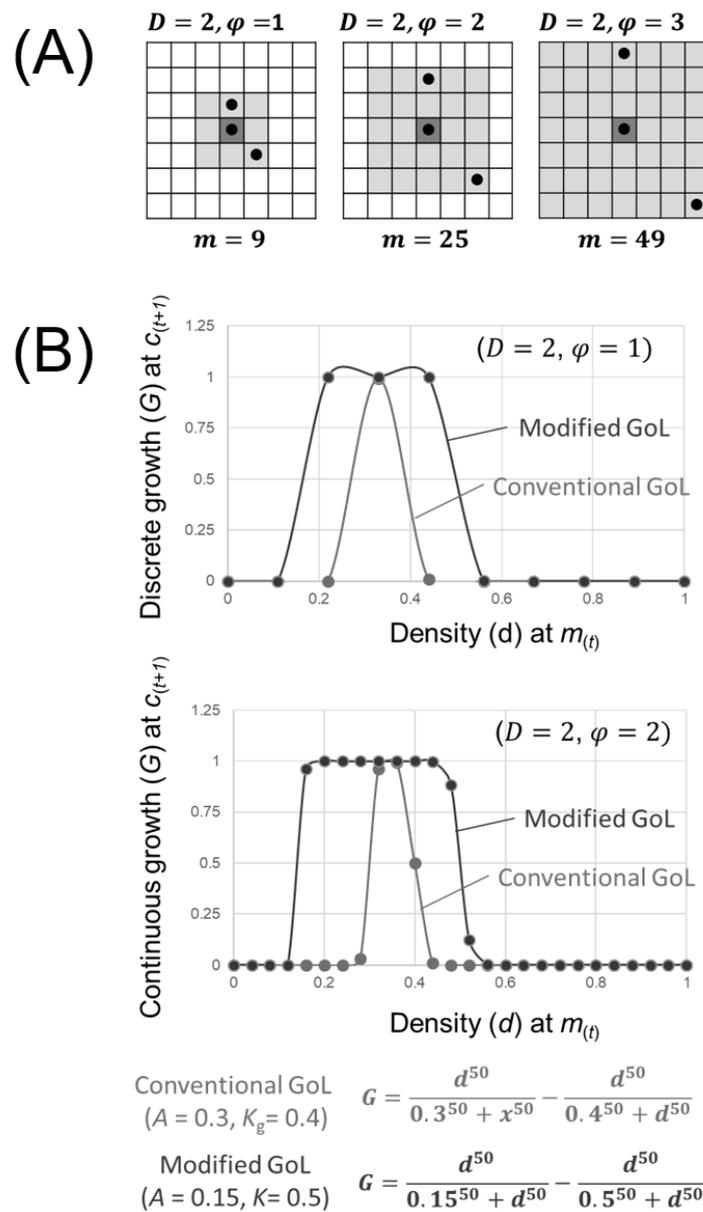


FIGURE 3. The parameters equivalent to A and K corresponding to the lower and higher density effects determined in conventional and modified GoL models

modified model (Figure 3(B)), designed to be used for further simulation in this study, an altered A (lower than carrying capacities in original GoL) and unified K were introduced for simplification and for enhanced growth.

3. Results and Discussion.

3.1. **Effect of the neighborhood size.** As shown in Figure 4(A), the size of Moore neighborhood to be employed in the modified GoL can be modulated depending on the purpose. By employing the Hill-type algorithm based on Equation (11), growth of the cells in conventional and modified GoL models was simulated as function of density in the Moore neighborhoods. In Figure 4(B), discrete growth profiles and continuous growth profiles resulted from different neighborhood sizes are compared.



3.2. Comparison with logistic equation-based simulation. For further simulation (to be compared with conventional logistic kinetics), the modified GoL model with smallest Moore neighborhood ($\varphi = 1$) was used (Figure 5). The oscillation of population size in the logistic simulation shown in Figure 5(B) is apparently due to the selection of extremely high r value. In fact, the oscillating dynamism is readily lost as r was set below *ca.* 1.7; thus, smoothly attaining the plateau within 6-7 generations and the high population level is maintained throughout the range of simulation period (data not shown).

By comparison of the growth curves for modified GoL and logistic model, it seems that the growth of live cell population in the modified GoL obeys the logistic growth

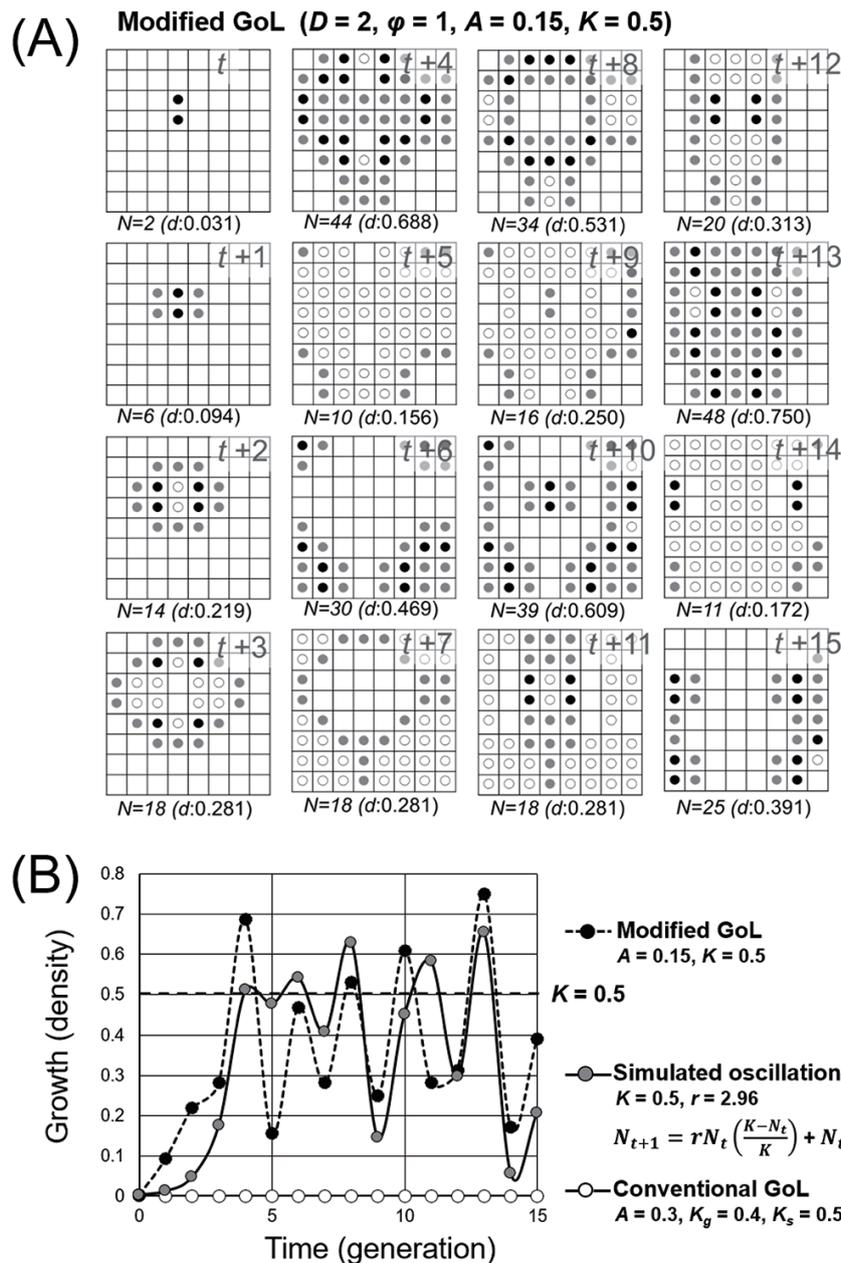


FIGURE 5. Trace of the population growth initiated by two adjacent live cells in the modified and conventional GoL on a 2D cellular space of 8×8 square lattice under periodic boundary conditions, followed by comparison with a logistic simulation

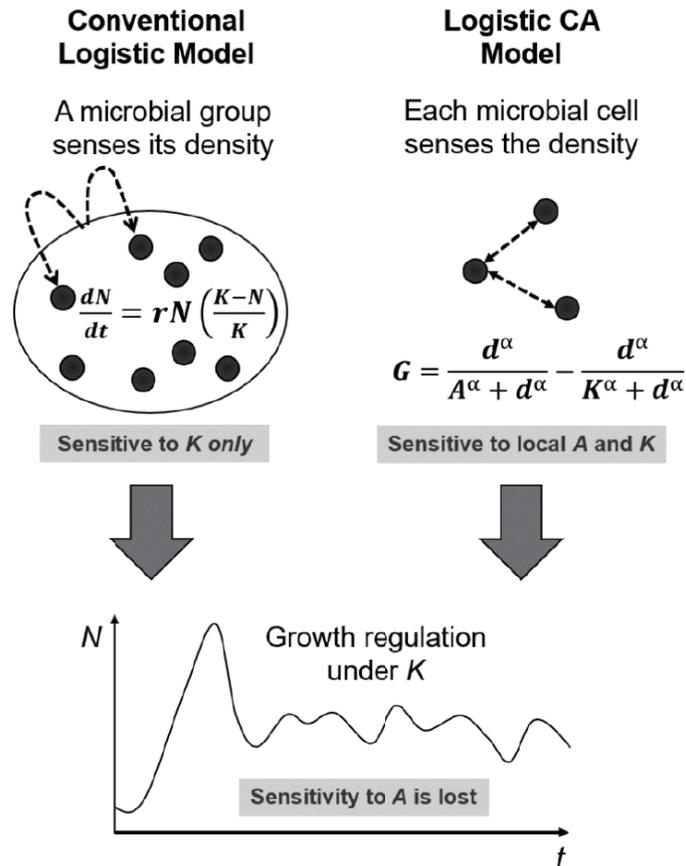


FIGURE 6. Comparison of the microscopic CA-based approach and macroscopic population-targeting logistic equation-based approach for simulating the oscillatory changes in cellular population in modified GoL

patterns under strong influence of K . This study could be viewed as a good example for microscopic CA model reflecting the behaviors of individual cells collectively reproducing the macroscopic ecological outcome as summarized in Figure 6.

Interestingly, the data implies that the low-density effect (harm) can be overcome in GoL-based CA model with specific local conformation possibly reflecting the nature of non-uniformly aggregating natural microbial cells with tendency to form colonies or biofilms; thus, unlike uniformly growing culture systems such as paramecium and cyanobacterial cultures [25], Allee threshold (A) effective at cellular/individual level can be no-longer found in the whole culture. This could be a likely answer to the fundamental question why microbial communities in the natural ecosystem rarely show sensitivity to low density effect. In contrast, K effective at cellular level and/or individual level resembles the one found in the whole population or community levels, and therefore, K could be reproduced both in the micro- and macro-organisms. In the future, greater impacts could be expected if this GoL-derived logistic CA model could be applicable for simulation of the growth or behavior of macro-organisms, chiefly plants and animals.

4. Conclusion. Here, an attempt to remodel the GoL as the parameter-adjustable ecological models was presented. The strategy taken here is that a novel Hill-type density-responsive function could be the core algorithm behind the actions of this logistic CA model extended from GoL. Strong emphasis was made for comparison of the modes of density effects in the modified and conventional GoL and the standard logistic population

dynamics, by focusing on two parameters, namely A and K . In the near future, this model must be applied for simulation of a wider range of organisms covering the communities of plants and animals.

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