Dynamic Analysis and Optimization of Agro - ecosystems Based on the LV Model

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Abstract. With the advancement of agriculture, deforestation for farmland has disrupted ecological balance and species patterns. This study constructs multiple models for analysis: the Basic Farmland Ecosystem Model (BFW) established based on the Lotka-Volterra competition model, and the Marginal Species Regression model (MSR) that combines improved cellular automata with the LV model. Results demonstrate that the return of marginal species enhances system stability. The impacts of reducing pesticide application and introducing bats are also investigated. An Eco-Sustainability Indicator (ESI) is developed to optimize organic farming models, identifying the optimal parameter combination. Specifically, a 0.5 increase in the fertilizer factor and a 20% increase in secondary-consumer biomass yield the maximum ESI of 0.7098. This research provides theoretical foundations and model support for the sustainable development of agro-ecosystems, integrating ecological dynamics and human intervention strategies through interdisciplinary modeling approaches.

Keywords: L-V model, Improved cellular automaton, ESI, EWM.

1. Introduction

1.1. Motivation

Forests, covering about 31% of the global land, are vital for the ecosystem with multiple functions. However, due to human activities, extensive deforestation for farmland conversion occurs, leading to soil erosion, fertility loss, biodiversity decline, and reduced ecosystem stability. Thus, achieving the sustainability of agricultural ecosystems, considering ecological, economic, and social aspects, is a crucial challenge. This research aims to analyze this issue through model construction for sustainable development.

1.2. The related work

Benalcazar et al. found boreal forest - to - farmland conversion reduced key soil indices. Soil health score decreased but stayed relatively high; its change related to organic matter decline, regardless of conversion time [1]. Kefa Lew et al. studied Ethiopia's Gura Ferda Forest and found 1984 - 2016 forest - to - farmland/ecotone conversion altered woody species diversity and carbon storage. The ecotone had intermediate diversity, and natural forests had 1.53 - 2.67 times more carbon storage [2]. Li et al. analyzed a global dataset and showed natural forest conversion to other ecosystems changed soil microbial communities and negatively impacted carbon sequestration and nutrient cycling, more so in warm - humid areas [3]. HilleRisLambers et al. showed that in a changing world, organisms' trophic flexibility is crucial for ecosystems to cope with environmental changes. It affects species interactions, community structure, and ecosystem functions. They also analyzed the influencing factors and mechanism of action [4].

1.3. Our work

This paper focuses on post - deforestation farmland ecosystems, using multiple models.

First, the BFW model is developed with the Lotka - Volterra competition model, considering factors like pesticides and crop seasonality. Applied to a 5000 m² farmland, it shows that a 2% initial pesticide concentration leads to periodic stability.

Second, the MSR model combines an improved cellular automaton and the LV model. By introducing species like snakes and sparrows and setting diffusion rules, it reveals that marginal species return stabilizes the ecosystem.

Then we studied human - decision impacts. Reducing pesticides alone destabilizes the system, but introducing bats improves it, increasing crop yield by 19.45%.

Finally, the ESI, consisting of cost - benefit, ecosystem - stability, and soil - organic - matter indices, is constructed. With weights determined by the Entropy Weight Method, the optimal organic farming model is found: a 0.5 increase in the fertilizer factor and a 20% increase in secondary - consumer biomass, with a maximum ESI of 0.7098.

2. Preliminary

2.1. L -V model

In a resource - limited environment, the population dynamics of species can be effectively described by the improved Lotka - Volterra (LV) model. The original LV model, based on the logistic equation, mainly characterizes the predation relationship between two species:

$$\begin{gathered} \frac{dP_i(t)}{dt} = P_i(t)\left(a - bP_i(t)\right) \\ \frac{dP_{i+1}(t)}{dt} = P_{i+1}(t)\left(cP_i(t) - d\right) \\ i = 0, 1, 2, \cdots \end{gathered} \tag{1}$$

Where, $P_i(t)$ denotes the population of prey at time t, $P_{i+1}(t)$ denotes the population of predators at time t, and a, b, c, d are positive constants.

In this paper, to simulate the complex agro - ecosystem, the LV model was improved in several aspects:

2.2. Growth Factor r

For agro - ecosystem producers, data shows that due to human cultivation, their growth rate is closely related to artificial fertilizers, as follows:

$$r_{P_0}(t) = r_0 R_0 \tag{2}$$

Where R_0 represents the fertilizer promotion coefficient.

For consumers, their growth rate is related to the predation rate and population size, that is:

$$r_{P_i} = r_{P_i} \frac{\alpha_{P_{i-1}}(t) P_{i-1}(t-1)}{P_i(t-1)}, i = 1, 2, \cdots \tag{3}$$

Where $\alpha_{P_i}(t)$ is the predation rate of consumer level i at moment t, r_{P_i} is the growth rate base of consumer level i.

2.3. Predation Rate $\alpha_{P_i}(t)$

Since the predation rate $\alpha_{P_i}(t)$ at a specific trophic level is proportional to the change in the number of predators at the previous trophic level, we can determine the predation rates of producers and consumers in week t.

$$\alpha_{p_i}(t) = \alpha_{P_i}\left(1 + \frac{P_{i+1}(t-1) - P_{i+1}(t-2)}{P_{i+1}(t-2)}\right),\ i = 0, 1, 2, \cdots \tag{4}$$

Where α_{P_i} represents the baseline predation rate of organisms at trophic level i.

2.4. Pesticide Impact Factor β

Pesticides reduce organism populations via bio-concentration and toxicity, with trophic-level differences. The pesticide impact factor characterizes these effects, where weeds face general pesticidal and specific herbicide inhibition

Herbicides and insecticides were grouped as pesticides for similar ecosystem impacts, with effects integrated into overall pesticidal ecosystem impact.

Assuming stable environments, pesticide concentration dynamics follow exponential decay: $C(t) = C_0 e^{-k\left(t - \left\lfloor \frac{t}{T} \right\rfloor T\right)}$

Where $C(t)$ is the pesticide concentration at moment t, C_0 is the initial pesticide concentration, k is the degradation rate constant, and T is the crop growth cycle.

2.5. Seasonal Crop Growth

The biomass of crops grows seasonally and cyclically, and its expression is:

$$P_{0,f}(t) = P_0(1 - e^{-\lambda t}) \cdot \sin(wt) \tag{5}$$

Where P_0 is the maximum biomass of the crop.

2.6. Final LV model

Combining the above and considering pesticide effects, the population - size change over time is described by the improved LV model:

$$\frac{dP_i(t)}{dt} = r_{P_i}(t)P_i(t)\left(1 - \frac{P_i(t)}{K_{Pi}}\right) - \alpha_{P_i}(t)P_i(t) - \beta_{P_i}C(t),\ i = 0, 1, 2, \cdots \tag{6}$$

Where, K_{P_i} represents the maximum environmental carrying capacity for species i, β_{P_i} denotes the inhibitory factor of pesticides on species i, and $C(t)$ stands for the pesticide concentration at cycle t.

Differentiating the above equation yield:

$$P_i(t) - P_i(t-1) = r_{P_i}(t)\left(1 - \frac{P_i(t-1)}{K_{Pi}}\right) - \alpha_{P_i}(t)P_i(t-1) - \beta_{P_i}C(t-1) \tag{7}$$

The above is the basic model of how the population size changes over time.

2.7. Notations

The key mathematical notations used in this paper are listed in Table 1.

Table 1. Notations used in this paper

Symbol	Description	Unit
$P_0(t)$	Biomass of producers in the t-th week	individual
$P_i(t)$	The biomass of the i-th level consumer in week t.	individual
C_0	Initial pesticide concentration	mg/L
k	Degradation rate constant	-
T	Crop growth cycle	$week$
r_{p_i}	Growth rate base for level i consumers	-
α_{p_i}	Base predation rate of consumers at level i	-
β_{p_i}	Impact factor of pesticide concentration on level i consumers	-
R_0	Fertilizer promoter	-
K_{p_i}	Carrying capacity at each food web level.	-

3. Basic food web (BFW) model of agro-ecosystems

3.1. The establishment of BFW model

Producers, consumers, and human factors (such as pesticides) are key elements of agricultural ecosystems. Based on this ecosystem, this paper uses logistic model and Lotka and Volterra model [1] to construct a model of the population size changes of various species in different levels of ecosystems under limited resource environment over time.

The original L-V model focused on predator-prey scenarios between two populations. In order to enable the Lotka Volterra model to effectively simulate complex multi-level agricultural ecosystems, we improved the L-V model and took into account other factors such as pesticide concentration.

According to the hierarchical resource utilization model [2], agricultural ecosystem producers exhibit a growth rate directly influenced by artificial fertilization through human cultivation. Their survival and growth rates are positively associated with resource availability (e.g., nutrient uptake during critical growth phases) and negatively regulated by population density due to intraspecific competition.

$$\begin{cases} r_{P_0}(t) = r_0 R_0 \\ r_{P_i} = r_{P_i} \dfrac{\alpha_{P_{i-1}}(t) P_{i-1}(t-1)}{P_i(t-1)}, i = 1, 2, \cdots \end{cases} \tag{8}$$

Where R_0 represents the fertilizer promotion coefficient, $\alpha_{P_i}(t)$ is the predation rate of consumer level i at moment t , r_{P_i} is the growth rate base of consumer level i.

Since the predation rate $\alpha_{P_i}(t)$ at a specific trophic level is proportional to the change in the number of predators at the previous trophic level, we can determine the predation rates of producers and consumers in week t.

$$\alpha_{p_i}(t) = \alpha_{P_i}\left(1 + \frac{P_{i+1}(t-1) - P_{i+1}(t-2)}{P_{i+1}(t-2)}\right), \ i = 0, 1, 2, \cdots \tag{9}$$

Due to their biological concentration and toxicity, pesticides can cause a decrease in the population of various organisms, resulting in different impacts on their nutritional levels. We introduce the pesticide impact factor β_{P_i} to describe these effects. Weeds are affected by general pesticide impacts and specific herbicide inhibition, denoted as $\beta_{P_{0,z}}$.

Considering that human activities make the ecological environment of farmland stable, pesticide concentration naturally decays during the crop cycle. We use an exponential decay function to describe the changes in pesticide concentration over time.

$$C(t)=C_0 e^{-k\left(t-\left\lfloor\frac{t}{T}\right\rfloor T\right)} \tag{10}$$

Where $C(t)$ is the pesticide concentration at moment t, C_0 is the initial pesticide concentration, k is the degradation rate constant, and T is the crop growth cycle.

Under the intervention of human activities, the calculation of crop biomass for seasonal growth, exponential growth, and periodic growth is as follows:

$$P_{0,f}(t)=P_0(1-e^{-\lambda t})\cdot\sin(wt) \tag{11}$$

Where P_0 is the maximum biomass of the crop.

Combining the above and considering pesticide effects, the population - size change over time is described by the improved LV model:

$$\frac{dP_i(t)}{dt}=r_{P_i}(t)P_i(t)\left(1-\frac{P_i(t)}{K_{Pi}}\right)-\alpha_{P_i}(t)P_i(t)-\beta_{P_i}C(t),\ i=0,1,2,\cdots \tag{12}$$

Where, K_{P_i} represents the maximum environmental carrying capacity for species i, β_{P_i} denotes the inhibitory factor of pesticides on species i, and $C(t)$ stands for the pesticide concentration at cycle t. Weeds are affected by general pesticide impacts and specific herbicide inhibition, denoted as $\beta_{\mathrm{P_{0,z}}}$

Differentiating the above equation yield:

$$P_i(t)-P_i(t-1)=r_{P_i}(t)\left(1-\frac{P_i(t-1)}{K_{Pi}}\right)-\alpha_{P_i}(t)P_i(t-1)-\beta_{P_i}C(t-1) \tag{13}$$

When calculating the total producer output at time in this human - driven agroecosystem, we mainly consider crop biomass. Despite predation and pesticide effects, crops grow exponentially in an ideal environment. Weeds stabilize at a certain level due to the unfavorable environment.

In agricultural ecosystems, consumer population dynamics exhibit significant intra trophic synchronicity [3] [4]. For instance, bats' trend is like that of secondary consumers. So, the overall consumer trend can be inferred from individual predators.

In summary, the complete BFW model is obtained as follows:

$$\begin{cases}\dfrac{dP_i(t)}{dt}=r_{P_i}(t)P_i(t)\left(1-\dfrac{P_i(t)}{K_{P_i}}\right)-\alpha_{P_i}(t)P_i(t)-\beta_{P_i}C(t),\ i=0,1,2\\ P_0(t)=P_0(1-e^{-\lambda t})\cdot\sin(wt)+P_{0,z}(1-\beta_{P_{0,z}}C(t))\\ r_{P_0}(t)=r_0R_0\\ r_{P_i}(t)=r_{P_i}\dfrac{\alpha_{P_{i-1}}P_{i-1}(t-1)}{P_i(t-1)},\ i=1,2\\ \alpha_{P_i}(t)=\alpha_{P_i}\left(1+\dfrac{P_{i+1}(t-1)-P_{i+1}(t-2)}{P_{i+1}(t-2)}\right),\ i=0,1,2\\ C(t)=C_0e^{-k\left(t-\left\lfloor\frac{t}{T}\right\rfloor T\right)}\end{cases} \tag{14}$$

For the top - level predators in the food chain, the base number of their being preyed upon is zero.

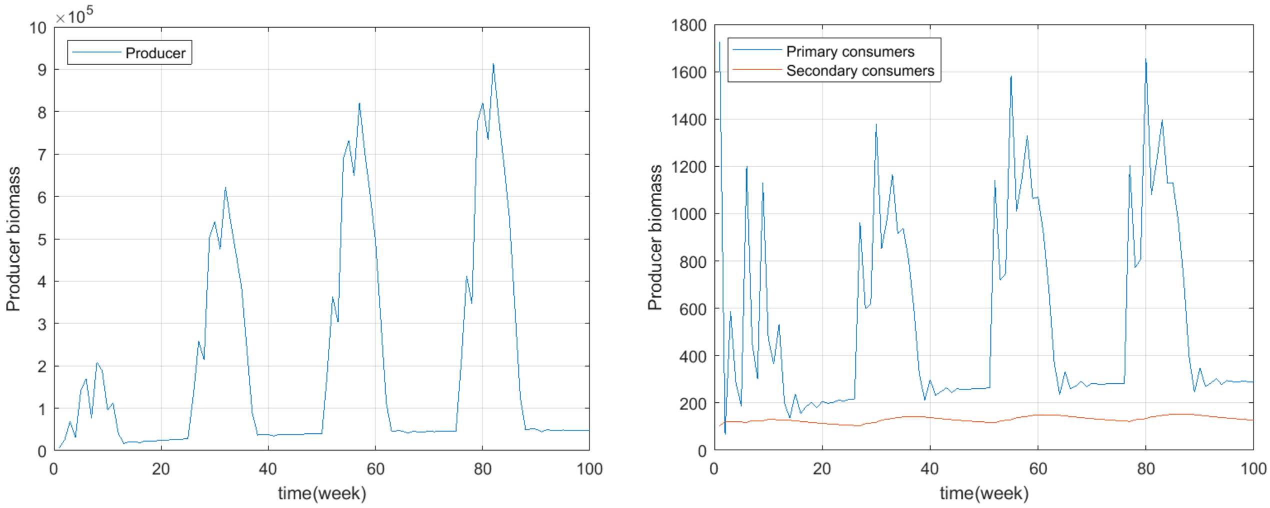
3.2. The Application of BFW Model

Apply the BFW model to the following scenarios which is shown in Table 2:

Table 2. The size of the application scenario and the species it contains

Species	K	$\beta(1\% \cdot week^{-1})$	α	r
Weeds	250000	0.9	0.21	0.56
		0.3		
lettuce	1125000	0.3	0.21	0.56
Aphids	11250000	18	0.77	1.4
Insectivorous birds	120	2	0.49	0.35
Bats	21	2	0.14	0.14

Assuming the crop cultivation cycle $T = 100$, we used the fourth - order Runge - Kutta method for programming. The changes in population size of producers and consumers over time are shown in Figure.1.



(a) producers (b) consumers

Figure 1. Change in the number of trophic levels at T = 100

In Figure.1. (a), producer numbers rose from 0. In the first cycle, they fluctuated little due to ecosystem instability, leading to low yields. As the agro - ecosystem stabilized and conditions improved, numbers increased significantly and steadily, with crop yield around 9.1×10^5. The sharp biomass decline meant harvest.

In Figure.1. (b), primary consumers' population dropped due to natural enemies, then rebounded and cycled, controlled below 2000. Secondary consumers, with limited initial numbers and low capacity, had small population fluctuations.

4. Model of Marginal Species Regression (MSR)

Over time, marginal habitats gradually mature, promoting the return of native species. These species interact with the environment and alter the agricultural ecosystem. However, the complex and nonlinear ecological environment makes traditional deterministic ecological dynamics models difficult to use [5]. To better describe marginal - species return and ecosystem changes, we combined the BFW model with metacellular automata. This combination overcomes traditional model limitations [6].

The stability of the agricultural system allows its response to different consumption levels of species to be classified into two categories: same level superposition and cross level regulation. [7]. To simplify the explanation, we introduce one species in each category, and further species regression can be summarized into the above two situations.

Birds are enriched at the edges due to the edge effect [8]. So, introducing sparrows is reasonable. Normal insectivorous birds were in the original web. However, the sparrow, which feeds on both grains and insects, will have a complex impact on the system. Also, as forests are snake habitats, snakes preying on birds and chicks return with bird migration.

Thus, we included snakes and sparrows in the model to study their impact on the ecosystem.

4.1. A Model of A Metacellular Automaton

In this paper the Moore neighborhood is adopted for snakes. Since sparrows can fly, which leads to a wider diffusion range, the Margolus neighborhood is used when determining the next state of sparrows [9].

We used two - dimensional cellular automata for modeling. Each grid is a cell, and its state represents the number of snakes $S_{i,j}(t)$ and the number of sparrows $B_{i,j}(t)$ in this region respectively.

The ecosystem outside the edge is stable. The number of snakes in boundary cells is S_{es}, and sparrow number remains stable at S_{es}. Initially, the number of both in internal cells is 0.

During non - hibernation, snakes and sparrows diffuse from cells with more individuals to those with fewer. The diffusion probability of snakes is P_s, and the state - update formula for cell (i,j) at time $t+1$ is:

$$S_{i,j}(t+1) = (1-P_s)S_{i,j_{new}}(t) + \frac{P_s}{n}\sum_{(m,n)\in N_{i,j}} S_{m,n_{new}}(t) \tag{15}$$

Where, $N_{i,j}$ represents the set of neighboring cells.

Sparrows follow the same rule with a diffusion probability of P_b. The state - update formula for cell (i,j) at time $t+1$ as follows:

$$B_{i,j}(t+1) = (1-P_b)B_{i,j_{new}}(t) + \frac{P_b}{n}\sum_{(m,n)\in N_{i,j}} B_{m,n_{new}}(t) \tag{16}$$

Since Sparrows diffuse faster, $P_s < P_b$.

Due to the predation relationship, when the number of snakes in a cell reaches $S_{threshold}$, the number of sparrows in that cell halves:

$$B_{i,j}(t+1) = \begin{cases} \frac{1}{2}B'_{i,j}(t+1), & S_{i,j}(t+1) \geqslant S_{threshold} \\ B'_{i,j}(t+1) \quad , & S_{i,j}(t+1) < S_{threshold} \end{cases} \tag{17}$$

Among them, $B'_{i,j}(t+1)$ represents the original number of sparrows in cell (i,j) in the $t+1$-th week.

During hibernation, only sparrows diffuse, unaffected by snakes.

4.2. Improved Lotka Volterra model

In species regression models, the improvement of BWF models requires customized design based on the ecological characteristics of the introduced species. In our model, we consider the hibernation habits of snakes and birds as DTL consumers [2]. For other more general cases, we can simplify by setting specific parameters to zero or one, indicating that our model has good universality.

Let the number of snake hibernation cycles be TD. During non - hibernation $t \notin TD$, snake population change follows the model in 3.1. During hibernation $t \in TD$, as snakes can't hunt, their population is mainly affected by pesticides.

In this agro - ecosystem, sparrows have diverse food sources. Pesticide impacts on organisms vary. This leads to a difference between the pesticide impact factor β_{P_b} and the β_{P_2} corresponding to secondary consumers. Although sparrows are secondary consumers, we discuss them separately [10].

In the post - species - return ecosystem, producers face new predation from sparrows and primary consumers have new predation from sparrows. we assume $P_2'(t)$ is the original secondary - consumer population.

Based on the above changes, the improved LV model is:

$$\begin{cases} \dfrac{dP_b(t)}{dt} = r_{P_b}(t)P_b(t)\left(1-\dfrac{P_b(t)}{K_{P_b}}\right) - \alpha_{P_2}(t)P_b(t) - \beta_{P_b}C(t) \\ r_{P_b}(t) = r_{P_b}\dfrac{\alpha_{P_0}(t)P_0(t) + \alpha_{P_1}(t)P_1(t-1)}{P_b(t-1)} \\ \dfrac{dP_2'(t)}{dt} = r_{P_2}(t)P_2'(t)\left(1-\dfrac{P_2'(t)}{K_{P_2}}\right) - \alpha_{P_2}(t)P_2'(t) - \beta_{P_2}C(t) \\ r_{P_2}(t) = r_{P_2}\dfrac{\alpha_{P_1}(t)P_1(t-1)}{P_2(t-1)} \\ \alpha_{P_2}(t) = \alpha_{P_2}\left(1+\dfrac{P_3(t-1)-P_3(t-2)}{P_3(t-2)}\right) \end{cases} \tag{18}$$

The update formula for secondary consumers in the current ecosystem is as follows:

$$P_2(t) = P_b(t) + P_2'(t) \tag{19}$$

4.3. The Mapping between Cellular Automata and the LV Model

We map the population size in the LV model to the cell state in cellular automata. If the total number of snakes is N_s and sparrows is N_b, then the proportion of the number of snakes $S_{i,j}(t)$ and sparrows $B_{i,j}(t)$ in each cell (i,j) to their respective total populations are:

$$\begin{aligned} f_{S_{i,j}}(t) &= \frac{S_{i,j}(t)}{\sum\limits_{i,j} S_{i,j}(t)} \\ f_{B_{i,j}}(t) &= \frac{B_{i,j}(t)}{\sum\limits_{i,j} B_{i,j}(t)} \end{aligned} \tag{20}$$

In the cell (i,j), the updating formula for the number of species is as follows.

$$\begin{aligned} S_{i,j_{new}}(t) &= S_{i,j}(t) + f_{S_{i,j}}(t)\Delta N_s \\ B_{i,j_{new}}(t) &= B_{i,j}(t) + f_{B_{i,j}}(t)\Delta N_b \end{aligned} \tag{21}$$

4.4. MSR Model

The MSR model integrates the cellular automaton in 4.1, population calculation formulas in the LV model in 4.2, and mapping rules in 4.3. We list core formulas for simplicity.

$$\begin{cases} S_{i,j}(t+1) = (1-P_s)S_{i,j_{new}}(t) + \dfrac{P_s}{n}\sum\limits_{(m,n)\in N_{i,j}} S_{m,n_{new}}(t) \\ B_{i,j}(t+1) = \begin{cases} (1-P_b)B_{i,j_{new}}(t) + \dfrac{P_b}{n}\sum\limits_{(m,n)\in N_{i,j}} B_{m,n_{new}}(t), & S_{i,j}(t+1) < S_{threshold} \\ \dfrac{1}{2}\left((1-P_b)B_{i,j_{new}}(t) + \dfrac{P_b}{n}\sum\limits_{(m,n)\in N_{i,j}} B_{m,n_{new}}(t)\right), & S_{i,j}(t+1) \geqslant S_{threshold} \end{cases} \\ S_{i,j_{new}}(t) = S_{i,j}(t) + \dfrac{S_{i,j}(t)}{\sum\limits_{i,j} S_{i,j}(t)}\Delta N_s \\ B_{i,j_{new}}(t) = B_{i,j}(t) + \dfrac{B_{i,j}(t)}{\sum\limits_{i,j} B_{i,j}(t)}\Delta N_b \end{cases} \tag{22}$$

4.5. The Application of MSR Model

Increased data related to snakes and sparrows are shown in Table 3:

Table 3. Data relating to snakes and sparrows

Species	K	$\beta(1\%\cdot\text{week}^{-1})$	α	r
Snakes	40	0.4	0	0.07
Sparrows	500	2	0.3	0.18

Based on our MSR model, we obtained heat maps of population size changes for snakes and sparrows during regression, Figure.2 and Figure.3, respectively.

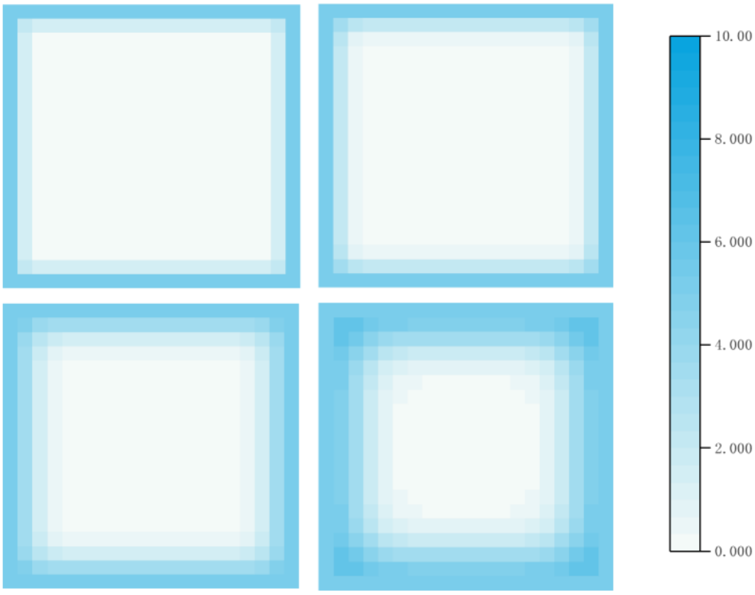


Figure 2. Introduce a heat map depicting the change in the number of snakes in the scenario

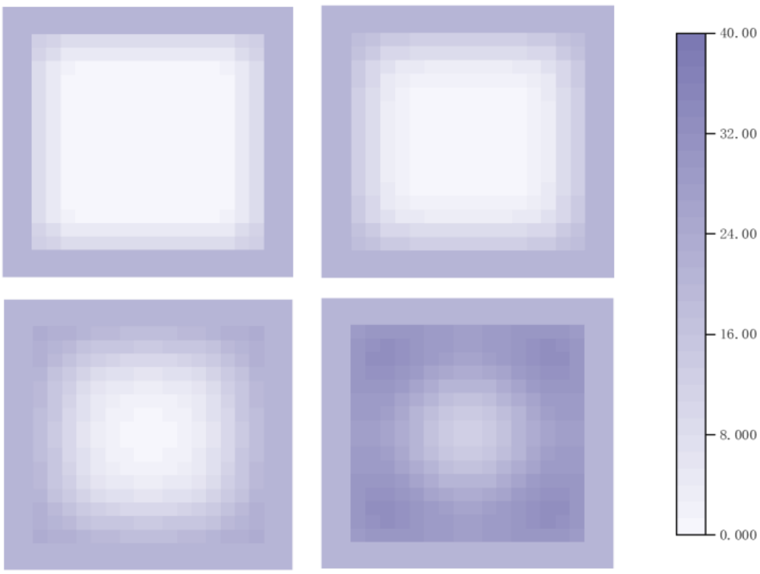


Figure 3. Introduce a heat map depicting the change in the number of sparrows in the scenario

By comparing Figure.1. and Figure.2., it can be seen that sparrows spread faster and have more numbers. Snakes are limited by their own range of activity and the unfavorable environment of the agricultural ecosystem, and often move in the forest areas around the agricultural ecosystem; And sparrows benefit from the widespread presence of insects in farmland, gradually accumulating towards the center of the field. This result is consistent with real life and proves the empirical reliability of our model.

5. Conclusion

This paper systematically analyzed the dynamic evolution mechanism of agricultural ecosystems by constructing a basic food web model (BFW) and a marginal species regression model (MSR). The BFW model, based on the improved Lotka Volterra equation, successfully simulated the periodic fluctuations of biomass in a 5000 m^2 agricultural ecosystem. The MSR model innovatively combines cellular automata and LV equations to achieve population change prediction of regression species in complex and nonlinear ecological environments. The simplification of high trophic level interactions and climate factors in the model may limit its universality. Future research can further integrate higher trophic level species and dynamic environmental parameters to enhance the predictive ability of complex ecological scenarios.

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