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Annotation

The model proposed by W. Dieckmann and R. Law[1][2] takes into account the behavior of each individual and its impact on the entire population and effectively describes the interaction of species. The third chapter discusses two approaches to modeling - numerical method and simulation, and also describes the advantages and disadvantages of each of them. In the fourth section, several graphs were analyzed showing the dependence of the equilibrium density and the radii of dispersion and competition. All input data for running simulations were prepared, the necessary approaches and formulas were studied. The task for the future works - is using one of the modeling methods - simulation, to obtain results and compare them with the results obtained by solving integro-differential equations, as well as to assess how reliable the results are and can be used for further research.

Аннотация

Модель предложенная У. Дикманом и Р. Лоу[1][2] учитывает поведение каждого индивида и его влияние на всю популяцию, и эффективно описывает взаимодействие видов. В третьей главе рассматриваются два подхода к моделированию - численный метод и симуляции, а также описываются преимущества и недостатки каждого из них. В четвертой главе были проанализированы несколько графиков показывающих зависимость равновесной плотности и радиусов рассеивания и конкуренции. Были подготовлены все входные данные для запуска симуляций, изучены необходимые подходы и формулы. Цель для будущих работ - это, используя один из методов моделирования - симуляции, получить результаты и сравнить их с результатами полученными при помощи решения интегро-дифференциальных уравнений, а так же оценить насколько полученные результаты достоверны и могут быть использованы для дальнейших исследований.

Keywords

Mathematical biology

Biological models

Math modeling

1 Introduction

Currently, various types of mathematical models of biological communities, which are used to predict the behavior of populations in ecosystems, are being actively developed. Each individual model has its benefits and drawbacks depending on the application. This paper considers a spatial biological model proposed by Ulf Dieckmann and Richard Law[1][2] to study the dynamics of plant populations. The behavior of populations and all changes are described using integro-differential equations. This paper will also consider various modeling approaches that allow you to monitor the behavior of populations and analyze it without huge time costs, as well as indicate the advantages and disadvantages of each of the approaches. The work will pay attention to the change in the equilibrium density of populations depending on some factors and lay the foundation for running simulations that will enable more detailed analysis in the future.

2 Dieckmann-Law biological model

Let us first describe the model in its classical form. In area A belonging to space \mathbb{R}^N ($N = 1, 2, 3$), there is a population of plants. Region A is finite and not equal to zero. Individuals are material points and do not differ from each other in any way, except for their position in space. The set of all points located in space is denoted by X. Time in the model is continuous and at any moment can occurs one of two events - birth or death. Death can occur due to natural factors and competition between species. It is assumed that the environment is homogeneous and acts on all individuals equally.

b - birth rate, $b > 0$

d - death rate, $d \geq 0$

d' - strength of competition, $d' \geq 0$

$m(x)$ - birth kernel

$\omega(x)$ - competition kernel

The functions $m(x)$ and $\omega(x)$ are spherically symmetric and have the following restrictions:

$$\begin{aligned} m(x) &\geq 0, \int_{\mathbb{R}} m(x) dx = 1, \lim_{|x| \rightarrow +\infty} m(x) = 0 \\ \omega(x) &\geq 0, \int_{\mathbb{R}} \omega(x) dx = 1, \lim_{|x| \rightarrow +\infty} \omega(x) = 0 \end{aligned}$$

An individual at point ξ can give birth to a new individual at point ξ' with probability $m(\xi - \xi')$. Similarly, an individual located at the point ξ , can kill an individual located at the

point ξ' with probability $(\xi - \xi')$, respectively.

To describe the spatial structure of Dieckmann-Law biological model, some definitions must be introduced. To do this, a moment of time t_0 is fixed and the set $X = X(t_0)$ is considered.

$$I_{X \cap A}(X) = \begin{cases} 1, & X \in A, \\ 0, & X \notin A. \end{cases} \quad (1)$$

This is a characteristic function of $X \cap A$ showing that there is an individual at a particular point A.

Definition 1:

The correlation density of order m in the area A for a fixed configuration of the community X is the function

$$C_m(\xi_1, \xi_2 \dots \xi_{m-1}, X) = \frac{1}{\mu(A)} \sum_{x \in X \cap A} I_{X \cap A}(x) \prod_{i=1}^{m-1} I_{X \cap A}(x + \xi_i)$$

Where $\mu(A)$ - measure of set A.

Correlation density of order m is a characteristic of groups consisting of m individuals living in area A, in which the distance from the first individual to the second is ξ_1 , the distance from the first to the third is ξ_2 , and so on. The first-order correlation density is the average population density in area A, and the second-order correlation density is the number of pairs in which the distance between individuals is equal to ξ divided by the measure of area A.

Let's introduce a new function $\lambda(X)$

$$\lambda(X) = \begin{cases} 1, & |x| = 0, \\ 0, & |x| \neq 0. \end{cases}$$

with which we introduce a new definition - *the corrected correlation density*.

Definition 2:

The corrected correlation density of order m in the region A for a fixed configuration of the community X is the function

$$\tilde{C}_m(\xi_1, \xi_2 \dots \xi_{m-1}, X) = C_m(\xi_1, \xi_2 \dots \xi_{m-1}, X) \prod_{i=1}^{m-1} \lambda(\xi_i) \prod_{i=1}^{m-2} \prod_{j=i+1}^{m-1} \lambda(\xi_j - \xi_i)$$

where $C_m(\xi_1, \xi_2 \dots \xi_{m-1}, X)$ - correlation density of order m in the region A.

Definition 3:

The spatial moment of order m in region A is the expected value of the corrected correlation density of order m for all possible community configurations, that is, a function of the form

$$C_m(\xi_1, \xi_2 \dots \xi_{m-1}) = \int_{\rho} \tilde{C}_m(\xi_1, \xi_2 \dots \xi_{m-1}, X) dP(X),$$

where ρ - probability space on the set of possible community configurations, $P(X)$ - probability measure in this space.

Spatial moments:

To describe the numerical characteristics of the model at each moment of time we use three main functions - spatial moments.

$N = C_1$ - first spatial moment, describing only the average abundance in area A .

$C(\xi) = C_2(\xi)$ - second spatial moment, describing the density of all possible pairs of individuals in A .

$T(\xi, \xi') = C_3(\xi, \xi')$ - third spatial moment, describing the triplets density, the first term of which is separated from the second and third at distances ξ and ξ' , respectively.

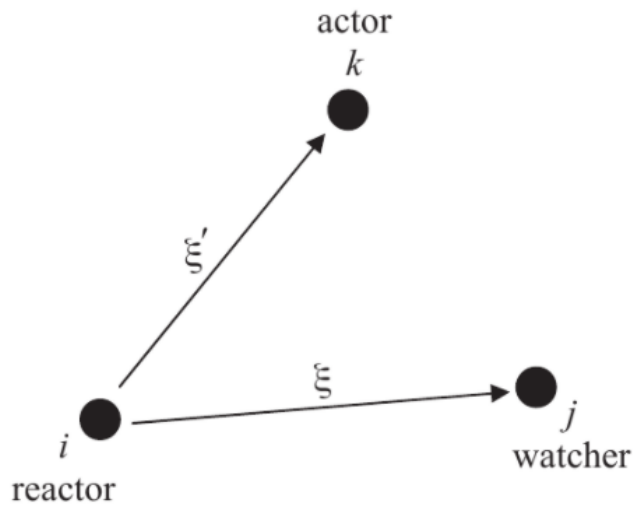


Figure 2.1

At each moment t , the probability $P(x)$ of the configuration of the community X is different, which means that the introduced spatial moments depend on time, which indicates the existence of not only the dynamics of the population, but also the dynamics of its spatial moments.

This system of integro-differential equations was derived by Ulf Dieckmann in his work and reflects the dynamics of the first two spatial moments.

$$\begin{cases} 0 = (b - d)N - d' \int_{\mathbb{R}^n} C(\xi)w(\xi) d\xi, \\ 0 = bm(\xi)N + \int_{\mathbb{R}^n} bm(\xi')C(\xi + \xi') d\xi' - (d + d'w(\xi))C(\xi) - \\ - \int_{\mathbb{R}^n} d'w(\xi')T(\xi, \xi') d\xi'. \end{cases} \quad (2)$$

This system of equations can be expanded up to any $k \in N$, taking into account spatial moments, and will be a system of $k + 1$ equations. From the point of view of ecology, the equilibrium point of the system is of interest, when the spatial moments cease to change in time. In mathematics, this problem is called finding the stationary point of the system.

There is condition that the solution must not be trivial is also important, because the problem always has a zero solution if the community has died out and all spatial moments are equal to zero.

Equation (2) shows that the dynamics of the first spatial moment depends on the second spatial moment, and the second - on the third. No matter how much we expand the system, this problem will remain. To cope with this problem, it was proposed to use the closure method.

The essence of the method is that the unknown spatial moment of the highest order among all those considered is expressed in terms of the rest, thus, the number of unknowns decreases. Such an expression of the spatial moment is called a closure.

This approach of course leads to an error, but its size depends on the selected closure. If you successfully pick up the closure, then the error will be quite acceptable.

3 Modeling approaches

There are two main approaches to modeling - numerical method and simulations.

1. Simulations - Poisson Point Process
2. Numerical method - Neumann series method

Nowadays, a serious problem in the study of the behavior of populations is their long lifespan compared to humans. Thus, a person simply does not have time to really study population changes properly, but here computer simulations come to the rescue and make this process much faster. Simulations make it possible to obtain a fairly accurate description of the population and its

spatial characteristics, and the values of spatial moments obtained by simulations are considered reference. Simulations do not require serious analytical calculations, but at the same time I give a fairly truthful result, however, compared to the numerical method, they work for a long time and it is not clear when exactly it is worth stopping the simulation.

The numerical method also has its advantages and disadvantages. It works much faster than simulations, but it is very dependent on the input data, if you change them a little, the result becomes completely wrong. Also, this approach requires a lot of complex mathematical calculations in order to write an algorithm and improve it.

4 Graph analysis

Article [1] describes various dependencies in a Spatial Logistic Equation.

Birth. The probability per unit time $B(x, x', p)$ that a plant, located at point x in a pattern $p(x)$, gives rise to a daughter plant at location x' is given by

$$B(x, x', p) = bm^{(b)}(x' - x)$$

Death. The probability per unit time $D(x, p)$ that a plant, located at x in a pattern $p(x)$, dies is given by

$$D(x, p) = d + d' \int \omega^{(d)}(x' - x)[p(x') - \delta_x(x')]dx'$$

Equation for the dynamics of the first spatial moment of the stochastic process:

$$\frac{d}{dt}N = (b - d)N - d' \int \omega^{(d)}(\xi')C(\xi')d\xi'$$

Equation for dynamics of the second moment of the stochastic process:

$$\begin{aligned} \frac{1}{2} \frac{d}{dt}C(\xi) = & +b \int m^{(b)}(\xi'')C(\xi + \xi'')d\xi'' \\ & +bm^{(b)}(\xi)N \\ & -dC(\xi) \\ & -d'C(\xi) \int \omega^{(d)}(\xi')C(\xi')/Nd\xi' \\ & -d'\omega^{(d)}(\xi)C(\xi) \end{aligned}$$

Equilibrium of the first spatial moment for a given second moment:

$$\hat{N} = \frac{b-d}{d' \int \omega^{(d)}(\xi') \hat{c}(\xi') d\xi'}$$

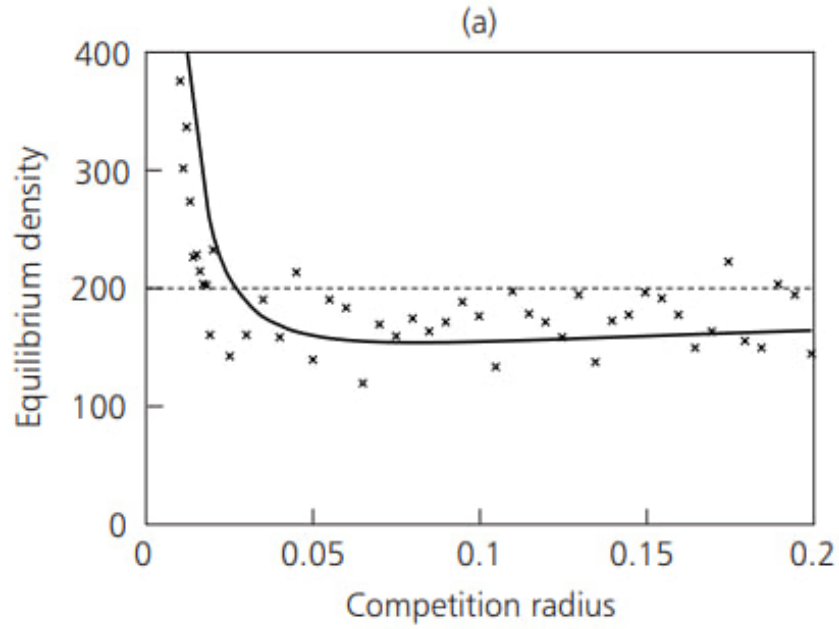


Figure 4.1

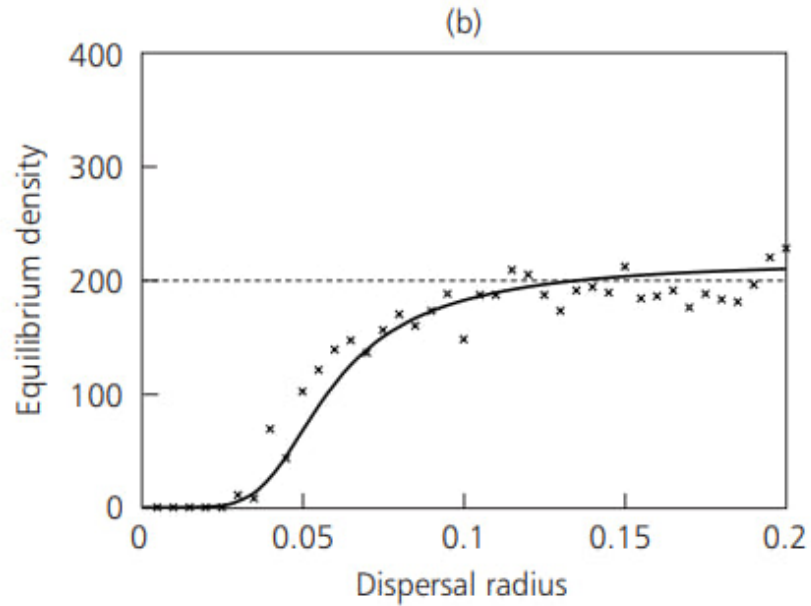


Figure 4.2

These graphs reflect the results of stochastic realizations (crosses), the mean-field results (dashed lines) and the deterministic approximation based on spatial moments (continuous curves). It is

the continuous curves that give a fairly acceptable description of how the equilibrium densities depend on competition radius and dispersal radius.

In further research, it is planned to conduct computer simulations on the basis of which it will also be possible to draw conclusions regarding the dependence of the equilibrium density and external parameters. The following are the data on the basis of which simulations will be carried out.

$b = 0.4$ - birth rate

$d = 0.2$ - death rate

$d' = 0.001$ - strength of competition

When running simulations, parameters such as the standard deviations of the dispersion kernels - $s^{(b)}$ and the standard deviations of the dispersion and competition kernels - $s^{(d)}$, which are normal distributions, will also be taken into account. On the figure 4.1 competition radius $s^{(d)}$ is varied between 0 and 0.2, $s^{(b)} = 0.08$. Figure 4.2 shows the effect of varying $s^{(b)}$ over the same interval for $s^{(d)} = 0.05$.

When the simulations will be ready, it will be possible to accurately assess how accurate the calculations by the numerical method were and how corresponded to reality.

5 Conclusion

In this paper, Ulf Dieckmann's model of biological communities was considered, which describes the behavior of individuals and their influence on the interaction of communities. Various approaches to modeling were studied and an example of the application of the numerical solution method was considered. A graph was considered on which, based on the solution of integro-differential equations, the dependence of the equilibrium density on other parameters was shown. The possibility of creating a simulation that could confirm the validity of the results obtained and assess their reality was explored. All data and mathematical base were collected to run simulations and further research in this area.

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