THEORETICAL FOUNDATIONS FOR CONSTRUCTING MATHEMATICAL MODELS OF DEVELOPMENT AND DISTRIBUTION OF CROP PESTS

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Abstract. Issues of development for mathematical models are considered on development and dissemination of harmful organisms of agricultural crops, built on the basis of the specifics populations, the nature of their reactions to environmental factors, which makes it possible to model pest populations dynamics and effectively manage them. The ways and principles of choosing essential factors in the development of mathematical models, as well as the issues of zoning territories according to their weather and environmental characteristics are given. Mathematical models of biological plant protection have been developed using the "predator-prey" and "parasite-host" procedures.

Keywords: mathematical models, essential factors, zoning of territories, biological protection, "host-parasite" procedure.

INTRODUCTION

Relevance. At the present stage of specialization and intensification of agriculture, due to the need for a general improvement in the strategy and tactics of plant protection, the importance of forecasts for the spread and development of pests of agricultural crops, especially cotton, has sharply increased. The use of mathematical methods based on the specifics of populations, the nature of their reactions to environmental factors, makes it possible to model the dynamics of pest populations and effectively manage them. At present, with very large investments in plant protection, errors in forecasting or in choosing a management method can be very costly.

Based on the above, this article discusses:
• development of a methodology for selecting significant factors in predicting the dynamics of pest populations;
• methods of phytosanitary zoning of territories using pattern recognition algorithms;
• development of mathematical models of biological plant protection using the "predator-prey" and "parasite-host" procedures.

RESULTS

Methodology for the selection of significant factors in predicting the dynamics of pest populations. Effective management of crop production requires the timely collection and processing of extensive agro technical, agro economic, agrometeorological and agro ecological information. The collection, storage and appropriate processing of the above information is necessary for making optimal decisions. The collection of such diverse and extensive information and the solution of prognostic problems require huge labor costs. In this regard, the tasks of developing mechanized data collection systems, improving forecasting methods with a focus on

more accessible types of initial information and using modern computer and microprocessor technology for processing, storing information and creating a database (DB) arise.

Moreover, mathematical modeling of the process of pest population dynamics is a complex multifactorial complex, where, along with essential factors, less significant and insignificant ones act. Very often, the mathematical model and the empirical curve do not coincide due to the fact that the presence of insignificant factors obscures the main aspects of the process under study, and some significant factors that give this process a certain character may not be taken into account. In addition, numerous factors contribute to a sharp increase in the amount of work associated with the collection and processing of information. In view of these circumstances, when modeling the dynamics of agricultural pest populations, it is advisable to divide the entire factorial process into areas of significant, less significant and insignificant factors. The solution of this problem will be much easier if we introduce some quantitative measure to assess the significance of a particular factor.

To solve the stated problem, a class of pattern recognition algorithms is used, which are mainly based on calculating estimates [6, 7]. The main problem of pattern recognition can be solved by various methods, for example, correlation (using the theory of statistical decisions), algorithms "Generalized portrait", "Kora-2", "Kora-3", etc. All these methods and algorithms were applied to solve the series applied tasks and gave good results. Their common distinguishing feature is that when implementing the recognition process, the concepts of importance (in formativeness) of the features defining the object are not explicitly used. Therefore, the concept of the measure of importance (information weight) of features is also not introduced and it is not calculated [7]. However, in recent years, methods in which the main stage is the calculation and consideration of information weights of features are becoming more widespread. The informational weights of the features are calculated by the frequency of occurrence, the analysis of dead-end tests, and algorithms for calculating estimates.

Let us consider some general principles on which the algorithms for calculating estimates are built.

Let the table Tnm be given. In it, each line S_j (j=1,2,…,m) is an object that can be represented as Sj = (Xj1 , Xj2 , …, Xjn),

where Xji (i=1,2,…,n) are elements of a set of numerical or qualitative values that identify an object. Usually these elements are called signs, and their values are obtained, as a rule, as a result of experiments. Let now a set of sets qi be given, which we will consider as some alphabet of features. As an alphabet can:

a) a set of two elements {0 , 1}, where "1" means the presence of some property, 0 means its absence;

b) a finite set of integers { 1,2,…,P }. The meaningful value of each such attribute reflects the degree of expression of the corresponding property.

Object Sj is called accessible if $X_{ji} \cap q_i$. Note that the concept of a valid object is equivalent to the concept of a valid string.

The set of m admissible objects, each of which is characterized by a set of features, can be reduced to a table Tnm, which we will call an admissible table. Now suppose that there is a partition of all admissible rows into classes $k_1, k_2, ...,k_l$, and $K_u \cap K_j \neq 0$ при $u \neq j$. This partition induces a partition of the rows of the table into l non-overlapping classes.

$$K_1, K_2, …, K_l$$

We assume that the last partition is given.

Let us denote the number of elements of class K_e as $m_u - m_{u-1}$ and represent the division of strings by class as

$$K_1: S_1, S_2, \ldots, S_{m1}$$
$$K_2: S_{m1+1}, S_{m1+2}, \ldots, S_{m2}$$
$$\ldots\ldots\ldots\ldots\ldots$$
$$K_e: S_{me-1+1}, S_{me-1+2}, \ldots, S_{me-1}$$

The table T_{nm}, whose rows are divided into L classes, will be denoted by T_{nml}.

The introduced concepts and definitions allow us to proceed to the consideration of the principle caused by the principle of calculating some quantitative estimates obtained by comparing admissible objects or parts and representing the basis of algorithms for calculating estimates.
Let two admissible objects be given:

$$S_1=(x_{11}, x_{12}, \ldots, x_{1n})$$
$$S_1=(x_{21}, x_{22}, \ldots, x_{2n})$$

where x_{jn} $(j=1,2)$ takes the values of one of the above alphabets.

Let further it is required to establish a degree of "proximity". We will understand this term on an intuitive level, comparing it with the concepts of similarity, sameness, etc. The proximity of S1 and S2 can be established, for example, based on the analysis of the identifying sets or their parts. This approach is associated with obtaining some quantitative estimate using certain transformations of the sets. Based on this assessment, proximity is established by a certain criterion.

Thus, if the identifying sets of objects are denoted by x_1 and x_2, and the estimate by B , then for the latter one can write

$$B=B(x_1, x_2)$$

The value of B can be intermediate, and, in turn, make it possible to obtain some final estimate characterizing the proximity of the object. This assessment in quantitative terms characterizes the total effect of comparing objects.

Therefore, if the total effect is denoted by G, then we can write $G=G(B)=G(B(x_1, x_2))$

In the theory of recognition algorithms based on the calculation of estimates, the value Γ is usually called the number of votes given by objects, for example, for the object S_2. It is clear that the number of votes cast by objects S_2 for $S_1(G_{1,2})$ is equal to the number of votes $G_{1,2}$.

Procedures for obtaining the value of G for comparing objects S_1 and S_2 are called voting procedures. Voting procedures can be carried out not only to establish the proximity of two objects, but also a group of objects summarized in a specific table. So, if some table T_{nm} consists of objects, each of which is characterized by a set of n features, then the following voting matrix can be obtained by the voting procedure:

$$G_{11}, G_{12}, \ldots, G_{1m}$$
$$G_{22}, \ldots, G_{2m} \qquad\qquad (1)$$
$$\ldots\ldots\ldots\ldots\ldots$$
$$G_{nm}$$

Matrix (1) actually makes it possible to obtain all the necessary values of the votes given by individual objects both for themselves and for other objects of this table. In practical problems, the votes cast for oneself are usually excluded from the matrix (1).

Note that the effectiveness of voting procedures depends on the method of counting votes. The procedure, from the point of view of the speed of implementation, is the more effective, the simpler the method of counting votes.

In the theory of evaluation algorithms, such an apparatus has been obtained, with the help of which the number of votes is calculated relatively simply. The works [22, 23] describe the derivation and proofs of the following expressions for counting votes (the value of G), as well as various modifications of the counting formulas, which differ from each other in the specifics of specifying certain stages of the algorithms for calculating estimates. Let us write out expressions for counting votes, which will be used later in this paper.

If the table T_{nml}, is given, divided into classes $K_1, K_2, \dots , K_l$ then the number of votes cast by row S for class K_u is equal to

$$\Gamma_u(S) = \sum_{q=m}^{m} C_{n-r}^h (S, S_h) \tag{2}$$

where $S=(x_1, x_2, \dots ,x_n)$, $S_q=(x_{q1}, x_{q2}, \dots ,x_{qn})$ are compared pairs of strings; h is the length of the voting set, i.e. the number of columns by which the rows S u S_q ; - compared; $r(S, S_q)$ - Hamming distance between strings S and S_q (if the table is given by binary characters), i.e. the number of columns where rows do not match.

When the table is filled with elements that take a value from an arbitrary alphabet, then instead of a value, you should use $r(S, S_q)$- - the distance between the rows S and S_q, equal to the number of fulfilled inequalities where $abs(x_l-x_{qi}) \geq V_i$ - the proximity threshold of the i -th feature. If $h \geq n-r(S, S_q)$, then expression (2) vanishes.

According to [6, 7, 17], the value

$$P_1 = \sum_{u=1}^{e} \frac{1}{m_u - m_{u-1}} \sum_{q=m_{u-1}+1}^{m_u} \left[\Gamma_u(S_q^i\right]$$

is called the information weight of the i- feature.

Thus, the above method for determining the information weights of signs was used to select the essential factors necessary in the development of mathematical models for predicting the development of harmful objects of agricultural crops [17].

Tasks and methods of phytosanitary zoning of territories by agricultural pests. The task of optimized zoning of territories described below, in our opinion, can be used to create an ACS for plant protection (APCS). Establishment of the APMS is unthinkable without an objective preliminary zoning of the territories in relation to the objects of management.

The zoning of agricultural territories according to weather and environmental characteristics are essential links in the scientific knowledge of the continuous environment. Works in this direction are of great practical importance, since zoning is an essential element in many studies, in particular, when predicting the size of the dynamics of the population of agricultural pests, the size of infested areas by pests, the date of appearance of pests, planning pest control measures, and analyzing the causes of outbreaks. breeding pests, etc.

Against the background of the modern development of science and changes in the demands of practice, the traditional group of zoning methods does not always provide satisfactory results.

Zoning in plant protection is a systemic process consisting of a number of interrelated elements, such as the choice of a presentation model, the scale of research, the type of primary objects of observation, methods for locating and describing these objects, as well as subsequent

processing of information and interpretation of zoning results. The heterogeneity of these elements creates different possibilities for formalization. The formalization of even individual stages of the zoning process entails a restructuring of the entire system of this process as a whole. Due to the use of formalization methods, an important place is occupied by the linking of all elements of zoning, the development of general rules for making decisions at each stage, the development of general rules for interpreting the results.

At the stage of obtaining the actual source material, the task of primary selection of information is of particular importance. Depending on the specific tasks, it is possible to zoning at the level of farm territories, territories of an administrative district, region, or at the level of observation sites. The objects of zoning include sets of indicators representing the territory being zoned, and they can be conditionally divided into groups of indicators. The first group includes:
• annual and long-term average indicators of the number of harmful objects, the intensity of development of diseases, the percentage of crops populated by pests, the size of infected areas, the percentage of spread of the disease;
• annual and average long-term indicators of reproduction, survival and the timing of the passage of the main phenological phases. These indicators should be collected from different areas of the zoned territory over a number of years according to a single methodology.

The second group of indicators includes parameters that characterize the conditions for the development of harmful organisms and their habitat. These include:
• hydrometeorological factors - the sum of effective temperatures, average ten-day, average monthly, maximum, minimum air temperatures. Hydrothermal coefficient (HTC), the amount of precipitation by decades and months. The timing of the onset of phenological phases and their duration.
• agrotechnical factors - the timing of sowing, harvesting. The timing of the main agro technical and protective measures.

Zoning according to the characteristics of reproduction and the timing of the passage of the main phenological phases of harmful organisms makes it possible to identify zones with different intensity of reproduction of pests.

To solve the problems of zoning in plant protection, the same class of pattern recognition algorithms [6,7, 17], which was considered above, is used.

In this case, the classification of objects without a standard is used. The problem of spontaneous partitioning of a set of objects is solved using algorithms for calculating estimates using some quantitative measures that characterize the information content of both features and the objects themselves. The in formativeness of the object is obtained from expression (3). Computation for all given objects, the information weights are then ordered in descending order.

The division of objects into classes in this case is based on the assumption that when ordering objects by the value of the latter, they will be grouped by rank. The partition obtained in this way is an intermediate stage of spontaneous classification. The final splitting is obtained only after the voting confirms that the object belongs to its class.

The proposed zoning method is based on the rational processing of multidimensional arrays of biological, ecological, agrometeorological and agro technical information. Such information is contained in the archival data of the meteorological station network, PPS(plant protection station), strong points and observation points for pests and diseases. The use of recognition algorithms in rational data processing makes it possible to reduce the amount of information required for

decision-making by combining points - information meters into groups, and observations - into time classes, according to the principle of similarity of the information contained in them. At the same time, the quality of the initial information is improved by eliminating gross errors while maintaining its information content.

As an example, Table 1 shows the results of zoning the territory of the Andijan region in relation to the cotton bollworm on cotton in terms of abundance, timing of the main phenological phases, hydrometeorological (the sum of effective temperatures, the HTC, the sum of precipitation) indicators.

Thus, as can be seen from Table. 1, districts of Andijan region can be divided into classes:
• Andijan, Asaka, Buz, Shakhrikhan districts - 1st grade;
• Balykchinsky, Bulakbashinsky, Zhalakuduksky, Izboskansky districts - 2nd class;
• Kurgantepa, Markhamat, Ulugnar districts - 3rd grade;
• Oltinkul, Pakhtaabad, Khuzhaabad districts - 4th grade.

Table 1.

Information weights of districts of Andijan region in relation to cotton bollworm on cotton

№№	Districts	District Information Weights	The class of District
1.	Andijan	0.961	1
2.	Asaka	0.915	1
3.	Balikchi	0.890	2
4.	Bulakbashi	0.813	2
5.	Buz	0.971	1
6.	Jalakuduk	0.872	2
7.	Izboskan	0.810	2
8.	Kurgantepa	0.702	3
9.	Marhamat	0.785	3
10.	Oltinkul	0.621	4
11.	Pakhtaabad	0.544	4
12.	Ulughnar	0.796	3
13.	Shakhrikhan	0,909	1
14.	Khujaabad	0.508	4

Formation of predictive models of the dynamics of populations of agricultural pests. The formation of crop yields and their quality is greatly influenced not only by cultivation methods, but also by measures to combat diseases and pests of crops. In the conditions of modern trends, farming technologies and concentration of production, programming, and other phytosanitary problems become even more complicated. This requires strengthening research on the development of automated and remote methods for collecting, storing and evaluating data on the phytosanitary state of crops in order to increase the reliability and efficiency of pest development forecasts.

In practice, it is very important to establish the possible expansion or narrowing of the range of pests, to foresee the degree of their development, the timing of individual infections and manifestations. The possibility of foresight is the essence of plant pest forecasting.

The task of predicting common pests is as follows:

• determination of general tendencies towards the growth of pests or, conversely, towards attenuation;
• prediction of outbreaks of a particular pest, indicating for each region (zone) the intensity of damage and the amount of possible damage (crop shortage);
• setting in advance the timing of individual infections and their manifestations in a given season in relation to the conditions of each region;
• timely informing the agricultural authorities and farms about the possible timing of the appearance of pests, the intensity of damage to crops and the extent of damage, as well as recommendations for the necessary protection measures.

It follows that, based on the forecast, it is possible:
• rational organization and timely implementation of preventive measures to protect plants from mass damage by pests, i.e. planning of means of protection and their distribution to areas of cultivation of agricultural crops according to the expected outbreaks and probable crop losses, as well as the timing of protective control measures according to the predicted timing of plant infection;
• recommendations to planning organizations for the production of the necessary protective equipment and the implementation of appropriate measures for the procurement of products;
• recommendations to the agricultural bodies of appropriate organizational, economic, preventive, agrotechnical measures in cases of expected changes in the dynamics of pests.

Mathematical methods for predicting the dynamics of agricultural pest populations consist in using the available data on the characteristics of the predicted object, processing these data by mathematical methods, obtaining a dependence linking these characteristics with time and calculating, using the found dependence of the characteristics of the object under study at a given point in time.

The pest population can be considered as a certain process [17], represented by the diagram shown in the figure. The set of parameters $(V_1, V_2, ..., V_n)$ and $(Z_1, Z_2, ..., Z_m)$ forms the input of the research object and the set $(Y_1, Y_2, ..., Y_k)$ is the output. Obviously, the inputs and outputs of an object can be considered as some multidimensional vectors in the parameter space. So, for the vector V, the space has n dimensions, for the vector Z - m dimensions, and for the vector Y - k dimensions.
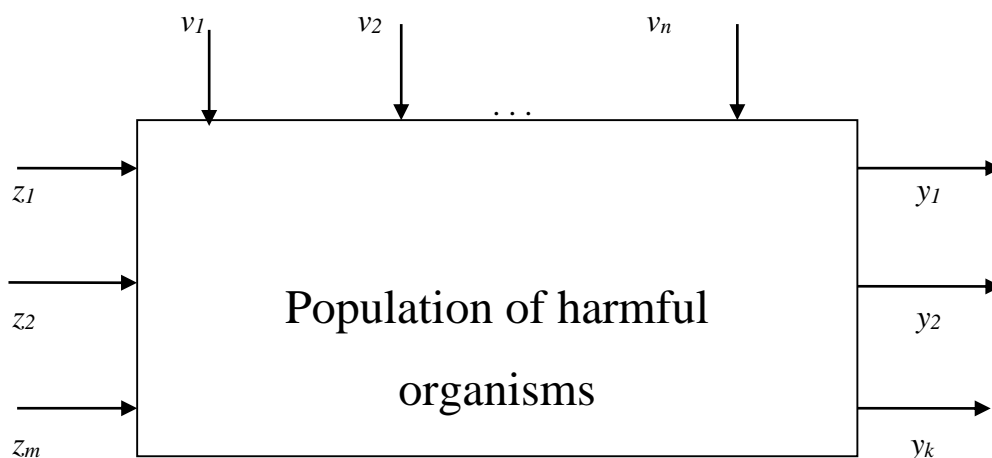
Interactions of the object of study and influencing his factors

The output of an object is connected to its inputs in a certain way, for example, using the operator F,

$$Y = F\ (V,\ Z) \tag{4}$$

which characterizes the structure of this object.

Finding a quantitative relationship between parameters (4), i.e. the full disclosure of the operator F is the essence of the problem of the object under consideration. As a result of modeling, a mathematical model of this object is obtained.

In expression (4), the set V forms (in terms of ecology) a set of biotic factors, Z is a set of abiotic factors, and Y is a set of factors characterizing the pest population. They can be such indicators as the number (density) of pests, the size of the areas of agricultural crops infected with pests, the dates of appearance of pests, etc.

Let us assume that in expression (4) the vectors Y, V, Z are available for observation and their components can be measured. Then, if the structure of the operator F is known, then the problem of mathematical modeling of the dynamics of the population of agricultural pests, which consists in establishing the influence of factors of the biotic and abiotic environment on the dynamics of the population of agricultural pests, is reduced to finding an unknown vector of parameters $A = (a_1,\ a_2,\ ...,\ a_s)$, whose components are quantities that depend on factors V and Z.

The solution of this problem allows us to move on to the range of problems associated with solving the problems of predicting the dynamics of the population of agricultural pests and developing optimal plans for combating them.

Let us assume that for some ecological process the analytical form of expression (4) is found, i.e. the values of the parameters of the vector A are determined. Let us assume that the resulting model, described by expression (4), is adequate to the process under study. Then the determination of the value of Y_t at the output of the model of some future moment $t+1$ is the essence of the forecasting problem for the vector Y.

Various methods are used to find the analytical form of expression (4). Since the factors of the biotic and abiotic environment can be considered as subsets of the set of input factors, i.e.

$$X = V \cap Z$$

then expression (4) will take the form:

$$Y = F\ (\ X\ ) \tag{5}$$

Expression (5) can be written as

$$y_m = f_m(x_{m1},\ x_{m2},\ ...,\ x_{nm}) \tag{6}$$

where the index m indicates the type of pest.

Thus, expression (6) in general terms shows the relationship between the dynamics of the population of agricultural pests and the factors influencing it.

As mentioned above, the predicted parameters of the pest population (ym) can be such characteristics as the number (density), the size of the infected areas of agricultural crops, the dates of the appearance of pests, etc., and their meters (factors of the biotic and abiotic environment) are established by a specialist, well knowing the object of forecasting.

To identify the analytical form of expression (6), various identification methods are used. We will focus on regression analysis and the method of group accounting of arguments (MGAA).

The least squares method can be applied to objects for which, based on a priori information (observation during experiments, meteorological data, data on plant growing methods), the structure of equations describing their behavior and nominal values of parameters is known.

In the simplest case of identification, the least squares method is based on the study of deterministic input and output signals (without taking into account random measurable perturbations). Regression analysis algorithms are described in detail in [17].

The purpose of the MGAA is to obtain the result of a complete enumeration according to the selection criterion. MGAA belongs to the group of methods based on the mathematical processing of historical data and is designed to solve the so-called interpolation problems of technical cybernetics. Examples of such problems are the problems of pattern recognition, forecasting random processes, identifying the structure and parameters of complex objects based on the results of observing their work, optimal control with forecast optimization. These enumerated tasks can in principle be solved by a complete enumeration of all variants according to a criterion called the selection criterion. The choice of such a criterion is heuristic; belongs to the programmer and is determined by the goal of solving the problem.

The complete enumeration occurs in the process of gradual complication of the mathematical description or model. In this case, the complication proceeds discretely, i.e. in each series, new terms are added, or the degree of the polynomial increases, or both occur simultaneously. Gradually increasing the complexity of the mathematical model and setting a number of discrete values of its coefficients with a certain small step, it is possible to organize a complete enumeration of all possible variants of the model according to the specified selection criterion and thus find the best model (from those reviewed). The presence of a minimum selection criterion makes it possible to find a single model of optimal complexity. The search method is alternate testing of models (enumeration).

There are various MGAA algorithms [8, 9], which differ from each other in the form of the approximating function. One of the algorithms is polynomial MGAA algorithms. These algorithms are used to implement multi-row selection when solving problems of finding the optimal model, given in the form of a power polynomial.

According to the polynomial MGAA algorithms, the complete description of the object (6) is replaced by a certain set of so-called partial descriptions, which are functions of two arguments. In the first row of the selection, particular descriptions look like:

$$Y_{1k} = f_k\left(X_{kj}, X_{kl}\right) ,$$

in the second and subsequent rows:

$$Y_{ik} = f_k\left(Y_{i-1,k}, Y_{i-1,k+1}\right)$$

As approximating functions f_k, polynomials of no higher than the second degree with respect to two arguments are used, on the first selection row:

$$Y_{1k} = a_{1k}^{(0)} + a_{1k}^{(1)}X_{jk} + a_{1k}^{(2)}X_{lk} + a_{1k}^{(3)}X_{jk}X_{lk} + a_{1k}^{(4)}X_{jk}^2 + a_{1k}X_{lk}^2$$

on the second and subsequent rows:

$$Y_{ik} = a_{ik}^{(0)} + a_{ik}^{(1)}Y_{i-1,k} + a_{ik}^{(2)}Y_{i-1,l} + a_{ik}^{(3)}Y_{i-1,k}Y_{i-1,l} + a_{ik}^{(4)}Y_{i-1,k}^2 + a_{ik}^{(5)}Y_{i-1,l}^2$$

Here i is the number of selection rows, $i = 2,3, ..., N$;

k - number of particular descriptions, $k = 1, 2, ..., C_n^2$;

$$j = 1, 2, ..., N\text{-}1; \quad l = j+1, j+2, ..., N$$

where N is the number of arguments.

The partial description coefficients are determined from the training sequence (TS) data, for which the least squares method is used. It should be noted that in order to obtain stable solutions, the available data set is divided into training and testing sequences (TS).

The degree of regularity is estimated by the value of the root-mean-square error on a separate test sequence (the minimum of this error is searched for).

To obtain the most regular mathematical description, either the correlation coefficient or the value of the mean square measurement error on a separate test sequence can be used as a selection criterion.

The regularity criterion has the advantage that it changes very smoothly with increasing model complexity, which makes it possible to abandon the complete enumeration of models and apply multi-row MGAA algorithms, in which only a part of the models is compared by the criterion.

The disadvantage of the regularity criterion is its extrapolating properties: in the interpolation section (where the points of the training sequence are given), it gives a good approximation of the function. But in the extrapolation section, the regression curve goes up or down relatively quickly, so the regularity criterion is recommended for a short forecast lead time or identification task.

From series to series of selection, with the help of threshold selections, the most regular variables, called intermediate variables, are skipped from all particular descriptions. With an increase in the complexity of intermediate variables, the complexity of the model increases and on some series it becomes equal to the complexity of the object, while the value of the self-selection criterion reaches its extreme value. One of the intermediate variables of the last row is chosen as the final solution. A complete description of the object is obtained as a set of intermediate variables.

Application of "host-parasite", "predator-prey" procedures in plant protection. Biological control of harmful insects has now taken a permanent leading position in the concept of integrated pest control. In some cases, one form or another of biological suppression of their populations is sufficient to successfully control the number of insect pests; in a number of others, suppression is often supplemented by some other method, and finally, it plays only an auxiliary role. However, what is important is that the effective use of biological agents has now become a method that should be considered and widely applied in all possible cases. In this regard, it is necessary to study interspecies ecological relationships, which play an important role in the life systems of populations. Interspecific relations are usually classified according to the sign of the impact of one population on another: positive (+), negative (-) or neutral (0).

The vast majority of models of antisymmetric interspecies relations are oriented towards the description of the "predator-prey" or "parasite-host" system [1, 5, 14, 18, 25, 27, 28]. In such models, three main links are distinguished: 1) reproduction of the victim (host); 2) eating the prey by a predator (infection of the host with a parasite) and 3) reproduction of a predator (parasite).

The most important models of the second link, in turn, are divided into 4 options:
1. Model of predation (parasitism) with continuous time;
2. Model of predation with discrete time with a random nature of the search activity of a predator;
3. Model of parasitism with discrete time with a random nature of the search activity of the parasite;
4. Discrete-time parasitism model for random search, i.e. with unequal susceptibility to attack by individual host individuals.

Models of the 1st option are described by the differential equation

$$\frac{dx}{dt} = x(r - f(x,y))$$

where x and y are the population densities of prey and predator (parasite), respectively; r is the birth rate of victims $f(x,y)$- the rate of eating (infection) of prey by predators (parasites) per one individual of the prey. Examples of functions $f(x,y)$ are: $f=y/xt_h$ - victim processing during random search; $f=ay$ - in case of a random search for a victim[20,27]; $f=ay/(1+at_hx)$ [3, 14] - for random search and processing of the victim.

Models of other options are described by the difference equation

$$x_{t+1}=x_tkg(x_t,y_t)$$

where x_t and y_t are the density of prey and predator (parasite) populations in generation t; k is the multiplication factor of the prey; g - survival rate of victims from predators (parasites). Examples of such functions $g(x_t, y_t)$ - for a predator conducting a random search for a prey: $g=1-y_t/x_t$ - when processing a prey [4]; $g=exp(-ay_tT)$ - when searching and processing a victim [24] (option 2); for a parasite conducting a random search - when processing the victim [1]; when searching for a victim $g=exp(-ay_tT$ [1, 24, 27]; - when searching for and processing a victim [21, 23, 26] (option 3); for a parasite conducting a non-random search $g=g^k$ - when processing the victim [25]; - when searching for a victim [25], $g=(1+ay_tT/K)$ - when searching and processing a victim [22] (option 4).

Here x_t и y_t are the population densities of prey and predator (parasite), respectively; T is the lifespan of a predator (parasite); T_a is the duration of the treatment of the victim; a - search efficiency indicator; K is the parameter of the negative binomial distribution.

It should be noted that the models of predation (option 2) and parasitism (options 3,4) differ as follows. The predator eats the prey once, and the parasite is able to repeatedly infect the same individual of the host. In addition, the parasite is less effective at killing hosts than the predator, as it wastes time re-infecting. Those models that do not take into account the time spent by the parasite to infect the host are equally suitable for describing both predation and parasitism [1, 25, 27].

The difference between the models of the 3rd and 4th versions is that in the models of the 3rd version, the distribution of parasite eggs among the host individuals obeys the Poisson distribution, and in the models of the 4th version - negative binomial. The survival rate of hosts from parasites is equal to the first term of these distributions, that is, the proportion of hosts on which zero parasite eggs are laid. The first member of the Poisson distribution is $exp(-\mu)$, and the negative binomial distribution is $(1+\mu_k)^k$, where μ is the average number of parasite eggs laid per host, $K=\mu^2/(\alpha^2-\mu)$ is the variance of the number of parasite eggs per host. one owner.

The Poisson distribution follows from the assumption of a random host search process, and the negative binomial distribution can be easily derived from the hypothesis that the degree of host risk of being infected obeys the gamma distribution [16]. The difference in the degree of risk often has a different nature: the host individuals are not the same in behavior, and therefore, to varying degrees, are available for infection. At the same time, the non-synchronous development of hosts is sometimes fraught with the fact that rapidly developing individuals will be less susceptible to attack by parasites than those that are lagging behind in development. Finally, in areas with high host density, their risk of being infected is higher than in areas with low density due to the concentration of parasites in host aggregations [17].

As practice has shown, in many cases it is preferable to modify the interpretation of the parameters than to build a different, more complex model. The pursuit of an illusory "complete adequacy" is hopeless, since the adequacy itself is assessed only at the current level of knowledge,

and further research will always show the inadequacy of an adequate model. The way out is to use a systematic approach aimed at finding a reasonable compromise between adequacy and simplicity in describing complex systems [17]. Therefore, we agree with [26] that the parameters of a theoretical model should have a strictly fixed meaning and, in particular, it is wrong to select their values using regression methods.

It should be added that regression methods for estimating the parameters of models of the "predator-prey" or "parasite-host" system have been repeatedly discussed in the literature [1, 26]. The main problem is to transform the original equation to obtain a linear regression equation.

There are many ways to complicate the models described above. According to the first of them, the indicator of the search activity of a predator or parasite is supposed to be dependent on the density of prey, and such a dependence is usually considered to be increasing and is expressed by the formula given in [21, 27]. An increase in the search activity of a predator (parasite) is explained by the stimulating effect of either the frequency of encounters with prey or kairomones secreted by prey [27].

The second way of modifying models involves taking into account the mutual interference of predators or parasites, which manifests itself in a decrease in the indicator of search activity with an increase in the density of predators or parasites [1, 23, 37].

The third way of modifying models, proposed in [22], is applicable only to models of the 4th variant. Based on data on the infection of the winter moth with the parasite *Cyzenis albicans Fll.* it is shown that the parameter of the negative binomial distribution increases with the average host density.

In connection with the mathematical models of the "predator-prey" and "parasite-host" systems, the following question is constantly discussed: are natural enemies capable of suppressing the number of prey and maintaining it at a lower level? This ability is extremely important for the biological control of harmful insects [1, 25]. As it turned out, in the simplest models of Thompson, Nicholson, Bailey, Holling, Lotka, Volterra, the equilibrium state of populations is marked by instability, which in the presence of a fluctuating medium is equivalent to a real instability [1, 25]. Stability was achieved only when additional stabilizing mechanisms were taken into account, which are: self-regulation of prey or predators, the presence of shelters for prey, mutual interference of parasites in the search for hosts, the dependence of the sex ratio of the parasite on the density of the host, and the attraction of parasites to host aggregations [25, 27, 28]. In addition, resistance also arises when the age structure of parasite and host populations is taken into account [28].

Thus, in the models, natural enemies destabilize the host population rather than stabilize it. If earlier this fact raised doubts about the ability of natural enemies to restrain the reproduction of pests, now it has become obvious that in order to assess this ability, it is not enough to consider a predator or parasite as the only cause of death of individuals in a population. Other causes of density-dependent mortality must also be taken into account, such as lack of food. The role of natural enemies in population dynamics is fully manifested only in interaction with other factors.

It should be noted, however, that simulation models are used not only for forecasting, but also for management purposes. The effectiveness of one or another method of artificial impact on the population can be assessed by direct simulation [17], although simulation does not add confidence that the method used to influence the population is optimal. To optimize control, an optimality criterion is required, which is usually chosen from economic considerations. As a rule,

profit is optimized, equal to the difference between the cost of agricultural products received and the cost of pest control [21, 24]. At the same time, control variables are selected, which can be changed to obtain the greatest profit. They, in particular, are the timing and frequency of chemical control [22], mortality from insecticides, and the number of released entomophages [17].

Currently, in addition to the models analyzed above, there are many different theoretical models for "predator-prey" or "parasite-host" systems, the use of which in solving practical problems is very difficult, and sometimes even impossible.

The interests of the development of agricultural production require constant systematic pest control in agriculture. This struggle was and is being carried out by mechanical, chemical and biological methods. The most natural, and therefore reasonable, biological way of fighting. Its application most rationally takes into account the need to preserve entomophages, acariphages and pollinating insects. In addition, this method is of particular importance also because it often solves the problem of not completely destroying a species, but maintaining it at a certain constant level in order to maintain balance in the biocenosis.

Many researchers seek to explain the fluctuations in the population size observed in nature using models [4, 16, 17]. There is a large amount of experimental data on the most diverse biological populations, the nature of fluctuations in the numbers of which researchers seek to describe using mathematical models [2, 3]. As a result, to date, a very heterogeneous set of models has developed that are of purely academic interest, and those that are used to describe the dynamics of various populations.

With the expansion of human intervention in the natural environment and with the development of planning for the exploitation of natural resources and related calculations, mathematical models of natural biogeocenoses are becoming increasingly important. One of the first such models was proposed by V. Volterra (*Volterra, d'Ancona, 1935* [4]) and, although many other models have been proposed since that time, the main ideas and methods used by Volterra continue to be used today.

It should be noted that the Volterra models are rarely used in practice, which is explained by a certain narrowness of the assumptions underlying them. Some of the models built later have the same drawback. Therefore, it seems interesting and useful to attempt to combine a wide range of different hypotheses in one model (or system of models) in order to make the model more flexible and diverse in functioning, which can increase the practical value of such models. One of such attempts is described below using the principle of limiting factors, first formulated by J. Liebig [26, 27].

We will consider a simple biocenosis consisting of two populations of different biological species, one of which ("prey") serves as food for the other ("predator"). Note that more complex models are just as easy to generalize and expand as a simple one, and the choice of a simple model is dictated by methodological considerations.

Volterra studied the kinetics of the population size of prey x and predator y under the following assumptions: (1) reproduction of the prey is proportional to its size (ax); (2) the mortality of the prey is due in part to natural (age-related) mortality, proportional to the number of prey (*bx*) and in part to the predation by the predator; the latter is proportional to the "number of meetings" predator - prey, i.e. the product of their numbers (or numbers per unit measure of range) - λxy); (3) reproduction of a predator is proportional to the amount of food consumed by it (number of prey eaten - *mxy*); (4) predator mortality is proportional to its abundance (βy).

As a result, the model reflecting the kinetics of numbers x and y is written as a system of ordinary differential equations:

$$\frac{dx}{dt} = \alpha x - \lambda xy$$

$$\frac{dy}{dt} = \lambda xy - \beta y$$

The system is written for real variables($x,\ y\ R^1{}_+$), although the size of any population is always expressed as an integer; x и y in (1) should be considered either as an average value over an ensemble of randomly taken cenoses, or as population biomass, or, which seems more natural to us, as fictitious values, which, by virtue of (1), form the trajectory of the system($x(t),\ y\ (t)$). Passing through discrete points (or close enough to them), corresponding to the real (integer) values of the number of prey and predators. Such continuous models of discrete objects have become a tradition not only in studies of biogeocenoses.

Therefore, for the practical application of models for the system "parasite-host" against pest control is to reduce the number of pests present and thus the damage they cause.

Assume that the above system of differential equation, we managed to somehow describe the growth rates $\mu_1=P_1-C_1$ и $\mu_2=P_2-C_2$ (where P_1 и P_2 are the birth rates, C_1 и C_2 are the death rates of the "parasite" and "host", respectively), and frequency of occurrence. Then it will be possible to determine the optimal value of x at a certain time t in order to reduce the value of y.

Then the equation can be written as:

$$N_1(t+1) = N_1(t) + \mu_1 N_1(t) - \lambda N_1(T)N_2(t)$$
$$N_2(t+1) = N_2(t) + \mu_2 N_2(t) - \lambda N_1(T)N_2(t) \tag{7}$$

Restrictions can be imposed on the desired parameters of this system:

$$N_1(t) \leq N_2(t)_{max}$$
$$0 \leq N_1(t) \leq N_1(t)_{min}$$
$$N_1(t)\big|_{t=t0} = N_{1np} \tag{8}$$

Where $N_1\ u\ N_{1np}$ - are the actual and predicted values of the pest, respectively;;

$N_1(t)_{min}$ - the minimum allowable value of the pest;

$N_2(t)_{max}$ – max is the maximum productivity of "parasites" produced by biological factories.

Quality functional in the form

$$\Phi = \sum_{k=1}^{K} CkN_2(t) \blacktriangleright min \tag{9}$$

где C_k – is the cost of releasing "parasites" and "host", respectively;

Thus, the problem is reduced to finding the optimal values of N2 from system (7), which satisfies the constraints (8) and ensures the minimum of the quality functional (9).

Functional (9) can be minimized using various random search algorithms. As you know, the existing search methods are divided into two classes: regular (deterministic) and non-deterministic, random methods. Among the regular search methods, the methods described in [13] are widely used.

In general, the idea of the random search method (RSM) was first clearly formulated by W. R. Ashby [13] and implemented in his homeostat. Subsequently, random search was reflected in a number of works, both by Soviet and foreign scientists [8, 9, 17]. Rastrigin L.A. made a particularly great contribution to the further development of SMEs. and his collaborators [15], in works where a rather rigorous theory of the method was actually developed and a significant number of efficient algorithms were given [16].

The essence of the idea of SMEs is as follows. In the space of optimizing parameters, the system takes a random step from some initial state. If this step does not lead to success (i.e., to a decrease in the quality functional), then a return to the original state occurs. When the functional decreases, the state that the system came to with a random step is taken as the initial one and a new random step is performed from it, etc. Each state of the system during a random walk generates a certain value, and naturally, the set of such states at the output of the system forms a certain set of quality functionals m$\{Q^*\}$. It is obvious that the task of optimization in this case is to select a subset $\{Q^*\}=\{Q\}$ corresponding to the fulfillment of some requirements imposed on the optimizing system. For example, this subset can include all those values of the quality functional that turned out to be less than a given value or equal to zero.

In this paper, the optimization of the functional is carried out by random search algorithms, the choice of which is due to two circumstances. First, one of the serious drawbacks of the regular search method is its slow convergence in the presence of restrictions. Secondly, in the process of further improvement of the model, additional parameters can be introduced that are not considered in the work due to the lack of the possibility of determining these parameters. In this case, the random search algorithm is able to give better convergence than the regular search method. Moreover, the inclusion of additional parameters will not require fundamental changes in the existing model optimization scheme. When solving the problem posed by us, the algorithm described in [12] and the program compiled on its basis [10] are used.

One of the promising methods of pest control is the biological method of plant protection. Among his means in protecting the cotton crop, a special place is occupied by the use of a trichogram for the destruction of the cotton bollworm, a cotton pest. Usually the required number of individuals of the "parasite" - trichogramma is grown in a laboratory - industrial way in biological factories, the rhythmic and effective work of which provides for:

a) population forecast of the "host" - cotton bollworm;

b) predicting the timing of the peak of the host population;

c) forecast of the population of the "parasite" population prepared by the biofactory, depending on the available forecast of the population of the "host".

Assume that aspects a) and b) are allowed, i.e. the period of appearance of the "host" population and its abundance N1 at time t are known (here t is the time during which the "parasite-host" interaction occurs in the model). It is required to predict the size of the "parasite" population. Then. that the forecast for N1 is feasible by the method of group consideration of arguments [17]. Aspect c) is also considered here, taking into account the biological characteristics of the interacting pair "trichogramma - cotton bollworm" and, by means of a qualitative analysis, the choice of a "reference" system and the mode of interaction of this pair is substantiated. A simple form of the reference mode makes it possible to construct an optimization relation that connects the quantities known from steps a) and b) and those predicted from step c) [17].

As an example, the release rates of the "parasite" (trichogramma) are determined for given predictive values of the "host" (cotton bollworm), which is shown in Table 2.

Table 2.

Trichogramma release rates at predicted values of the cotton bollworm

№ number	Approximately value of the host, per 100 plants	The optimal value of the parasite produced by biofactories

			piece	gramm
1.	7,0	158221.0		1,58
2.	7,5	158010.0		1,58
3.	8,0	152930.0		1,53
4.	8,5	152448.0		1,52
5.	9,0	150025.0		1,50
6.	9,5	147842.0		1,48
7.	10,0	146200.0		1,46
8.	10,5	145830.0		1,46
9.	11,0	143990.0		1,44
10.	11,5	142650.0		1,42
11.	12,0	141100.0		1,41

CONCLUSIONS

The pest control system practiced in the past decades, mainly due to the massive use of chemicals, especially when their use was not sufficiently substantiated, in ecological and economic terms, led to serious problems associated with a negative impact on the environment and the emergence of pest resistance to pesticides. plant protection. In part, this even contributed to a direct or indirect increase in the harmfulness of certain types of pests and diseases and the growing dependence of the crop on the effectiveness of measures to combat them. In this regard, in recent years, the biological method of combating agricultural pests has become more widespread, as it most satisfies the principles of environmental protection.

There are the following biological methods of combating agricultural pests: cultivation and reproduction of a predator (parasite) devouring a certain pest in order to suppress the reproduction of an agricultural pest; cultivation of pathogenic microorganisms that cause certain diseases in pests, leading to a reduction in their numbers, etc. But of the above methods of control, the most acceptable method is the cultivation and reproduction of predators (parasites). So, to combat sucking pests, the main position is occupied by the use of natural entomophages (trichogramma, brakon, lacewing, etc.). An important role in this is played by an increase in the number (density) of these beneficial insects through artificial breeding, seasonal colonization against pests. For this purpose, biological factories for the cultivation and reproduction of parasites have been built and are successfully operating.

For the most efficient operation of these biological factories, it is necessary to develop optimal pest control plans that will determine the plan for the release of parasites, depending on the available forecast of the abundance (density) of the host.

The specificity of the ecological interaction "parasite-host" is such that the pest (the cotton bollworm-host) appears much earlier than its entomophages (parasite-trichogramma). If the timing of the appearance of entomophages is delayed or their density (number) turns out to be small, then the abundance of the host will prevail and then human intervention is necessary, i.e. a person must maintain the necessary number of parasites by their artificial reproduction and release.

For insect populations that are characterized by a change in the stages of egg, larva and pupa, and reproduction occurs in the wake of a certain stage of an adult insect - imago, it is necessary to use equations in finite differences or differential-difference equation.

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