

4. Mathematical modeling of biological systems in Mathcad

Abstract. Modern challenges associated with climate change, population growth and the need to ensure sustainable development require new, highly accurate and predictive tools from agronomy and ecology. Traditional methods of agricultural production management often turn out to be insufficiently flexible and accurate for making informed decisions in a dynamic and complex environment. In this context, mathematical modeling appears as one of the most powerful and promising approaches. It allows not only to quantitatively describe complex biological and ecological processes, but also to predict their dynamics, optimize management decisions and minimize environmental risks. The subject of the study is methods, algorithms and mathematical models used to describe, analyze and predict the state and development of biological systems. *The methodological basis* of the study is based on a systems approach and the paradigm of mathematical modeling, which allows moving from a qualitative description of biological and ecological phenomena to their quantitative analysis and forecasting.

The purpose of the work is to systematize, analyze and provide an in-depth presentation of the theoretical foundations and practical application of mathematical modeling methods for effective analysis, optimization and forecasting of key processes in agronomy and ecology. In particular, attention is paid to the study of the Leslie matrix model, which allows predicting the population size and its age composition over time; the Lotka-Volterra model, which analyzes the dynamics of the interaction of two or more species; plant growth models, which are central to the optimization of agricultural technologies.

Conclusions. The results of the study have direct practical significance for the development and implementation of information systems for decision-making support in agriculture, and can be used as a methodological base for students of the faculties of agronomy, horticulture and plant protection and ecology, forestry and horticulture.

Introduction

Mathematical modeling of natural processes consists of sequentially passing through certain stages and using different types of models to describe and predict phenomena. The process of constructing and using a mathematical model usually includes the following main techniques:

1) analysis of the subject area and problem statement: defining the object and its boundaries, for example, population, ecosystem; highlighting key factors that influence the process and ignoring secondary ones; clear formulation of the modeling goal, id est forecasting, understanding mechanisms, optimization,

2) construction of a mathematical model: choosing a mathematical apparatus (differential equations, probabilistic methods, algebraic relations); recording the basic laws and relationships to which the object is subject; establishing initial and boundary conditions,

3) analysis and solution of the model: using analytical methods, if possible, to obtain an exact solution; applying numerical methods for complex systems,

4) verification and adequacy: checking the compliance of the modeling results with real observations; calibration (selection of model parameters for the best fit to experimental data); model adjustment in case of inconsistency,

5) interpretation and prediction: analysis of the obtained results in the context of the real process; prediction of the behavior of the system under new conditions [1].

The main types of mathematical models used in agronomy and ecology can be classified according to their purpose, structure and nature of the processes they describe. These models help to predict the dynamics of systems, optimize resource management and assess the impact of various factors.

Table 1 shows the classification of models according to the mathematical approach.

Table 1

Classification of mathematical models

View	Description	Application
Deterministic	The process is described by precise, single-valued equations (e.g., differential equations). The result is determined by the initial conditions.	Population dynamics, energy flows, crop growth patterns.
Stochastic	They take into account the element of chance. They use probability theory and statistics.	Disease spread modeling, weather forecasting, risk assessment.
Empirical	They are based on establishing relationships between variables through regression analysis of data, without an in-depth description of the mechanisms.	Rapid yield forecast, correlation between pollution and health.
Imitation	Reproduce the behavior of a complex system step by step, allowing you to experiment with different scenarios.	Complex ecosystems, management of large agro-industrial systems.

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Mathematical models in agronomy are focused on predicting yields, optimizing resource use (fertilizers, water) and risk management.

Crop growth and development models are known as yield models or crop system models. They can be very detailed. Phenological models predict the onset of key phases of plant development (emergence, flowering, ripening) based on temperature. Physiological models describe the processes of photosynthesis, transpiration, nutrient uptake and biomass formation.

Agroclimatic and soil models describe the interaction of a plant with its environment. Soil water balance models predict soil moisture, the required amount of irrigation and the risk of drought, taking into account precipitation, evaporation and transpiration. Nutrient dynamics models calculate the transformation of nitrogen, phosphorus and potassium in the soil, which allows optimizing fertilizer application rates (precision farming).

Risk management and optimization models are used for decision-making. In particular, pest and disease distribution models predict the time and rate of

development of pest populations or infections, helping to determine the optimal moment for the application of protective measures. Optimization models use linear or nonlinear programming to determine the best solutions. For example, the optimal distribution of crop areas, minimizing costs at a given yield.

Mathematical models in ecology are aimed at describing the dynamics of populations, energy and matter flows in ecosystems, as well as the impact of pollution. Population dynamics is the most classic type of model that describes changes in the number of organisms. The exponential growth model describes population growth in the absence of resource constraints. The logistic growth model takes into account resource constraints and the concept of environmental carrying capacity. The Lotka-Volterra model describes fluctuations in the number of two interconnected populations. The Leslie matrix model is also a powerful tool in ecology, using matrix algebra to model discrete population dynamics, especially those with age or stage structures. Unlike simple differential equations, these models allow us to track in detail how life events of survival, fertility, and transitions between stages affect overall population growth. System and simulation models of ecosystems include many interconnected components: plants, animals, soil, water, and atmosphere. Matter and energy flow models describe the transfer of carbon, nitrogen, phosphorus, water, and energy through different trophic levels and between biotic and abiotic components of an ecosystem. Spatial models use geographic information systems to model the distribution of species, pollutants, or soil degradation in a given area. Pollution and self-cleaning models describe the transport and transformation of pollutants in different environments. Transport models use differential equations to describe the diffusion, advection, and dispersion of pollutants in water or air. Balance models calculate the overall balance of a pollutant in a system, taking into account input, output, decay, and accumulation.

4.1 Leslie Matrix Model

One of the early versions of the matrix model was developed by Leslie [2]. It is a discrete model of population dynamics that takes into account its age structure. It allows to determine the future age structure of the female population from the known structure at a given time and hypothetical survival and fecundity coefficients.

The population is divided into $n + 1$ age groups (i.e. $0, 1, 2, \dots, n$, with each group consisting of individuals of the same age) so that the oldest group, or the group in which all individuals survive to this age, has the number n . Denoting by x_n the number of individuals in each age group, we obtain a vector $\vec{a}_t = (x_{0t}, x_{1t}, \dots, x_{nt})$ that represents the age structure at time t . The variable t takes into account discrete changes in time (generations).

The model is described by the matrix equation $\vec{a}_{t+1} = A \cdot \vec{a}_t$ (1), which we write in expanded form by transposing the matrix-vector $\vec{a}_t$:

$$\begin{bmatrix} x_{0,t+1} \\ x_{1,t+1} \\ \vdots \\ \vdots \\ \vdots \\ x_{n,t+1} \end{bmatrix} = \begin{bmatrix} f_0 & f_1 & f_2 & \dots & f_n \\ p_0 & 0 & 0 & \dots & 0 \\ 0 & p_1 & 0 & \dots & 0 \\ 0 & 0 & p_2 & \dots & 0 \\ 0 & 0 & 0 & \ddots & 0 \\ 0 & 0 & 0 & p_{n-1} & 0 \end{bmatrix} \cdot \begin{bmatrix} x_{0,t} \\ x_{1,t} \\ \vdots \\ \vdots \\ \vdots \\ x_{n,t} \end{bmatrix} \quad (1)$$

where A – the Leslie matrix,

the quantities $f_i, (i = 0, 1, \dots, n)$ represent the number of females born to a female of age i ,

$p_i, (i = 0, 1, \dots, n - 1)$ – the probability that a female of age i will survive to age $i + 1$.

For example, consider a population consisting of individuals of 5 age groups.

$$A = \begin{pmatrix} 2 & 4 & 1 & 5 & 8 \\ \frac{1}{2} & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{3} & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{4} & 0 & 0 \\ 0 & 0 & 0 & \frac{1}{3} & 0 \end{pmatrix}, \quad (2)$$

where the numbers 2, 4, 1, 5, 8 – the number of females born to females of the corresponding age group,

$\frac{1}{2}$ – the probability that the female of the youngest age will survive to the next.

Let us show that the behavior of the model can be predicted by analyzing some formal properties of the matrix A .

First, by successively multiplying equation (1) by the matrix A (2), it is easy to obtain more general equations for the number of age groups by time t_{0+k} : $\vec{a}_{t_0+k} = A^k \cdot \vec{a}_{t_0}$.

Second, since the matrix A is square with $(n + 1)$ rows and columns, it has $(n+1)$ eigenvalues $(n + 1)$ (taking into account multiplicity) and $(n + 1)$ eigenvectors. The elements of A are positive numbers, or zeros, so the largest (in absolute value) eigenvalue and the coordinates of its corresponding eigenvector are positive and have some ecological meaning.

Let us illustrate this with one of the simplest models proposed by Williamson. The initial population has a vector representing the age structure $\vec{a}_0 = (0,0,1)$, that is, the population consists of one older female. The matrix A , which is called the Leslie matrix, has the form:

$$A = \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} \quad (3)$$

After one time interval, multiplying the matrix A (3) by the transposed vector $\vec{a}_0$ (using the matrix multiplication rule), we have

$$A \cdot a_0 = \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} = \begin{pmatrix} 12 \\ 0 \\ 0 \end{pmatrix}. \quad (4)$$

i.e. $a_1 = (12,0,0)$ and there will already be 12 younger females in the population. Re-applying the model gives the following results:

$$A \cdot a_1 = \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} \cdot \begin{pmatrix} 12 \\ 0 \\ 0 \end{pmatrix} = \begin{pmatrix} 0 \\ 4 \\ 0 \end{pmatrix} = a_2, \quad (5)$$

$$A \cdot a_2 = \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} \cdot \begin{pmatrix} 0 \\ 4 \\ 0 \end{pmatrix} = \begin{pmatrix} 36 \\ 0 \\ 2 \end{pmatrix} = a_3, \quad (6)$$

$$A \cdot a_3 = \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} \cdot \begin{pmatrix} 36 \\ 0 \\ 2 \end{pmatrix} = \begin{pmatrix} 24 \\ 12 \\ 0 \end{pmatrix} = a_4. \quad (7)$$

So, after three time intervals, each older individual, before dying, manages to produce an average of 12 offspring, each middle-aged individual, before dying (or with the same probability moving to the next class), manages to produce an average of 9 offspring. Young individuals do not produce offspring and with probability $\frac{1}{3}$ fall into the middle age group.

Let us find the main eigenvalue λ (λ - indicates the population growth rate, $\lambda > 0$ - the population is growing, $\lambda < 0$ - it is decreasing, $\lambda = 0$ - the number is constant) and the eigenvector $\vec{v}$ of the matrix A . They can be found by the methods described in the section Eigenvalues and Vectors, having

$$A \cdot \vec{v} = \lambda \cdot \vec{v} \quad (8)$$

Let us denote the coordinates of the eigenvector $\vec{v} = (x, y, z)$. To find them, we will compose a system of three linear algebraic equations:

$$\left. \begin{aligned} 9y + 12z &= \lambda x \\ \frac{1}{3}x &= \lambda y \\ \frac{1}{2}y &= \lambda z \end{aligned} \right\}, \quad (9)$$

determinant of which

$$\begin{vmatrix} -\lambda & 9 & 12 \\ \frac{1}{3} & -\lambda & 0 \\ 0 & \frac{1}{2} & -\lambda \end{vmatrix} = -\lambda^3 + 3\lambda + 2 = (2 - \lambda) \cdot (\lambda + 1)^2. \quad (10)$$

By equating (10) to zero, we find the principal eigenvalue $\lambda_1 = 2$. This means that the population size doubles for each time interval.

To find the eigenvector that determines the stable age structure of the population, we substitute $\lambda_1 = 2$ into each equation of system (9). We have:

$$\begin{cases} -2x + 9y + 12z = 0 \\ \frac{1}{3}x - 2y = 0 \\ \frac{1}{2}y - 2z = 0 \end{cases} \quad (11)$$

Since the system is homogeneous, it has many solutions. Express y and z in terms of x in the second and third equations and substitute into the first. We have: $y = \frac{1}{6}x$, $z = \frac{1}{24}x$, then $z = 1$, to $y = 4$, $x = 24$.

The eigenvector of equality $\vec{v}_1 = (24, 4, 1)$. The other eigenvalues of equality have the form $\lambda_2 = -1$, $\lambda_3 = -1$. Similarly, the eigenvector of $\vec{v}_2$ has the form $\vec{v}_2 = (6, -2, 1)$. Since the eigenvalue is -1 of multiplicity 2, to find the vector $\vec{v}_3$, we solve the system of equations $(A - \lambda_2) \vec{v}_3 = \vec{v}_2$:

$$\begin{pmatrix} 1 & 9 & 12 \\ \frac{1}{3} & 1 & 0 \\ 0 & \frac{1}{2} & 1 \end{pmatrix} \cdot \begin{pmatrix} x \\ y \\ z \end{pmatrix} = \begin{pmatrix} 6 \\ -2 \\ 1 \end{pmatrix}. \quad (12)$$

It is easy to verify that the corresponding system admits the solution $\vec{v}_3 = (0, -2, 2)$.

Based on the concept of a basis of vectors and its geometric interpretation, we assume that the age structure of the population is represented by a vector in three-dimensional space, for which the vectors $\vec{v}_1 = (24, 4, 1)$, $\vec{v}_2 = (6, -2, 1)$ and $\vec{v}_3 = (0, -2, 2)$ – the basis, i.e.

$$\vec{a}_0 = \alpha_0 \cdot \vec{v}_1 + \beta_0 \cdot \vec{v}_2 + \gamma_0 \cdot \vec{v}_3, \quad (13)$$

where $\alpha_0, \beta_0, \gamma_0$ – some positive numbers.

For example, if $\vec{a}_0 = (258, 30, 17)$, then we find the coordinates of this vector in the new basis $\vec{v}_1, \vec{v}_2, \vec{v}_3$ by composing and solving the system of linear algebraic equations:

$$\begin{cases} 24\alpha_0 + 6\beta_0 + 0\gamma_0 = 258 \\ 4\alpha_0 - 2\beta_0 - 2\gamma_0 = 30 \\ 1\alpha_0 + 1\beta_0 + 2\gamma_0 = 17 \end{cases}. \quad (14)$$

We have $\alpha_0 = 10$, $\beta_0 = 3$, $\gamma_0 = 2$.

Since $\frac{k}{2^k} \rightarrow 0, k \rightarrow \infty$, then at $t = +k \rightarrow \infty$ the population grows exponentially

$$\vec{a}_{+k} \approx 2^k \cdot a_0 \cdot \vec{v}_1. \quad (15)$$

Therefore, the principal eigenvalue λ_1 gives the rate at which the population size grows (in our example, the population doubles in each time interval), and the eigenvector $\vec{v}_1$ determines the stable age structure of the population, i.e. the ratio of the numbers of individuals of different age groups remains constant and equal to 24:4:1.

Knowing the principal eigenvalue λ_1 and using the following formula, we can also estimate the number of individuals that need to be removed from the population so that its size is equal to the initial one:

$$H = 100 \frac{\lambda - 1}{\lambda}. \quad (16)$$

The remaining eigenvalues and vectors can characterize the stability and oscillatory tendencies in the models.

It is easy to see that if at the end of each time interval we remove half of the population and use it for food, then its size will become equal to the initial $\vec{a}_0$.

Therefore, matrix models are indispensable in conservation biology in determining the most critical life cycle stages for endangered species. This helps to direct efforts to protect those groups whose survival has the greatest impact on $\bar{\lambda}$; in resource management to predict population growth of commercial species (e.g., fish) to set catch quotas; in ecological toxicology to assess the impact of pollutants on specific life stages of organisms; in modeling stage development using a stage transition matrix instead of a pure age structure, which is better suited for plants, invertebrates, and other organisms whose development depends on size or stage, rather than just age.

The algorithm for individual calculation stages in the Mathcad environment is shown in (Listing 1).

Listing 1

Which displays the population characteristics over time intervals: $t=3,30,100,300$, where t is the generation time

$$\begin{aligned}
 \mathbf{A} &:= \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} & \mathbf{A} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} 12 \\ 0 \\ 0 \end{pmatrix} & \mathbf{A} \cdot \begin{pmatrix} 12 \\ 0 \\ 0 \end{pmatrix} \rightarrow \begin{pmatrix} 0 \\ 4 \\ 0 \end{pmatrix} & \mathbf{A} \cdot \begin{pmatrix} 0 \\ 4 \\ 0 \end{pmatrix} \rightarrow \begin{pmatrix} 36 \\ 0 \\ 2 \end{pmatrix} \\
 & & \mathbf{A}^3 \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} 36 \\ 0 \\ 2 \end{pmatrix} & \mathbf{A}^{30} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} 2863311408 \\ 477218628 \\ 119304628 \end{pmatrix} = \begin{pmatrix} 2.863 \times 10^9 \\ 4.772 \times 10^8 \\ 1.193 \times 10^8 \end{pmatrix} \\
 & & \mathbf{A}^{100} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} \rightarrow \begin{pmatrix} 3380401600608611737324541880600 \\ 563400266768101956220756980300 \\ 140850066692025489055189244976 \end{pmatrix} = \begin{pmatrix} 3.38 \times 10^{30} \\ 5.634 \times 10^{29} \\ 1.409 \times 10^{29} \end{pmatrix} \\
 & & \mathbf{A}^{300} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} = \begin{pmatrix} 5.432 \times 10^{90} \\ 9.053 \times 10^{89} \\ 2.263 \times 10^{89} \end{pmatrix} & \mathbf{A}^{1000} \cdot \begin{pmatrix} 0 \\ 0 \\ 1 \end{pmatrix} = \begin{pmatrix} 2.857 \times 10^{301} \\ 4.762 \times 10^{300} \\ 1.191 \times 10^{300} \end{pmatrix}
 \end{aligned}$$

Determining the eigenvalues of a matrix

$$\begin{aligned}
 \mathbf{A} &:= \begin{pmatrix} 0 & 9 & 12 \\ \frac{1}{3} & 0 & 0 \\ 0 & \frac{1}{2} & 0 \end{pmatrix} & \left| \mathbf{A} - \lambda \cdot \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \right| \rightarrow 3 \cdot \lambda - \lambda^3 + 2 \\
 & & 3 \cdot \lambda - \lambda^3 + 2 \text{ solve} \rightarrow \begin{pmatrix} -1 \\ -1 \\ 2 \end{pmatrix} \\
 & & \begin{pmatrix} 24\alpha + 6\beta + 0\gamma = 258 \\ 4\alpha - 2\beta - 2\gamma = 30 \\ 1\alpha + \beta + 2\gamma = 17 \end{pmatrix} \text{ solve, } \alpha, \beta, \gamma \rightarrow (10 \ 3 \ 2)
 \end{aligned}$$

4.2 Lotka-Volterra Mathematical Model

The classical Lotka-Volterra mathematical model describes the dynamics of the number of two interacting populations in a predator-prey ecosystem. The model is a system of two first-order nonlinear differential equations that show how the number of each population changes over time, depending on their interaction.

Let there be two biological species that live together in some isolated territory. The environment is considered stationary and provides the «prey» species with everything necessary for existence. The other species, the «predators», is also in stationary conditions, but feeds only on representatives of the first «prey» species. Such simple models can approximately describe the interaction of populations of hares and wolves, crucian carp and pike, competition between producers of products, competition between sellers.

The predator-prey system is a complex ecosystem for which long-term relationships between predator and prey species are implemented in a common territory. One of the important problems in studying this ecosystem is the problem of its stability and its manageability.

Let us consider a simplified Lotka-Volterra mathematical model of the coexistence of two biological species. It consists of two components: Y_0 – the number or biomass of the prey or plant population and Y_1 – the number of the consumer (predator) population.

The predator-prey model describes the dynamics of average values. This is a system of two first-order ordinary differential equations that describes the dynamics of the population size with one type of predator and one type of prey.

Let us consider the case when, in the absence of a predator, the prey population will grow along an exponential curve.

Let us construct the simplest model of the development of predator and prey populations. To simplify the model, we will consider their numbers as continuous functions of time, the number of prey is unlimited. The limitations of the proposed model also include the fact that it does not take into account the spatial parameters of

the interaction of predators and prey, the dependences between the values are considered linear. Also, this model does not take into account the existing evolution of prey and predator species.

The variables in the model will be:

$$Y_0 = Y_0(t) - \text{number of victims,}$$

$$Y_1 = V_1(t) - \text{number of predators.}$$

Let's write an equation that describes the change in the number of victims over time. The change in the number dY_0 of victims over time dt will occur due to three reasons. Since there are no restrictions on the number of food resources for victims, they will multiply indefinitely in proportion to their number:

$$dY1_0 = \alpha Y_0 dt, \quad (17)$$

where α – the generalized proportionality coefficient, which depends on the living conditions and birth rate of the victims.

The decrease in the number of victims will occur due to the extinction of the population: the number of such deceased victims will be proportional to the total number of existing victims:

$$dY2_0 = -\beta Y_0 dt, \quad (18)$$

where β – the proportionality coefficient that takes into account natural mortality.

The change in the number of victims due to natural causes (if predators are absent) can be written as:

$$dY_0 = dY1_0 + dY2_0 = \alpha Y_0 dt - \beta Y_0 dt = (\alpha - \beta) Y_0 dt = \mu Y_0 dt, \quad (19)$$

where $\mu = \alpha - \beta$ – the total coefficient, $\mu > 0$, which reflects environmental conditions, birth rate and mortality of victims in the absence of predators.

Let us determine the value of the coefficient μ . To do this, we solve the differential equation (19) for some time interval $[0, t]$:

$$dY_0 = \mu Y_0 dt. \quad (20)$$

Let's separate the variables:

$$\frac{dY_0}{Y_0} = \mu dt.$$

Let's integrate:

$$\begin{aligned} \int_{V_0^0}^{V_0^t} \frac{dY_0}{Y_0} &= \int_0^t \mu dt \\ \ln V_0^t - \ln V_0^0 &= \mu(t - 0), \\ \ln \left(\frac{V_0^t}{V_0^0} \right) &= \mu t, \\ \ln \left(\frac{V_0^t}{V_0^0} \right) &= \mu t \ln e = \ln e^{\mu t} \\ \frac{V_0^t}{V_0^0} &= e^{\mu t}. \end{aligned} \tag{21}$$

We obtained the equation of simple exponential growth:

$$V_0^t = V_0^0 e^{\mu t}, \tag{22}$$

In real ecological systems, the food resource for victims is limited, so the number of victims for real systems is described by a system of equations of simple exponential growth:

$$\begin{cases} V_0^t = V_0^0 e^{\mu t} \text{ при } 0 \leq t \leq t^* \\ V_0^t = V_0^{t^*} \text{ при } t > t^* \end{cases}. \tag{23}$$

Let the number of victims increase by a factor of $V_0^\tau = eV_0^0$ over a period of time τ , then according to (21) we can write:

$$\begin{aligned} \ln \left(\frac{V_0^\tau}{V_0^0} \right) &= \ln \left(\frac{eV_0^0}{V_0^0} \right) = \ln e = 1 = \mu\tau, \mu\tau = 1, \\ \mu &= \frac{1}{\tau}, \end{aligned} \tag{24}$$

i.e. the coefficient μ is the reciprocal of the time it takes for the number of prey to increase by e times. But since there are also predators in the ecosystem that feed on prey, the number of prey will decrease as a result of their destruction by predators. The number of prey that will be destroyed is proportional to the number of predators and the number of prey: $dY_0^3 = kY_0Y_1dt$. The proportionality coefficient k – a total coefficient that takes into account the probability of a predator meeting a prey, as well as the number of prey that can be eaten by one predator.

Therefore, the first equation of the model is written as follows:

$$\begin{aligned} dY_0 &= \mu Y_0 dt - k Y_0 Y_1 dt, \\ Y_0' &= \frac{dY_0}{dt} = \mu Y_0 - k Y_0 Y_1. \end{aligned} \quad (25)$$

Let's write the second equation of the model, which will describe the change in the number of predators. Since predators feed only on prey, without the presence of prey the population of predators will decrease. The number dY_1^Π of those who died without food dt during the time of predators will be proportional to the number of predators: $dY_1^\Pi = m Y_0 dt$, where the coefficient m – the proportionality index, obtained similarly to the same index for the first equation of the model (see equation (17-25)).

But in the presence of prey, predators will be able to increase their population proportional to their number and the number of prey: $dY_1^3 = b Y_0 Y_1 dt$, where b – the proportionality index, which takes into account the ability of predators to reproduce and the probability of a predator meeting a prey. Therefore, the second equation of the model can be written:

$$dY_1 = -m Y_0 dt + b Y_0 Y_1 dt,$$

or

$$Y_1' = \frac{dY_1}{dt} = -m Y_1 + b Y_0 Y_1. \quad (26)$$

System of differential equations:

$$\begin{cases} \frac{dY_0}{dt} = \mu Y_0 - k Y_0 Y_1 \\ \frac{dY_1}{dt} = -m Y_1 + b Y_0 Y_1 \end{cases} \quad (27)$$

is called the Lotka-Volterra model. The coefficients μ, k, m, b are the parameters of the model.

The steady state of the system is described by the system of equations:

$$\begin{aligned} &\begin{cases} Y_0 = const \\ Y_1 = const \end{cases}, \\ &\begin{cases} \frac{dY_0}{dt} = 0 \\ \frac{dY_1}{dt} = 0 \end{cases}, \\ &\begin{cases} \mu Y_0 - k Y_0 Y_1 = 0 \\ -m Y_1 + b Y_0 Y_1 = 0 \end{cases}, \end{aligned}$$

$$\begin{cases} \mu - kY_1 = 0 \\ -m + bY_0 = 0 \end{cases}.$$

Therefore, stationary solutions of the system of differential equations (27) can exist under the condition:

$$Y_0 = \frac{m}{b}, \quad (28)$$

$$Y_1 = \frac{\mu}{k}. \quad (29)$$

$$\begin{aligned} \text{System of differential equations} \quad & \begin{cases} \frac{dY_0}{dt} = \mu Y_0 - k Y_0 Y_1 \\ \frac{dY_1}{dt} = -m Y_1 + b Y_0 Y_1 \end{cases} \text{ with initial conditions:} \\ & \begin{cases} Y_0(0) = YZ \\ Y_1(0) = YV \end{cases} \end{aligned} \quad (30)$$

(where YZ – the number of victims at time $t = 0$, YV – the number of predators at time $t = 0$) is solved in Mathcad by numerical methods.

For solving differential equations and their systems by numerical methods, Mathcad has more than 30 different functions built in.

For the system of differential equations (27), the built-in function *rkfixed* gives quite good results. It gives a solution to the system of differential equations of the problem on a given interval by the Runge-Kutta method with a constant step.

The function has the format:

$$Z = rkfixed(y, t1, t2, N, D), \quad (31)$$

where Y – the vector of initial conditions, $t1, t2$ – the initial and final points of the integration segment of the system; N – the number of nodes on the segment $[t1, t2]$; when solving a problem on a segment, the result contains $N + 1$ lines; D – the name of the vector function $D(t, y)$ of the right-hand side of the system of differential equations (it contains expressions for the derivatives of the system of differential equations), Z – the result of the function-matrix, the format of which depends on the type of problem, for example, for first-order differential equation systems of type (27), their first column contains the coordinates of the grid nodes t_i (time), the second column – the calculated approximate values of the solution Y_{0i} (number of victims), the third – Y_{1i} (number of predators).

To analyze predator-prey systems, phase diagrams are used. A phase diagram – a graph that quantitatively characterizes the dependence of one population on another. If the phase diagram on the plane is a smooth closed curve, and the phase diagram in space is a spiral line, then the system exists in a stable state the pitch of the spiral line characterizes the cyclicity of the system in time.

If the phase diagram on the plane is a non-smooth closed curve and the phase diagram in space is a distorted spiral-shaped line, then the system may exist but it is weakly stable, the connections between its elements are inharmonious, and any minor disturbances in the system can lead to its collapse.

If the phase diagram on the plane is an open curve, and the phase diagram in space is not a spiral line then the system cannot exist.

Let us consider the Mathcad program-document for studying the simplified Lotka-Volterra predator-prey model, for a system with parameters: $\mu = 0,5$, $k = 0,002$, $m = 0,2$, $b = 0,0015$. The initial number of hares $YZ = 200$, wolves – $YV = 150$, the time interval is 300 conventional units, the number of nodal integration points $N = 1000$. The solution to the problem is given in (Listing 2).

The developed mathematical model (Listing 2) makes it possible to change the values of the system parameters, that is, to investigate the behavior of the system at different parameter values, therefore it can be attributed to the class of simulation models.

Simplified Lotka-Volterra predator-prey model

Model parameters:

$$\mu := 0.5 \quad k := 0.002 \quad m := 0.2 \quad b := 0.0015$$

$$YZ := 200 \quad \Leftarrow \text{Number of hares at the initial time } t_1=0$$

$$YV := 150 \quad \Leftarrow \text{Number of wolves at the initial time } t_1=0$$

$$t_1 := 0 \quad \Leftarrow \text{Initial time (in conventional units)}$$

$$t_2 := 300 \quad \Leftarrow \text{Final point in time (in conventional units)}$$

$$N := 1000 \quad \Leftarrow \text{The number of points for which a solution to a system of equations found}$$

Relationship between model parameters:

$$\frac{m}{b} = 133.333 \quad \frac{\mu}{k} = 250$$

Initial condition vector:

$$Y := \begin{pmatrix} YZ \\ YV \end{pmatrix} \quad \begin{matrix} \Leftarrow \text{Number of hares at the initial time } t_1=0 \\ \Leftarrow \text{Number of wolves at the initial time } t_1=0 \end{matrix}$$

The vector $D(t, Y)$, which contains the left-hand sides (values of derivatives) of the system of differential equations (27)

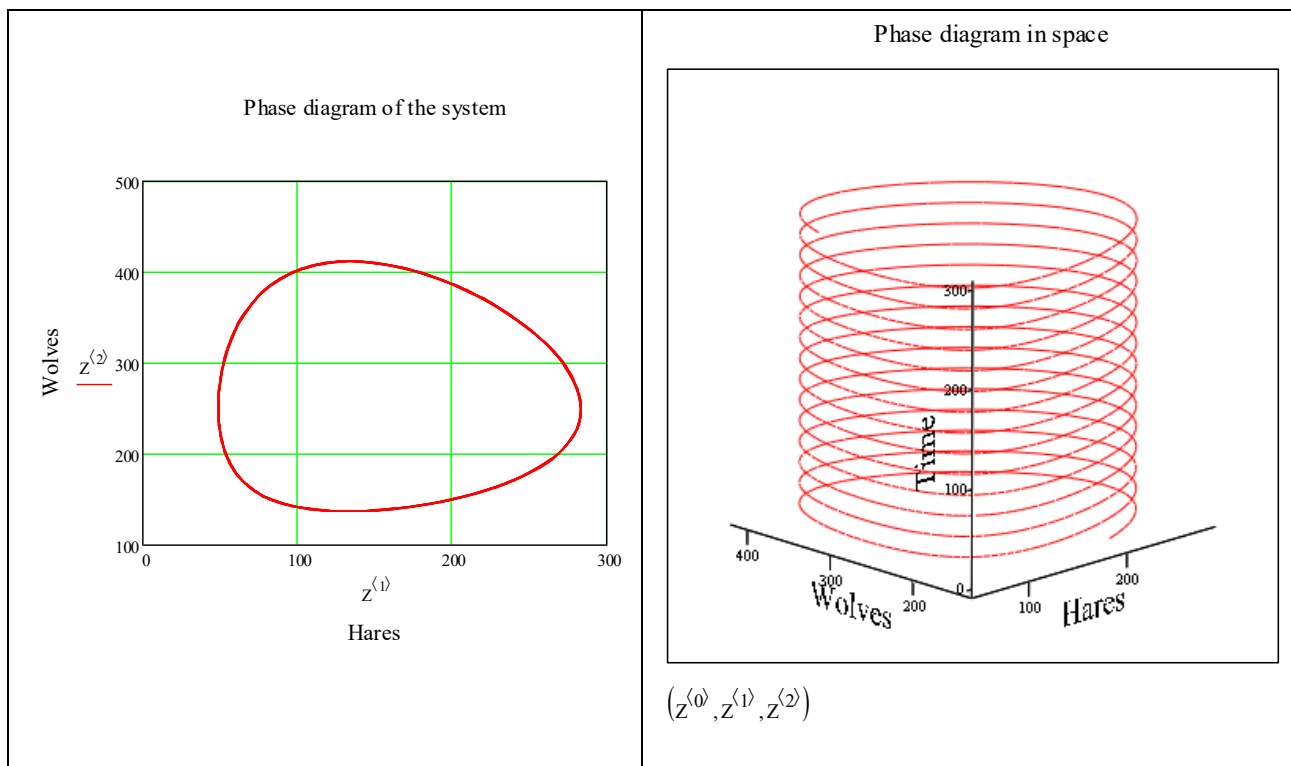
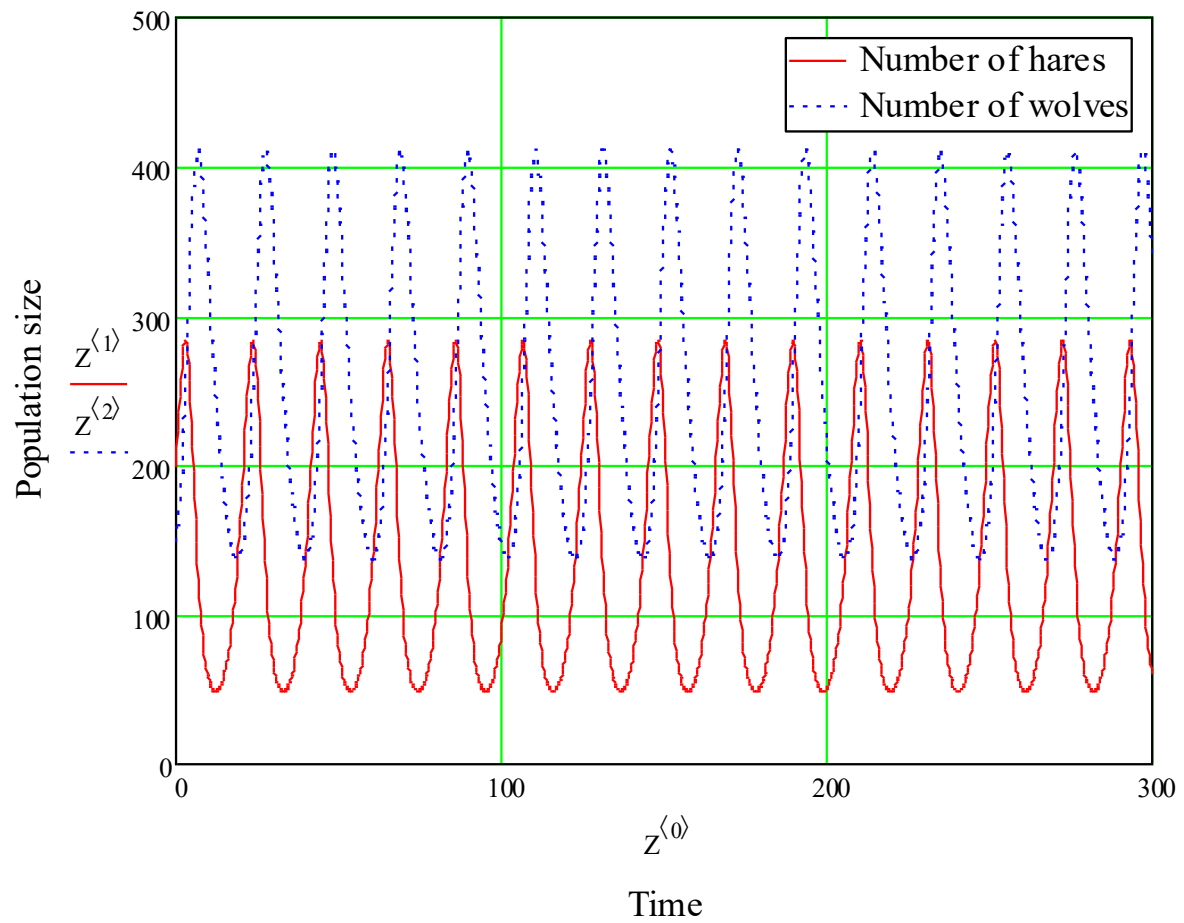
$$D(t, Y) := \begin{pmatrix} \mu \cdot Y_0 - k \cdot Y_0 \cdot Y_1 \\ -m \cdot Y_1 + b \cdot Y_0 \cdot Y_1 \end{pmatrix}$$

Solving a system of differential equations by the Runge-Kutta method (rkfixed function). Solution Z - a matrix of dimension $N \times 3$. Its first column contains the time t , the second Z^1 and the third Z^2 contain the values of the functions Y_0 and Y_1 corresponding to the given moments of time t

$$Z := \text{rkfixed}(Y, t_1, t_2, N - 1, D)$$

Continuation of Listing 2

Predator-prey system dynamics



4.3 Dynamic plant growth models

In agriculture, *S*-shaped models are often used to describe the dynamics of biomass accumulation over time. These curves reflect typical limited growth: a slow start, rapid exponential growth, and a slowdown until reaching a maximum or constant value. The most common such models used to model plant growth are the logistic growth equation, Gompertz, and Chanter [3].

The logistic model is the simplest and most common model of limited growth. It was first proposed by Pierre-François Verhulst. The growth curve is symmetric about the inflection point (the highest growth rate), which is exactly half the maximum mass. It is suitable for modeling growth where factors limiting growth (such as lack of space or nutrients) begin to act proportionally as the object increases in size.

The Gompertz model is often used in biology and medicine to describe the growth of tumors or organs, as well as plant growth. Unlike the logistic curve, the Gompertz curve is asymmetric. The inflection point (maximum growth rate) is located at $\approx 37\%$ of maximum mass. It better models those biological processes where the highest growth rate is achieved in the early stages (low mass), and the growth slowdown is more gradual in the later stages. In agronomy, it is often used to model fruit growth or dry mass accumulation.

The Richards equation, also sometimes called the Chanter equation in the context of plant growth, is a generalization of both the logistic and Gompertz models. It introduces an additional parameter that controls the shape of the curve. Chanter used specific forms of this equation to model the growth of agricultural crops, in particular root crops. The Richards equation can be reduced to either the logistic model or the Gompertz model. Due to its flexibility, the Chanter equation allows for the most accurate modeling of various growth patterns of agricultural crops (root crops, tubers, leaves), where the point of maximum growth rate can differ greatly from half of the final mass.

We analyze the growth dynamics of Brussels sprouts using a mathematical model constructed upon a system of differential equations. For every plant subsystem, a distinct differential equation is formulated to describe its development and

interconnection with other components. This system of equations is solved utilizing a numerical approach. The final step involves selecting solutions from the generated set where the cumulative sum of squared deviations from observed experimental values is minimal.

Plant subsystems undergo continuous dynamic transformations during the growth process, which poses several challenges for mathematical modeling. Conventionally, plant parameters are measured at specific time intervals. For these discrete time points, researchers often formulate regression equations, aiming to generalize the findings for intermediate and subsequent time moments by introducing time as a variable into the regression model. However, it is widely recognized that the results derived from simple regression equations frequently diverge from empirical observations. Such a semi-empirical approach may fail to capture the true dynamics of plant development, thereby leading to the construction of inefficient models.

An adequate mathematical description of the unique characteristics of a real agrobiological system requires a dynamic model. Such a model must inherently describe the interaction among plant subsystems, uncover the underlying mechanisms of their temporal change, and reveal the patterns governing the internal processes. Typically, dynamic models are constructed using differential equations and their systems [4, 5, 6]. Consequently, the task of developing methodologies for generating mathematical models to describe complex, multidimensional dynamic systems remains highly relevant.

Plant growth and developmental trajectories can be mathematically captured using growth functions that establish the relationship between accumulated dry matter and time. We will now examine some of the most widely recognized growth equations, including the logistic, Gompertz, and Chanter's models [4, 5, 14].

Focusing on the latter, we proceed to analyze the specifics of Chanter's equation:

$$M = \frac{M_0 \cdot B}{M_0 + (B - M_0) \cdot \exp\{-[\mu(1 - e^{-D \cdot t})/D]\}} \quad (32)$$

where, M, M_0, B, μ, D – parameters that have a biological meaning.

Let $M = 100 \text{ g}$ – the mass of dry matter for the period of harvest;

$M_0 = 1$ g – the mass of dry matter of the plant at the time $t = 0$;

B – availability of nutrient medium;

$$B = \frac{M \cdot M_0 \cdot (e^{\mu/D} - 1)}{M_0 \cdot e^{\mu/D} - M}, \quad (33)$$

$\mu = 0,5$ – specific growth rate;

D – an indicator of complication, which characterizes μ the change with plant development.

The derivation of the logistic equation is predicated on the assumption that the plant's growth rate is limited by the available nutrient resources in the medium. Conversely, the Gompertz equation posits that the nutrient medium resource is unlimited. Specifically, it assumes that the growth energy remains unaffected and is directly proportional to the dry mass, while the specific growth rate remains constant [4].

By selecting the value D for from the interval $0 \leq D \leq \mu/[\ln(M/M_0)]$, you can build a family of curves, which is bounded on the left by the logistic curve, and on the right – the Gompertz curve. When $D \rightarrow 0$ (for example, $D = 0,00086$), and B determined by formula (33), equation (32) becomes logistical. When $D \rightarrow \mu/[\ln(M/M_0)] = 0,1086$ – in the Gompertz curve, when $D = 0,05$ the curve is between the logistic curve and the Gompertz curve. All plotted growth curves share identical values for the initial and final dry weight of the plant, as well as the starting specific growth rate. As a parameter increases, the inflection point shifts towards later time values. The Gompertz curve is characterized by more rapid growth during the initial stages, a slower convergence towards the asymptote, and an extended linear segment around the inflection point. (Fig. 1).

Consequently, the Chanter, Gompertz, and logistic growth curves are suitable for integration as fundamental components within dynamic models designed for plant growth.

By integrating these specific growth curves (Chanter, Gompertz, and logistic), it is possible to construct a more robust mathematical model for plant growth dynamics,

typically represented by a system of differential equations.

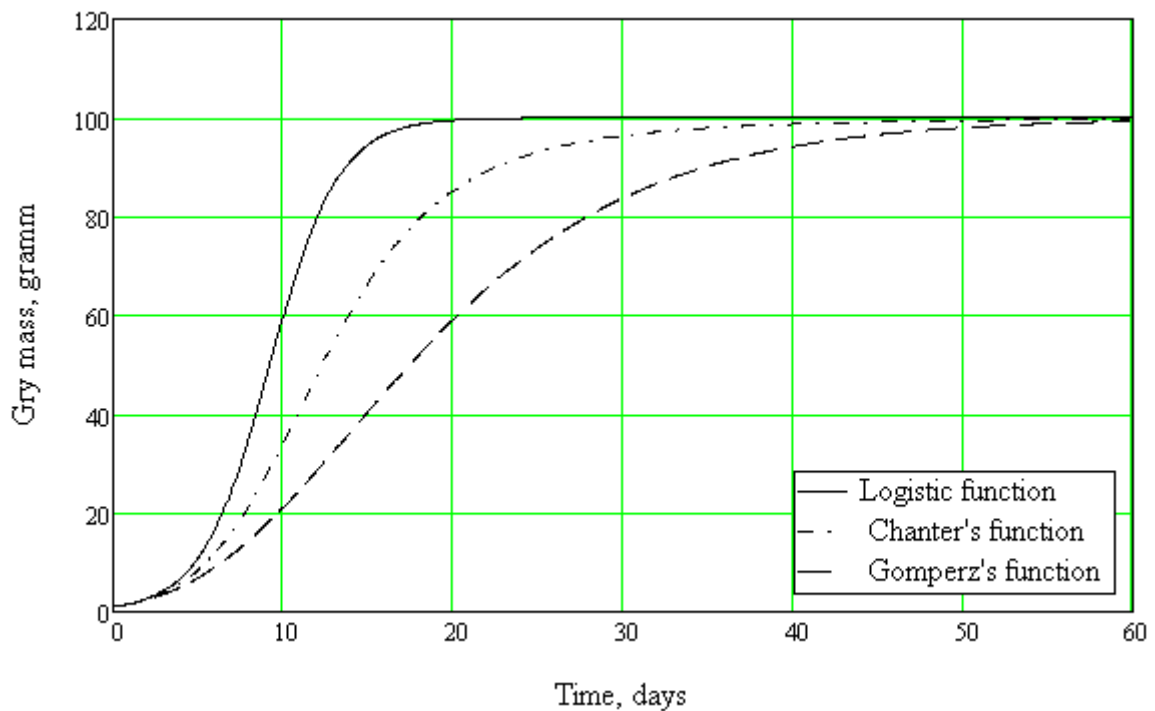


Fig.1 Chanter's growth function

The majority of differential equations and equation systems used to model the dynamics of agrobiological systems lack closed-form (analytical) solutions, or such solutions are excessively complex [4, 5, 6]. Consequently, the ability to solve these differential equations and their systems using numerical techniques is essential. The Mathcad system provides the necessary capabilities for this purpose [1].

The Mathcad environment provides capabilities for solving differential equations and their systems using both symbolic and numerical approaches. While symbolic methods for equation solving are unfortunately constrained, the system compensates with robust numerical techniques designed for solving problems such as the Cauchy problem (initial value problem). Numerical solution of the generalized differential equations (GDE) within the framework of the Cauchy problem constitutes a sophisticated and detailed process. Crucially, the ease of interpreting the results and analyzing how solutions respond to changes in system parameters are key advantages in this process.

The majority of computational tasks are straightforwardly managed (often solved using the standard Runge-Kutta algorithm). Conversely, particularly "stiff"

problems necessitate the application of specialized numerical techniques. Since all these algorithms are integrated into the Mathcad system, the user can select the appropriate method based on the specific characteristics of the equation being analyzed.

When modeling biological processes, systems, or ecosystems, one must assume the validity of fundamental laws from physics, chemistry, and biology. The core principles and laws governing processes in non-living nature maintain their relevance for living systems. Consequently, every robust mathematical model must be grounded in the laws of conservation (mass, electric charge, energy, linear and angular momentum) and the laws governing mass interaction, radioactive, and chemical transformations.

We now explore a methodology for constructing a dynamic plant growth model that relies on empirical data. Developing such a mathematical model necessitates a substantial volume of experimental measurements. Crops like potatoes [6], tomatoes, sugar beets [15], and cabbage are particularly suitable subjects for developing these growth models.

A significant contribution to the study of cabbage growth was made by Cherednichenko V.M. [7, 8, 10, 11], Lykhatsky V.I. [9], Chernensky V.M. [12, 13]. Cherednichenko V.M. during 2009-2013 conducted fundamental field experiments on the cultivation of cauliflower and broccoli at the experimental sites of Vinnytsia National Agrarian University. The effect of water-retaining granules, mulching with film and black agrofiber on plant growth was studied. Phenological observations, biometric measurements and records were carried out, the relationship between plant subsystems was studied, and a statistical analysis of plant growth indicators was performed.

As an illustrative case, we will construct a model detailing the growth dynamics of Brussels sprouts, basing our approach on the framework established by Zagorodny Y. V. [6]. In plants, we distinguish separate subsystems: W_1 – root, W_2 – stem, W_3 – leaves, W_4 – heads. The total dry weight of the plant is:

$$W = \sum_{i=1}^4 W_i, \quad (34)$$

The growth of subsystems (stem roots, leaves) for Brussels sprouts is described by the growth equation:

$$W_i = \frac{A_i \cdot B_i}{A_i + (B_i - A_i) \cdot e^{-\kappa_i t}}, \quad (35)$$

where A_i is the dry weight of the corresponding subsystem for seedlings;

B_i – dry mass of the relevant subsystem for the period of completion of harvesting.

The model is built according to the following algorithm:

1. In plants, we distinguish separate subsystems: W_1 – root, W_2 – stem, W_3 – leaves, W_4 – head.
2. We determine the dry weight of plant subsystems with a period of 5-7 days throughout the growing season.
3. Based on experimental data, we determine the unknown parameters of growth functions for each subsystem of the plant.
4. We write the differential equations for the dynamics of each subsystem.

We combine differential equations into a system:

$$\begin{cases} \frac{dW_1(t)}{dt} = a_{1,1}W_1(t) \cdot \rho(t) \cdot f(t) \cdot \frac{k_1 e^{-k_1 t}(B_1 - A_1)}{A_1 - e^{-k_1 t}(A_1 - B_1)} + a_{1,2}W_2(t) - a_{1,3}W_3(t) - a_{1,4}W_4(t) \\ \frac{dW_2(t)}{dt} = a_{2,1}W_1(t) + a_{2,2}W_2(t) \frac{k_2 e^{-k_2 t}(B_2 - A_2)}{A_2 - e^{-k_2 t}(A_2 - B_2)} + a_{2,3}W_3(t) - a_{2,4}W_4(t) \\ \frac{dW_3(t)}{dt} = a_{3,1}W_1(t) \cdot a_{3,2}W_2(t) + a_{3,3}W_3(t) \cdot f(t) \cdot \frac{k_3 e^{-k_3 t}(B_3 - A_3)}{A_3 - e^{-k_3 t}(A_3 - B_3)} - a_{3,4}W_4(t) \\ \frac{dW_4(t)}{dt} = [a_{4,1}W_1(t) + a_{4,2}W_2(t) + a_{4,3}W_3(t) \cdot f(t)]s(t) - a_{4,4}W_4(t) \end{cases} \quad (36)$$

where $\begin{bmatrix} a_{1,1} & a_{1,2} & a_{1,3} & a_{1,4} \\ a_{2,1} & a_{2,2} & a_{2,3} & a_{2,4} \\ a_{3,1} & a_{3,2} & a_{3,3} & a_{3,4} \\ a_{4,1} & a_{4,2} & a_{4,3} & a_{4,4} \end{bmatrix}$ – matrix of coefficients of the system of

equations, which characterizes the interaction of elements of plant subsystems;

$a_{1,1}$ – coefficient characterizing the strength of root growth;

$a_{1,2}$ – coefficient that characterizes the rate of exchange between the subsystem «root – stem»;

$a_{1,3}$ – coefficient that characterizes the rate of exchange between the subsystem «root – leaf» through the stem;

$a_{1,4}$ – coefficient that takes into account the decrease in the rate of root growth

due to the growth of the head;

$a_{2,1}$ – rate of exchange between subsystems «stem – root»;

$a_{2,2}$ – characterizes the growth rate of the stem;

$a_{2,3}$ – rate of exchange between subsystems «stem – leaf»;

$a_{2,4}$ – takes into account the decrease in the growth rate of the stem due to the growth of the heads;

$a_{3,1}$ – rate of exchange «leaf – root» through the stem;

$a_{3,2}$ – rate of exchange «leaf – stem»;

$a_{3,3}$ – characterizes the growth rate of leaves;

$a_{3,4}$ – takes into account the decrease in leaf growth due to the growth of heads;

$a_{4,1}$ – characterizes the influence of roots on the growth rate of dry weight of heads;

$a_{4,2}$ – characterizes the influence of the stem on the growth rate of dry weight of the heads;

$a_{4,3}$ – characterizes the influence of leaves on the growth rate of dry weight of heads;

$a_{4,4}$ – takes into account the decrease in the intensity of the growth rate of the heads due to the aging of the plant organism;

$\rho(t)$ – soil moisture function;

$f(t)$ – soil temperature function;

$F(t)$ – air temperature function;

A_1 – dry mass of seedling roots;

B_1 – dry mass of roots for the period of completion of harvesting;

K_1 – coefficient of the logistic equation of root growth;

A_2 – dry mass of seedling stem;

B_2 – dry weight of the stem for the period of completion of harvesting;

K_2 – coefficient of the logistic equation of stem growth;

A_3 – dry mass of seedling leaves;

B_3 – dry weight of leaves for the period of completion of harvesting;

K_3 – coefficient of logistic level of leaf growth;

$S(t)$ – a function that characterizes the growth rate of heads.

4. We set the initial conditions – values $W_{i,0}$ for the moment of time $t = 0$.

5. We give the initial approximations of the unknown coefficients $a_{i,j}$ of the system of differential equations.

6. We solve the system of differential equations in Mathcad by the Runge-Kutta method with a constant step. We use the built-in function:

$rkfixed(y, x1, x2, n, D)$.

7. We find the weighted sum of the squares of the deviations of the experimental values from the calculated ones $\sum_{i=1}^n \sum_{j=0}^m \left(\frac{W_{i,j} - WP_{i,j}}{WP_{i,j}} \right)^2$.

8. By the method of coordinate descent we change the values of the coefficients $a_{i,j}$.

9. We solve the system of equations and calculate the sum of squares of deviations.

10. The computational procedure is completed at

$$\sum_{i=1}^n \sum_{j=0}^m \left(\frac{W_{i,j} - WP_{i,j}}{WP_{i,j}} \right)^2 = \min. \quad (37)$$

11. We fix the optimal values of the coefficients $a_{i,j}$.

12. We substitute the obtained optimal values of the coefficients into the system of differential equations (36) and solve it.

13. We analyze the solution of the system of equations and investigate the interaction between the individual elements of plant subsystems. We build graphs.

To determine the dry weight of plant subsystems, field experiments were performed (table 2). The plants were cleaned from the soil, their components were isolated: root, stem, leaves, heads, placed in a thermostat with a temperature of 50-60°C and dried for 4-5 hours. After that, at a temperature of 103-110 °C the plants were dried (brought to constant weight) for 3-5 hours. The average value was determined by averaging the masses of 5-7 plants.

Table 2

Dry mass of plant subsystems

t	0	10	30	37	46	55	60	67	75	91	98	112
W_1, g	0.53	2.2	3.7	6	12.8	12.4	14.1	16.1	16.2	18.5	17.3	18.9
W_2, g	0.34	1.1	6.7	7	15.2	20.1	23.8	26.0	26.1	28.7	28.8	28.5
W_3, g	2.61	5.8	18.5	28	57.3	65.2	66.0	69.6	75.9	77	75.3	78.1
W_4, g	0	0	0	0	0.9	6.8	22.1	30	36	38	39.6	41.7

The function that characterizes the growth rate of Brussels sprouts has the form:

$$S(t) = \begin{cases} 0, & \text{if } t < 50 \\ e^{-\eta_1 t}, & \text{if } 75 < t \leq 50, \\ e^{-\eta_2 t}, & \text{if } t \geq 75 \end{cases} \quad (38)$$

where: τ – the period of time from planting seedlings to the beginning of tying the head,

η_i – exponent coefficients ($\eta_1 = 0.09704$, $\eta_2 = 0.09623$).

Unknown coefficients k_i of growth functions of plant subsystems were determined by a statistical method based on the results of field experiments, the value was obtained: $k_1 = 0,0880$; $0,0825$; $0,0995$.

Nonlinear equations were employed to approximate the mean daily values of soil temperature, air temperature, and soil moisture.

We will now construct a mathematical model for the growth of Brussels sprouts based on the experimental data provided in Table 1, following the previously described algorithm. The next step involves estimating the model parameters using the experimental dataset (Table 2) and specifying the initial conditions (the dry weight values of plant subsystems at the time of seedling transplantation):

$$W_1(0) = 0,53$$

$$W_2(0) = 0,34$$

$$W_3(0) = 2,6$$

$$W_4(0) = 0$$

The optimal solution of the system of differential equations (36) will be at the values of the coefficients $a_{i,j}$ (Table 3):

Table 3

Values of model coefficients

i \ j		1	2	2	4
		Root	Stem	Leaf	Heads
1	Root	0,047	0,0041	0,0038	0,0083
2	Stem	0,015	0,675	0,0031	0,0134
3	Leaf	0,069	0,0078	0,064	0,036
4	Heads	0,35	0,27	0,43	0,00068

The simulation results are shown in Fig. 2.

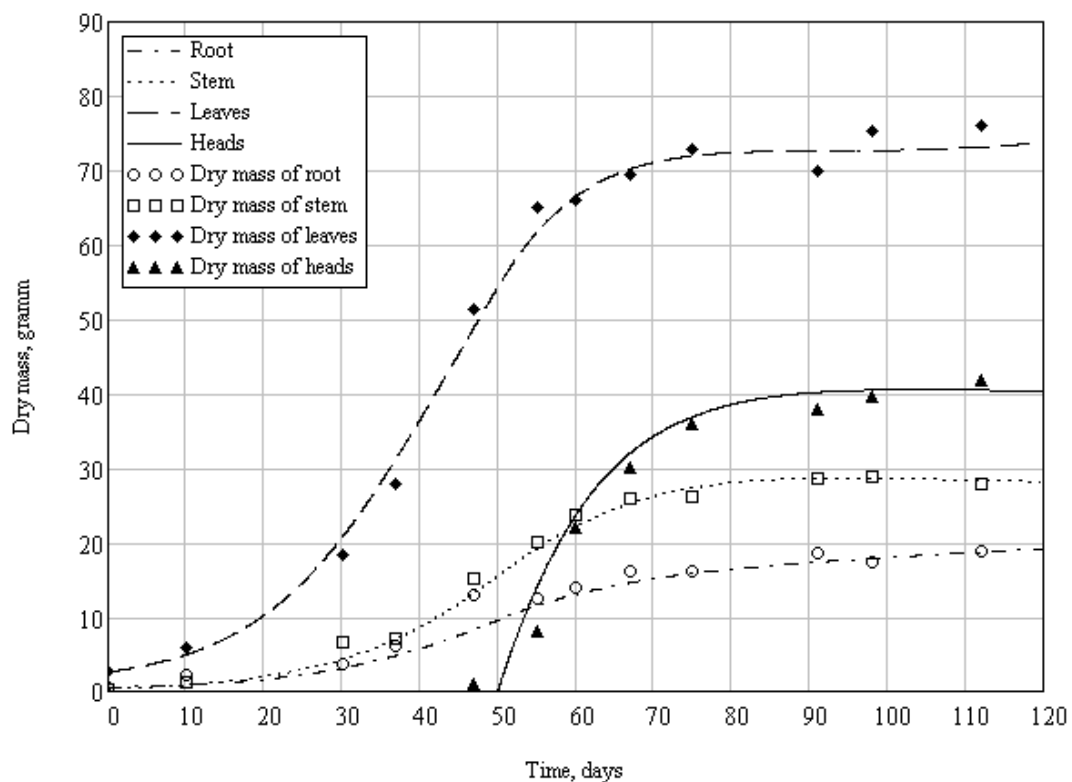


Fig.2. Dynamics of dry mass of Brussels sprouts

The developed model demonstrates significant sensitivity to parameter variation, enabling the simulation of plant growth. For instance, adjusting the coefficient a_{31} , which represents the rate of nutrient exchange between the leaf and root via the stem, from 0,069 to 0,076 results in a heavier head and a notable increase in leaf mass (Fig. 3). Further experimental testing is necessary to accurately quantify the actual impact of these coefficients on overall plant development.

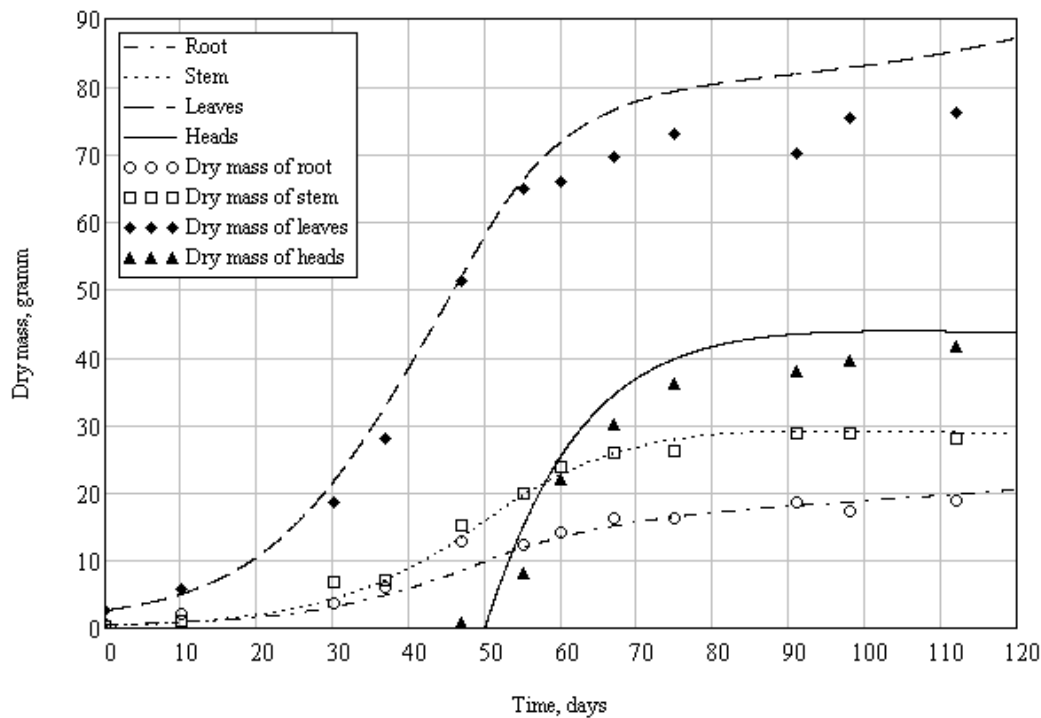


Fig. 3. The effect of changing parameters (the value of the coefficient of the model a_{31} changed from 0,069 to 0,076)

The creation of mathematical models for dynamic processes within the agro-industrial sector is pivotal. This modeling approach facilitates a detailed characterization of dynamic systems and enables computer-based process simulation. Such capabilities, in turn, accelerate the adoption of novel technologies, decrease the time needed for the design and refinement of new agricultural equipment and mechanisms, optimize crop growth, and ultimately lower the overall production cost of agricultural products. A primary benefit of this tool is its capacity to effectively convert empirical results from field experiments into a quantifiable digital format.

The presented mathematical model offers an accurate depiction of the plant development cycle. It allows for the investigation of how various external and internal parameters influence the growth process. These factors include, but are not limited to, irrigation levels, mulching practices, soil humidity, ambient temperature, light exposure, climatic variations, and the application of nutrients (fertilizers) and plant growth regulators.

Disadvantages of the mathematical model: the model is closed on itself; it requires a significant array of field experimental data; it is accompanied by cumbersome mathematical calculations.

Conclusions

The conducted study confirms the key role of mathematical modeling in agronomy and ecology. The considered models constitute a powerful analytical tool for quantitative assessment, prediction and optimization of complex biological and ecological processes. They allow to move from qualitative observations to quantitatively based decisions in the field of natural resource management and agricultural production.

The Leslie matrix model has demonstrated its effectiveness for analyzing the structure of populations (by age or stages of development) and predicting their long-term dynamics. It is an indispensable tool for assessing the impact of agrotechnical measures or environmental changes on the viability of populations, providing clear indicators such as growth rate and reproductive value.

The analysis of the Lotka-Volterra model emphasizes its fundamental importance for understanding species interactions (predator-prey, competition) in both natural ecosystems and agrocenoses. It provides a theoretical basis for studying the stability of ecological systems and developing integrated plant protection strategies that take into account the dynamics of natural enemies.

The logistic model of plant growth is the main tool for describing the S-shaped growth curve, which includes phases of acceleration, linear growth and saturation. Its use allows to estimate the yield potential and determine critical periods for fertilizer application or irrigation in agronomy.

The Gompertz model has been found to be particularly useful for describing growth, where maximum growth rate is reached early in the growth cycle and the deceleration is gradual. It often describes better than the logistic model the growth of fruits, plant organs or biomass accumulation, where the asymmetry of the curve is more pronounced.

The Chanter model, as an empirical model with practical application, is effective for predicting yield based on a limited number of parameters. Its advantage is its ease of use and sufficient accuracy for operational crop management.

The results of the monograph indicate the need for further development of hybrid and simulation models that integrate physiological knowledge such as the effects of temperature, moisture, nutrients with the considered classical dynamic approaches.

The main recommendation is to implement these mathematical models in decision support systems in agronomy and environmental monitoring. This will ensure the transition to precision agriculture and ecosystem management, minimizing environmental risks and maximizing production efficiency based on scientifically sound forecasts.

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