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THE LOGISTIC EQUATION IN POPULATION ECOLOGY AND EPIDEMIOLOGY

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Abstract: *In this paper we review the fundamental mathematical models in population biology and epidemiology, with particular emphasis placed on the exponential and logistic models. Exponential growth is described by the Malthusian model, in which unlimited resources are assumed, but environmental constraints are not taken into account. To overcome this limitation, the logistic equation was introduced by Verhulst, incorporating the concept of carrying capacity and providing a more realistic model of population dynamics. The logistic model is also applied in epidemiology, where it is used to describe the spread of infectious diseases.*

Keywords: *Malthusian exponential model, Verhulstian logistic model, allometry, epidemiology, mathematical models.*

INTRODUCTION

The ability to sustain growing populations under existing natural and economic conditions has been a fundamental issue throughout human history. In his book 'How Many People Can the Earth Support', published in 1995, Joel E. Cohen relies on two key assumptions. First, if the per capita growth rate remains constant and positive, the population grows exponentially, leading to the so-called "population explosion". Second, in the case of limited resources, the scale of this growth is controlled.

In population ecology, there are two main mathematical models – the exponential model of Malthus and the logistic model [1,2,3]. The exponential model is used to analyse populations in which all individuals develop independently, without environmental limitations and without competition for resources. Examples include assessing the growth rate of a parasite when it first enters the human bloodstream, analysing the initial spread of an infectious disease, calculating the degradation rate of a drug, or predicting the extinction rate of an endangered species.

Let us consider the following example. When cultivating bacteria in a petri dish, let the initial density be 10/ml, and the bacterial density doubles as a function of time. The exponential model describing this process is as follows

$$\frac{dx}{dt} = Cx,$$

where $x(t)$ is the bacterial density, and C is a constant. At the initial moment $x(0) = x_0$. After integrating the equation, we obtain

$$x(t) = x_0 e^{Ct}.$$

The constant C is determined from the condition that the density doubles in 20 hours, i.e. $x(20) = 2.x_0$. Thus $2.x_0 = x_0.e^{20.C}$, from which $\ln 2 = 20C$ and therefore

$$C = \frac{\ln 2}{20} \approx 0.0347\,.$$

In this way, the formula for the bacterial density as a function of time is

$$x(t) = 10\, e^{0.0347t} .$$

The exponential model assumes that the population increases or decreases at a constant rate, without accounting for limitations such as resource shortages or the presence of predators. In contrast, Verhulst's logistic model rakes into account that, in the long term, resources become depleted. As a result, when the population size approaches the environment's carrying capacity, its growth slows down.

LOGISTIC MODEL IN POPULATION ECOLOGY

The logistic model, introduced by Pierre-Francois Verhulst, is a modified exponential model in which an environmental limitation factor is added – the so-called carrying capacity K. The carrying capacity represents the maximum population size that the environment's resources can sustainably support. The logistic differential equation is as follows

$$\frac{dx}{dt} = = rx\left(1 - \frac{x}{K}\right), \tag{1}$$

where the constant r represents the intrinsic growth rate. When x is much smaller than K, the equation approaches the exponential model

$$\frac{dx}{dt} \approx rx.$$

In cases where $x \to K$, growth stops

$$\frac{dx}{dt} \approx 0.$$

The logistic differential equation can be solved by separating the variables and integrating as follows. From

$$\frac{dx}{x(K-x)} = \frac{r}{K} dt$$

and decomposing the left-hand side into two fractions

$$\frac{1}{x(K-x)} = \frac{1}{K}\left(\frac{1}{x} + \frac{1}{K-x}\right)$$

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it follows that

$$\int \frac{1}{x} dx + \int \frac{1}{K-x} dx = \int r\, dt + C_1$$

and

$$\ln \frac{x}{K-x} = rt + C_1 .$$

By transformation, the solution x(t) can be expressed in explicit from

$$x(t) = \frac{KC_2 e^{rt}}{1 + C_2 e^{rt}}.$$

From the initial condition $x(0) = x_0$, the constant C_2 is found

$$x_0 = \frac{KC_2}{1 + C_2} \quad \Rightarrow \quad C_2 = \frac{x_0}{K - x_0}$$

which gives

$$x(t) = \frac{Kx_0e^{rt}}{K + x_0(e^{rt} - 1)} = \frac{Kx_0}{x_0 + (K - x_0)e^{-rt}},$$

where x_0 is the initial population size. The final formula shows that if $0 < x_0 < K$, then $x(t) \to K$, as $t \to \infty$.

One of the conclusions that follow from the logistic equation is that limited resources constrain population growth. The logistic model predicts rapid initial growth, followed by stabilization around K. This corresponds to the actual behaviour of many biological populations and is used in demographic studies.

Let us consider the following example. If the population of Pacific halibut is modelled by a logistic equation in which the carrying capacity is 80,500 tons, the initial growth rate is 0.71 per year, and the initial fish population is one quarter of the carrying capacity, i.e. 20,125 tons, then after one year the halibut biomass will increase to 32,526 tons.

In biological science, there are many other laws that can be expressed mathematically. These include, for example, allometric laws. Allometry is a field that describes the proportion between body size and shape and studies the growth rate of one part of the body in comparison to other parts [4]. Let the *per capita* rates of two biological quantities $x(t)$ and $y(t)$ be proportional

$$\frac{1}{y}\frac{dy}{dt} = \alpha.\frac{1}{x}\frac{dx}{dt}.$$

The allometric law can be derived in its general form. By separating the variables in the above differential equation and integrating them term by term, we obtain successively

$$\frac{dy}{y} = \alpha.\frac{dx}{x} \iff \int\frac{dy}{y} = \alpha.\int\frac{dx}{x} + C \iff \ln y = \alpha.\ln x + C$$

Then the allometric law takes the form

$$y = K.x^{\alpha},$$

where y is the dependent variable, for example, the hight of the plant, and x is the independent variable, for example, the diameter of the stem. K is the proportionality coefficient, and α is the allometric coefficient, which defines the nature of the relationship between x and y.

Let us consider the following example. The metabolic rate MR is defined as the rate of energy expenditure per unit of time when the body is at rest. It is assumed that $MR = \rho.S$, where S is the surface area of an individual, and according to the allometric law $MR = K.W^{\alpha}$, where W is the body mass. For a spherical cow, the surface area is $S = 4\pi r^2$, and its volume is $V = \frac{4}{3}\pi r^3$, therefore $S = (36\pi)^{1/3}V^{2/3}$. Since the body mass W is proportional to the volume V, it follows that

$$MR = k_sW^{2/3}.$$

For a cubic cow, from $S = 6\,V^{2/3}$, in an analogous way as above, it follows that

$$MR = k_cW^{2/3}.$$

This shows that the allometric coefficient $\alpha = 2/3$ is the same in both cases. Furthermore,

$$k_s/k_c = \left(\frac{\pi}{6}\right)^{1/3}.$$

LOGISTIC EQUATION IN EPIDEMIOLOGY

The logistic equation in epidemiology describes the spread of an infectious disease within a limited population. The model assumes that, at the beginning, the number of infected individuals grows exponentially, and over time this growth slows due to the decreasing number of susceptible to diseases without long-term immune protection, in which recovered individuals become susceptible to the infection again.

The model involves the number of susceptible individuals $S\ (t)$ and infected individuals $I(t)$, with the total population size given by $N(t) = S(t) + I(t)$. The system of differential equations is

$$\frac{dS}{dt} = \Lambda - \beta \frac{S(t).I(t)}{N(t)} - \mu S + \gamma I$$

$$\frac{dI}{dt} = \frac{S(t).I(t)}{N(t)} - (\mu + \gamma)I \tag{2}$$

where Λ is the rate of new individuals entering the population, μ represents the mortality/emigration rate from the population, β reflects the level of infectiousness (called the infection rate and related to the law of mass action), and γ is the rate of recovery from the infection.

From the above system, a differential equation for the total population size N can be derived. From

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt}$$

it follows that

$$\frac{dN}{dt} = \left(\Lambda - \beta \frac{S(t).I(t)}{N(t)} - \mu S + \gamma I\right) + \left(\beta \frac{S(t).I(t)}{N(t)} - (\mu + \gamma)I\right)$$

which is equivalent to the linear differential equation

$$\frac{dN}{dt} + \mu N = \Lambda\,.$$

From the formula for the general solution of $y'(x) + p(x)y(x) = q(x)$,

$$y(x) = e^{-\int p(x)dx}\left(C + \int q(x)e^{\int p(x)dx}\,dx\right)$$

[5], the function $N(t)$ takes the form

$$N(t) = e^{-\int \mu dt}\left(C + \int \Lambda.e^{\int \mu dt}\,dt\right) = Ce^{-\mu t} + K$$

where $K = \frac{\Lambda}{\mu}$, and the constant C is determined from the initial condition $N(0) = N_0$.

$$N(0) = K + C.e^{0} \quad \Leftrightarrow \quad C = N(0) - K.$$

Thus

$$N(t) = K - \big(K - N(0)\big)e^{-\mu t}$$

where K is the equilibrium value toward which $N(t)$ approaches over time

$$\lim_{t\to\infty} N(t) = \lim_{t\to\infty}\left(K - \big(K - N(0)\big)e^{-\mu t}\right) = K$$

A MATLAB code has been written to visualize the solution of the equation, Figure 1. The following initial values and coefficients were used: $N(0) = 700$; $K = 1000$; $\mu = 0.1$; $t \in [0, 100]$.

The formula above shows that, regardless of the initial value $N(0)$, over time the total population $N(t)$ will tend toward the equilibrium level K, which depends only on the parameters Λ and μ.

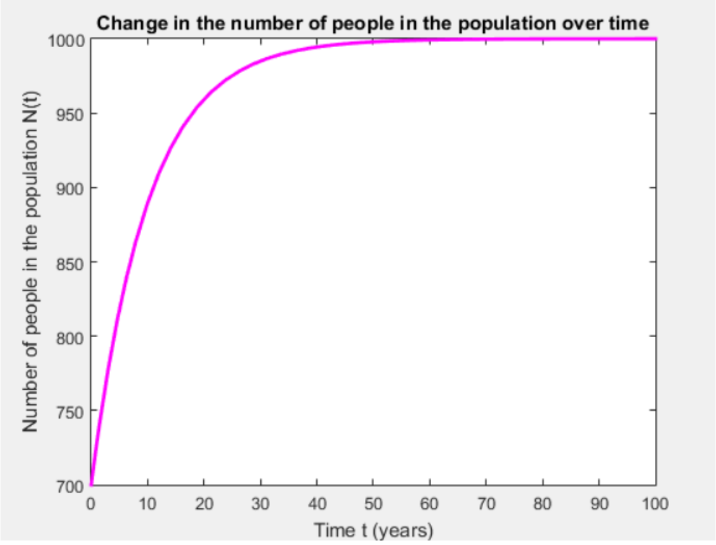

Figure 1. The solution $N(t) = K - \big(K - N(0)\big)e^{-\mu t}$ as a function of time

By using $S(t) = N(t) - I(t)$, $S(t)$ can be eliminated from equation (2). After substitution, the new equation for $I(t)$ is

$$\frac{dI}{dt} = \beta\frac{\big(N(t) - I(t)\big).I(t)}{N(t)} - (\mu + \gamma)I(t). \tag{3}$$

Since $N(t) \to K$ as $t \to \infty$, in equation (3) one can formally replace $N(t)$ with K, thus deriving the asymptotic equation

$$\frac{dI}{dt} = \beta\frac{(K - I).I}{K} - (\mu + \gamma)I. \tag{4}$$

Equation (4) is a logistic equation. Indeed, (4) is equivalent to

$$\frac{dI}{dt} = \big(\beta - (\mu + \gamma)\big)\,I - I\frac{\beta I}{K}$$

or

$$\frac{dI}{dt} = \big(\beta - (\mu + \gamma)\big)\,I\left(1 - \frac{\beta I}{\big(\beta - (\mu + \gamma)\big)K}\right)$$

or

$$\frac{dI}{dt} = \beta\left(1 - \frac{1}{R_0}\right) I \left(1 - \frac{I}{\left(1 - \frac{1}{R_0}\right) K}\right)$$

where $R_0 = \beta/(\mu + \gamma)$. The last equation matches the logistic equation (1), in which intrinsic growth rate is $\beta(1 - 1/R_0)$, and the carrying capacity is $\left(1 - \frac{1}{R_0}\right) K$. The number $R_0 = \beta/(\mu + \gamma)$ is called the basic reproductive number in epidemiology. If $R_0 > 1$, then the intrinsic growth rate $\beta(1 - 1/R_0) > 0$, and the epidemic spreads, with the number of infected individuals approaching $\left(1 - \frac{1}{R_0}\right) K$. However, if $R_0 < 1$, the disease fades away and disappears.

The above conclusions were derived using the asymptotic equation (4). To compare the results of the asymptotic equation (4) with the actual equation (3) of the system of differential equation, a MATLAB code was written using the following values for the initial conditions and parameters: $K = 1000,\ S_0 = 690,\ I_0 = 10,\ \mu = 0.1,\ \gamma = 0.25,\ \beta = 0.5,\ \Lambda = 100.$

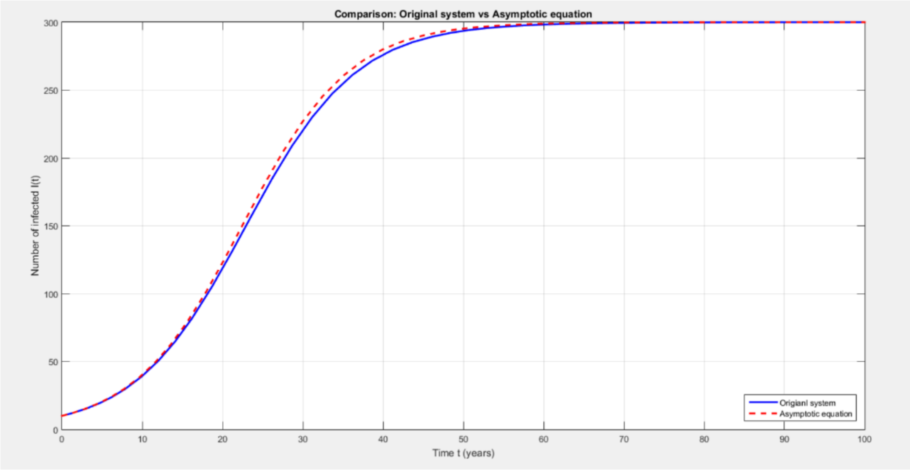

Figure 2. Numerical solutions for $I(t)$, obtained using the actual equation (3) of the system of differential equations and the asymptotic equation (4)

Figure 2 represents a numerical simulation of the number of infected individuals over time. The blue line represents the solutions of the original system for the population $N(t)$, while the red dashed line shows the solutions of the asymptotic equation, where it is assumed that $N(t) \to K$, and therefore $S(t) \approx K - I(t)$. The result shows a high degree of agreement between the two models.

Table 1. Numerical comparison between the original model and the asymptotic approximation of $I(t)$

t (years)	$I_{orig}(t)$	$I_{asymp}(t)$
10	39.35	40.33
20	118.80	122.90
50	293.61	295.27
60	298.31	298.93
100	299.98	299.99

From the table, it can be seen that at $t = 10$ there is a difference between the values of the two models. As time progresses, the values converge significantly, confirming the validity of the asymptotic model as a good approximation. The equilibrium value of the number of infected individuals is approximately $I^* \approx 300$, as observed in Figure 2 in both models. This value can also be calculated analytically. To do so, it is necessary to analyse the cases in which the right-hand side of the equation

$$\frac{dI}{dt} = I[\beta(1 - I/K) - (\mu + \gamma)]$$

is equal to 0. In the first case $I = 0$ corresponds to a state with no infection in the population. The other case is $\beta(1 - I/K) - (\mu + \gamma) = 0$. After rearranging, the equation takes the form

$$I^* = K\left(1 - \frac{\mu + \gamma}{\beta}\right).$$

After substituting the values used in MATLAB, we obtain

$$I^* = 1000(1 - 0.35/0.5) = 300$$

which is also observed in Figure 2.

CONCLUSION

In the first part of this work, two fundamental models in population dynamics were examined – the exponential and the logistic models – which are biologically grounded and from which a number of conclusions were derived. In the second part of the work, an epidemiological model was analysed, presented as a dynamic system concerning of already infected individuals in a given population. By substituting the total number of individuals in the population with its limiting value, an asymptotic equation for the number of infected individuals was derived, which is a logistic equation. The presentation is rich in examples, including numerical simulation that confirm the theoretical conclusions made.

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