

## Processes in nature - student modelling and simulation using mathematics and MATLAB

D. Schott

Hochschule Wismar - University of Applied Sciences Technology, Business and Design  
Wismar, Germany

**ABSTRACT:** Mathematics is at the heart of scientific knowledge. Besides, many findings and discoveries in all fields are based on data, models and computer simulations of real processes. The tool, MATLAB, is useful for implementing the necessary mathematical procedures. It is an important trend in modern teaching to bring all the aspects of the learning process together. So, a lot of interesting projects arise. Teachers and students are especially motivated to solve the corresponding problems and to present their results. This paper is a contribution in this direction. The dynamics of separate or interacting populations are studied. Further, the spreading of diseases is discussed. Simple, well-known models are used to interpret the mathematical results and to derive consequences. This paper contains many suggestions for further studies.

### MODELLING, SIMULATION AND MATHEMATICS

Modelling is a powerful scientific tool producing knowledge about nature and technology. Generally, a model in science grasps a whole class of phenomena by introducing *parameters*. Adapting these parameters to concrete systems can be used to study the behaviour of a system and to compare it with the actual behaviour. The results can be easily reproduced. Changing these parameters shows the influence of the magnitude of these parameters and the stability of the system. Often, unwanted effects in the system can be overcome by external control. In addition, virtual systems can be considered, which do not exist but which could be created in the future.

Modelling considerably saves costs. But there is a gap between models of systems and real systems. Therefore, one must be cautious about drawing hasty conclusions. A strict validation of a model's results is necessary to avoid unpleasant surprises. A comparison with real system results should be included.

Modelling is a control process. Starting with very simple models that can be refined step by step, the degree of coincidence with real systems increases more and more. So a *hierarchy* of models arises, with sophisticated models at the top. Sometimes, competing models with a similar level of complexity are developed. At the beginning, often *descriptive models* are used for the system behaviour without giving causes for the behaviour. Later, *causal models* replace them, based on some theory about the system. In this process students learn about the value and hierarchy of models.

Complex systems are described by mathematical models consisting of a system of equations and conditions. For processes, there are mostly systems of differential equations and initial conditions. Since the mathematical model does not contain specific properties limited to the field of application any more, it often has many applications in quite different fields. Beside high precision, it is the essential power of mathematics to reveal common qualitative properties of phenomena in various fields. It is remarkable that some of the considered population models lead to similar systems of differential equations and to similar qualitative behaviour as certain oscillator systems in engineering (see e.g. [4]). For complex systems, computer software is needed to simulate the model behaviour. The matrix laboratory, MATLAB, is a suitable tool for symbolic or numerical solutions and for graphical representations.

Nature is very complex. Sometimes, it seems to be rather static, but in the background, highly dynamical processes run. Fortunately, they are often balanced (stable steady-states). In other cases, the processes are periodic. Nevertheless, the influences of outer space, inner processes of the Earth, of human beings and other populations can end in dangerous situations or catastrophes. So, it is very important to model certain environments on Earth predicting the future development or weighing and rating possible alternatives. Students should gain knowledge about the interplay of modelling, mathematics and software tools in investigating biological or biomedical systems.

Starting with different kinds of growth processes and their modelling (for example, exponential or logistic growth) models for one or more interacting species can have several steady-states. Their meaning and stability is discussed. Models for interacting populations are considered (predator-prey models, competition models). Further, infection models (SI, SIS, and SIR) are outlined and studied.

## SINGLE SPECIES

If the size of a population is large enough, it can be modelled by a continuous function  $x = x(t) \geq 0$  varying in time  $t$ . Often, it can be assumed that the velocity of change in a population is proportional to its size:

$$x' = g(x) = a(x) \cdot x.$$

Here  $a(x)$  is the *net reproduction rate* (per capita) of the population (species or subspecies). The initial value  $x(0) = x_0$  must be known to determine  $x(t)$  uniquely. This approach is flexible enough to consider also declining resources (food or space) for increasing populations. Mathematical investigation shows, that the *steady-states*  $x_s$ , satisfying  $g(x_s) = 0$ , are stable for  $g'(x_s) < 0$  and unstable for  $g'(x_s) > 0$ , at least locally. If the rate  $a$  does not depend on the size of population  $x$ , then *natural growth* arises:

$$x'(t) = a \cdot x(t), \quad a > 0, \quad x(0) = x_0 > 0 \quad \Rightarrow \quad x(t) = x_0 \cdot e^{at}. \quad (1)$$

The population number  $x$  increases exponentially in time. This is only the case, if the resources are unbounded. Nevertheless, populations often grow in such a way in short periods of development.

For  $a < 0$  the given solution is also true. But, then, an exponential decline is obtained. A population without any food resources would follow this law. But here, one must recognise a gap between model and reality. While  $x(t)$  tends to 0 without reaching 0 the population would die out after a finite time.

A simple idea introduced by Verhulst in the 19<sup>th</sup> Century is to model limited resources by *logistic growth*:

$$x'(t) = a \cdot x(t) - b \cdot x^2(t) = \frac{a}{C} \cdot (C - x(t)) \cdot x(t), \quad a > 0, \quad b > 0, \quad x(0) = x_0 > 0, \quad C = \frac{a}{b}. \quad (2)$$

Here  $C$  measures the total *capacity* of the environment. A simple calculation shows that the population size is given by:

$$x(t) = \frac{C \cdot x_0 \cdot e^{at}}{C + x_0 \cdot (e^{at} - 1)} = \frac{C \cdot x_0}{x_0 + (C - x_0) \cdot e^{-at}}.$$

The limit of  $x$  is  $C$  as  $t$  tends to infinity. There are three cases. For  $x_0 = C$  the population is a constant  $C$ . If  $x_0 > C$ , the initial population is too large for the resources:  $x(t)$  monotonically decreases to  $C$ . If  $x_0 < C$ , the resources allow bounded growth,  $x(t)$  monotonically increases to  $C$ . The curve has the well-known sigmoid form (see Figure 1). Starting with slow growth, the velocity increases to the maximum when half of the capacity  $C$  is reached. Then, at the turning point of the curve, a growth drop happens and the growth becomes slower and slower. There are two steady-states, namely  $x_s = 0$ , which is unstable and not interesting, and  $x_s = C$ , which is stable and therefore attracting.

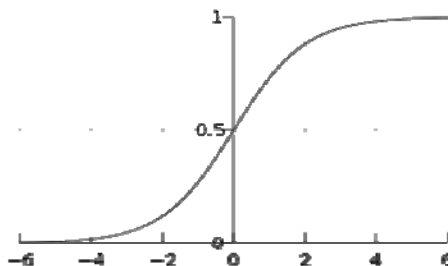


Figure 1: Standardised logistic function.

For a qualitative study, it is useful to introduce non-dimensional quantities. So, a whole class of models is standardised by a model where units are of no importance and the number of parameters is reduced. A disadvantage is that the solution ranges need not be realistic. Here we introduce:

$$T = a \cdot t, \quad X(T) = \frac{b}{a} \cdot x(t) = \frac{x(t)}{C}, \quad X_0 = \frac{x_0}{C} .$$

Then, we obtain:

$$X' = \frac{dX}{dT} = (1 - X) \cdot X, \quad X = X(T) = \frac{X_0}{X_0 + (1 - X_0) \cdot e^{-T}} .$$

Despite the simplicity of the logistic approach it has some features which distinguish real populations. There are many possible ways to modify this approach; for example, generalised logistic growth, logistic growth with time delay or combined with the influence of predation of another population. Then time arguments are changed or certain terms are added in Equation (2) (see [3: p. 7-17]).

## INTERACTION OF TWO SPECIES

The general model of one species can be extended to two or more species living in the same environment. Denoting the sizes of populations 1 and 2 by  $x_1 = x_1(t) \geq 0$  and  $x_2 = x_2(t) \geq 0$ , respectively, the model equations are:

$$x_1' = g_1(x_1, x_2) = a_1(x_1, x_2) \cdot x_1, \quad x_2' = g_2(x_1, x_2) = a_2(x_1, x_2) \cdot x_2 .$$

Here  $a_1 = a_1(x_1, x_2)$  and  $a_2 = a_2(x_1, x_2)$  are the reproduction rates. The initial sizes are denoted by  $x_1(0) = x_{10}$  and  $x_2(0) = x_{20}$ . The steady-states  $x_{1s}$  and  $x_{2s}$  satisfy the equations:

$$g_1(x_1, x_2) = 0, \quad g_2(x_1, x_2) = 0 .$$

It can be assumed that there is a so-called first integral  $P(x_1, x_2) = K$  with a constant  $K$ , relating the population sizes to each other without containing the time  $t$  explicitly. Geometrically, it represents a family of *trajectories* or *phase curves* in the  $x_1 - x_2$  coordinate system, where  $K = P(x_{10}, x_{20})$  is determined by the initial values. But the phases provide no information about the velocity of traversal. In reality, only those models are relevant where the phase curves and the steady states lie in the positive quadrant.

A simple model again arises following the logistic approach. For  $a_i$  affine linear expressions in  $x_i$  ( $i=1,2$ ) were chosen:

$$x_1' = (a_1 + b_1 \cdot x_1 + c_1 \cdot x_2) \cdot x_1, \quad x_2' = (a_2 + b_2 \cdot x_2 + c_2 \cdot x_1) \cdot x_2 . \quad (3)$$

This is the well-known model class of Lotka-Volterra.

Steady-states can be on the axes ( $x_1 = 0$  or  $x_2 = 0$ ) or positive solutions of the linear system:

$$a_1 + b_1 \cdot x_1 + c_1 \cdot x_2 = 0, \quad a_2 + b_2 \cdot x_2 + c_2 \cdot x_1 = 0 .$$

A unique solution exists if  $D = b_1 \cdot b_2 - c_1 \cdot c_2 \neq 0$ , namely:

$$x_{1s} = \frac{a_2 \cdot c_1 - a_1 \cdot b_2}{D}, \quad x_{2s} = \frac{a_1 \cdot c_2 - a_2 \cdot b_1}{D} .$$

Let the constants be arbitrary. First  $c_1 = c_2 = 0$  is assumed. Then, there are two separate populations without any interaction. If  $a_1 \neq 0$  and  $a_2 \neq 0$ , then depending on the sign of  $a_i$  the two populations grow exponentially or vanish exponentially. For  $a_i > 0$  and  $b_i < 0$  ( $i=1,2$ ) both populations grow logistically. Again, non-dimensional quantities can be introduced to simplify theoretical considerations. But the author will not elaborate this aspect in this discussion.

## Predator-Prey Model With Unbounded Capacity

Now, two populations are considered where the first lives on food readily available in the environment, and the second lives on consuming the first without other growth limitations. So, there is a *prey* Population 1 and a *predator* Population 2. Intuitively, oscillations of the two populations are expected. If there are only a few predators, the prey will increase. Then, the predators, having enough food, reduce the number of prey and will themselves increase. But, if their number becomes too great, there is not enough prey as food. Hence, the predators are reduced, and so on. Some simple assumptions are made for modelling. Put  $a_1 = \alpha_1 > 0$ ,  $b_1 = 0$  and  $a_2 = -\alpha_2 < 0$ ,  $b_2 = 0$ . Population 1 grows

exponentially, and Population 2 declines exponentially to die out, if there is no interaction between them ( $c_1 = c_2 = 0$ ). If the populations interact the number of meetings between prey and predators, as well as the number of sacrifices in the prey population should be proportional to both  $x_1$  and  $x_2$ . These meetings are on the whole losses for prey (*loss rate*  $c_1 = -\gamma_1 < 0$ ) and profits for predators (*profit rate*  $c_2 = \gamma_2 > 0$ ). Hence, we obtain:

$$x_1' = \alpha_1 \cdot x_1 - \gamma_1 \cdot x_1 \cdot x_2, \quad x_2' = -\alpha_2 \cdot x_2 + \gamma_2 \cdot x_1 \cdot x_2. \quad (3a)$$

This classical case is rather unrealistic but has some important consequences, which can be observed in real populations (for example, food fishes and sharks, rabbits and foxes or lynxes, beetles and scale insects). Therefore, it is the starting point for more sophisticated predator-prey models.

The solutions must be calculated numerically, but a first integral relating the populations to each other can be given analytically:

$$P(x_1, x_2) = \gamma_2 \cdot x_1 + \gamma_1 \cdot x_2 - \ln x_1^{\alpha_2} x_2^{\alpha_1} = \gamma_2 \cdot x_1 - \alpha_2 \cdot \ln x_1 + \gamma_1 \cdot x_2 - \alpha_1 \cdot \ln x_2 = K = P(x_{10}, x_{20}).$$

Now, the parameters are fixed. Geometrically, this is a family of bounded and closed phase curves in the first quadrant ( $x_1 > 0, x_2 > 0$ ) showing that the process is periodic. The curves are involved with each other for decreasing  $K$ . The direction of time flow is anti-clockwise (see Figure 2).

There are two steady-states, namely the unstable saddle point  $(0, 0)$  and the stable centre point:

$$(x_{1s}, x_{2s}) = \left( \frac{\alpha_2}{\gamma_2}, \frac{\alpha_1}{\gamma_1} \right).$$

The latter point is a degenerated phase curve with  $P(x_{1s}, x_{2s}) = P_{\min}(x_1, x_2)$  and lies in the centre of the whole family, marking also the mean values in time. Both populations coexist. The time functions of population numbers oscillate periodically with a certain shift to each other. The predator population follows the prey population. Important characteristics are the time period and the extremes  $x_{i,\min}$  and  $x_{i,\max}$  ( $i=1, 2$ ), which determine also the *amplitudes* of oscillation. The parameters influence the phase shape and the time period. This correlation can be investigated by experiment.

Figure 2 shows also a weakness of the modelling process: if it is running on a phase curve near the axes, then small perturbations can shift it to other curves with quite different amplitudes.

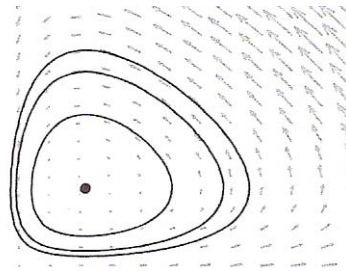


Figure 2: Phase portrait of predator-prey model with unbounded capacity.

#### Predator-Prey Model With Bounded Capacity

By including additionally the logistic terms  $b_i = -\beta_i < 0$  ( $i=1, 2$ ), we obtain:

$$x_1' = \alpha_1 \cdot x_1 - \beta_1 \cdot x_1^2 - \gamma_1 \cdot x_1 \cdot x_2, \quad x_2' = -\alpha_2 \cdot x_2 - \beta_2 \cdot x_2^2 + \gamma_2 \cdot x_1 \cdot x_2.$$

So, each population is assumed to have a limited capacity. The stable steady-state:

$$P_s = (x_{1s}, x_{2s}) = \left( \frac{\alpha_1 \cdot \beta_2 + \alpha_2 \cdot \gamma_1}{\beta_1 \cdot \beta_2 + \gamma_1 \cdot \gamma_2}, \frac{\alpha_1 \cdot \gamma_2 - \alpha_2 \cdot \beta_1}{\beta_1 \cdot \beta_2 + \gamma_1 \cdot \gamma_2} \right)$$

lies in the positive quadrant for  $\alpha_1 \cdot \gamma_2 > \alpha_2 \cdot \beta_1$ . The stability can be shown by the Lyapunov function:

$$L(x_1, x_2) = \gamma_2 \cdot (x_1 - x_{1s} \cdot \ln x_1) + \gamma_1 \cdot (x_2 - x_{2s} \cdot \ln x_2),$$

which defines the distance of points from the steady state  $P_s$ . The phases are spirals in the positive quadrant tending to  $P_s$ . The population sizes  $x_1 = x_1(t)$  and  $x_2 = x_2(t)$  oscillate in a damped manner around the steady states  $x_{1s}$  and  $x_{2s}$ , respectively. Sooner or later, a constant mixture of the two populations appears.

### Model for Two Competing Populations

Now, assume logistic growth of two populations and additionally losses by competition for common food or space resources in the environment. Put:

$$a_i = \alpha_i > 0, \quad b_i = -\beta_i < 0, \quad c_i = -\gamma_i < 0 \quad (i=1,2)$$

in the general Lotka-Volterra model (3) to obtain the equations:

$$x_1' = \alpha_1 \cdot x_1 - \beta_1 \cdot x_1^2 - \gamma_1 \cdot x_1 \cdot x_2, \quad x_2' = \alpha_2 \cdot x_2 - \beta_2 \cdot x_2^2 - \gamma_2 \cdot x_1 \cdot x_2. \quad (3b)$$

Under the assumption  $D = \beta_1 \cdot \beta_2 - \gamma_1 \cdot \gamma_2 \neq 0$ , there are four steady states, namely:

$$(0,0), \quad \left(0, \frac{\alpha_2}{\beta_2}\right), \quad \left(\frac{\alpha_1}{\beta_1}, 0\right), \quad P_s = (x_{1s}, x_{2s}) = \left(\frac{\alpha_1 \cdot \beta_2 - \alpha_2 \cdot \gamma_1}{D}, \frac{\alpha_2 \cdot \beta_1 - \alpha_1 \cdot \gamma_2}{D}\right).$$

The first three are on the axes. The fourth  $P_s$  is of special interest. The product  $\beta_1 \cdot \beta_2$  is a measure of *inhibition*, while the product  $\gamma_1 \cdot \gamma_2$  is a measure of *competition*. For  $D > 0$  inhibition dominates. An analysis shows that the point  $P_s$  is a nodal sink. Therefore, the two populations coexist peacefully tending to a fixed proportion. For  $D < 0$  competition is dominant. Then  $P_s$  is an unstable saddle point, whereas the other two nonzero steady states are stable nodal sinks. A *separatrix* divides the positive quadrant into two regions, each containing phases tending to the nearest sink. The populations cannot coexist. One population dies out, namely the population with the worst initial conditions. For theory and examples see Edwards et al [2: p. 544 f.].

### Models for More Than Two Populations

If there are several predator and prey populations, then they are reduced earlier or later to two populations, namely the strongest predators and the most resistant prey. If there are several competing populations, in many cases, only one population survives after some time. In some special cases, more than one can coexist. But the chance that many such populations survive is low. The various cases can be investigated by computer experiments and compared with real situations. If enough data are available, some assertions can be made. At the end of this process, one can look for a mathematical theory giving conditions for a balanced coexistence of different species. This is a true challenge for students to show power and creativity.

### SPREADING OF DISEASES

It is assumed that the number of people (or animals) in a relatively closed community is a constant  $K > 0$  at the beginning, and in the near future. One starts with the simplest model for the spreading of a single disease.

#### SI Model

The people are divided into two classes. There are healthy but *susceptible individuals* and *infectious individuals*, which cannot recover. Denoting the size of the first by  $x_1 = x_1(t)$  and the size of the second by  $x_2 = x_2(t)$  it is obtained:

$$x_1 \geq 0, \quad x_2 \geq 0, \quad x_1 + x_2 = K, \quad x_1' + x_2' = 0.$$

Obviously, the spreading velocity of disease is dependent on both, the number of infectious and the number of susceptible individuals. Simple proportionality is supposed, with an interaction factor  $c > 0$ , the *infection rate*. Observing the constraints, the decrease rate of healthy people is as a consequence:

$$x_1' = -c \cdot x_1 \cdot x_2, \quad x_2' = c \cdot x_1 \cdot x_2. \quad (4a)$$

Therefore,  $x_1$  is known if  $x_2$  is determined. Replacing  $x_1$  in the second equation gives:

$$x_2' = c \cdot (K - x_2) \cdot x_2 = a_2 \cdot x_2 - b_2 \cdot x_2^2.$$

This is a logistic growth equation with capacity  $C = K$  for  $x_2$ . Assuming  $0 < x_{20} < K$ , the disease infects sooner or later all people of the community, independently of the initial conditions. This is typical of *epidemics*.

### SIS Model

Again, there are two classes of *susceptible individuals* and *infectious individuals*. Thus, the constraints of the SI model are valid too. But more realistically, it is now supposed that ill people can recover. Introducing, apart from  $c > 0$ , a *rate of recovery*  $d > 0$ , the equations considered are:

$$x_1' = -c \cdot x_1 \cdot x_2 + d \cdot x_2, \quad x_2' = c \cdot x_1 \cdot x_2 - d \cdot x_2. \quad (4b)$$

Replacing  $x_1$  in the second equation supplies:

$$x_2' = c \cdot (K - x_2) \cdot x_2 - d \cdot x_2 = (c \cdot K - d) \cdot x_2 - d \cdot x_2^2.$$

If the parameters satisfy  $c > d$  and  $\frac{d}{c} < K < \frac{d}{c-d}$ , then  $a = c \cdot K - d > 0$  and  $C = \frac{a}{d} < K$ . This is again a logistic equation with limit capacity  $C$  for  $x_2$ . The sizes of the two classes tend to the steady-state  $(C, K - C)$ . If  $C > K$  all people become ill. For  $c < d$  the disease dies out.

### SIR Model

Now, consider that immunisation is possible. Three classes of people are introduced, namely susceptible, infectious and resistant individuals with sizes  $x_1 = x_1(t)$ ,  $x_2 = x_2(t)$  and  $x_3 = x_3(t)$ . This means:

$$x_1 \geq 0, \quad x_2 \geq 0, \quad x_3 \geq 0, \quad x_1 + x_2 + x_3 = K, \quad x_1' + x_2' + x_3' = 0.$$

The rate of recovery contributes positively to the resistant (and negatively to the infectious) individuals. The equations, due originally to Kermack and McKendrick in the 1930s, read:

$$x_1' = -c \cdot x_1 \cdot x_2, \quad x_2' = c \cdot x_1 \cdot x_2 - d \cdot x_2, \quad x_3' = d \cdot x_2 \quad (c > 0, d > 0). \quad (4c)$$

The first two equations do not contain  $x_3$ . They can be treated separately, and fit into the model class of Lotka-Volterra. The size  $x_3$  can be easily determined by the third equation. There are two steady-states, namely  $(0, 0)$  and  $(\sigma, 0)$  where  $\sigma = \frac{d}{c}$  is the *relative rate of recovery*. The first is unstable. The second is stable. The phases depending on the initial values have the explicit form:

$$x_2 = f(x_1) = x_{10} + x_{20} - x_1 + \sigma \cdot (\ln x_1 - \ln x_{10}), \quad x_{10} + x_{20} < K.$$

They are concave, having a common maximum  $x_{2m}$  at  $x_1 = \sigma$  and zeros  $x_{11}$  in  $(0, \sigma)$  and  $x_{12}$  in  $(\sigma, K)$ . Because of  $x_1' < 0$ , the phases are traversed backwards (from right to left). This has simple consequences. First: part of the people will not be infected. Second: there is a threshold  $\sigma$ : a) For  $x_{10} \leq \sigma$  both  $x_1$  and  $x_2$  decrease monotonically, the first to  $x_{1z}$  and the second to 0. The disease will die out rapidly; b) For  $x_{10} > \sigma$  again  $x_1$  decreases monotonically to  $x_{1z}$ , but  $x_2$  first increases to the maximum  $x_{2m}$  and decreases only afterwards to 0. The disease will become first an epidemic. If the number of susceptible individuals is small enough, the disease has lost power, and will die out after some time. Hence, the number  $\sigma$  is very important. If it is large enough, the danger of epidemic is low. This threshold number can be increased by appropriate health care.

### Soper Model

The disease, *measles*, is known for repeated fluctuations with varying power. In the 1930s, Soper introduced the following modelling equations:

$$x_1' = -c \cdot x_1 \cdot x_2 + e, \quad x_2' = c \cdot x_1 \cdot x_2 - d \cdot x_2, \quad x_3' = d \cdot x_2 - e \quad (c > 0, d > 0, e > 0). \quad (4d)$$

This is an extension of the SIR model. Considering again the first two equations, there is only one steady-state, namely:

$$(x_{1s}, x_{2s}) = \left( \frac{d}{c}, \frac{e}{d} \right).$$

An analysis shows that this state is stable. Further, both  $x_1$  and  $x_2$  oscillate in a damped manner around  $x_{1s}$  and  $x_{2s}$ , respectively. This model of measles is not very realistic. Further attempts to improve the model were also not very successful. Replacing the constant Soper term  $e$  by the variable term  $e \cdot x_1$ , the predator-prey model (3a) of Lotka-Volterra arises, where  $x_1$  plays the part of prey and  $x_2$  the part of predator. Here, there is true periodicity. All these models are not complex enough to explain certain features of measles.

## EXPERIMENTS AND PARAMETER ESTIMATION

Results for the following example of predator-prey Equations (3a) are given in Edwards et al [2: p. 544], where the time is in months:

$$\alpha_1 = 0.2, \gamma_1 = 0.005; \quad \alpha_2 = 0.5, \gamma_2 = 0.01; \quad x_{10} = 70, x_{20} = 40; \quad t_a = 0, t_b = 50.$$

They can be reproduced using MATLAB. The script file with several inputs calls the function file containing the differential equations (3a) with special parameter values. Then, it calculates the solution and supplies the phase curve.

```
% MATLAB function file lotka.m
function xd = lotka(t,x) % d: time derivative
xd = zeros(2,1);
xd = [(0.2 - 0.005*x(2))*x(1); (-0.5 + 0.01*x(1))*x(2)]; % Lotka-Volterra equations

% MATLAB script file lotkasol.m
ta = 0; tb = 50; % time interval (in months)
x10 = 70; x20 = 40; % initial populations
[t,x] = ode45('lotka',[ta,tb],[x10,x20],odeset('RelTol',1e-6)); % call of function file and calculation by ode45
plot(x(:,1),x(:,2)), xlabel('prey'), ylabel('predators') % plot of phase curve
```

The stable steady-state is (50, 40). Population 1 (prey) oscillates between 33 and 72; Population 2 (predators) between 20 and 70. The time period is slightly over 20 (months). It is not difficult to generalise these files in such a way that all models of the paper can be calculated.

To apply the results of the discussed models to real situations, realistic values of the parameters are required. The parameters must be estimated on the basis of real data. Using the method of least squares, minimising the sum of the squared residuals between the theoretical results and the given data, parameters can be fitted to the data in an optimal way. For the SIR model this is described in Chen et al [1].

## CONCLUSIONS

Students are especially motivated by using mathematical methods to gain new insights into nature and to solve practical problems. Therefore, projects are very interesting where processes in nature are modelled and simulated by mathematics. It is important to start with simple models. Following that, a hierarchy of models can be developed, depending on the level of the students.

Some features of real situations can be explained rather well, even surprisingly well, by simple models. Moreover, these simple models provide hints for reasonable strategies to control the corresponding real systems. Very sophisticated models are needed to understand and to control real systems with higher accuracy. Often, many populations are involved. The growth rates and interactions are more complicated than those discussed here. Such models often put high demands on computers and software. Thus, it is an interesting field of research.

The solutions (populations) develop within certain parameter ranges without qualitative changes. But, sometimes, there are critical parameters where small changes lead to quite different states. In chaotic systems no prediction of the behaviour is possible. Mathematics is needed. Without good modelling and without good mathematics nothing is possible. Complex models are simulated using computers and up-to-date numerical solution methods.

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