

Complex eco-biological systems modeling

Timofey Burak, Marina Lukashevich

Abstract—In this paper presented algorithm and methodology for computer modeling of complex eco-biological models, based on system approach of J. Forrester. Also specialties of modeling in ecology and biology are considered.

Keywords—computer modeling, system approach, biophysics, ecology.

I. INTRODUCTION

Computer modeling, as a field of science and engineering activity, connected to theory and practice of computing experiment. Complicated dynamic systems are special kind of mathematical models, and computer modeling – is a modern form of mathematical modeling, new technology of obtaining knowledge about objects.

Modeling is widely used in biology. Application examples are [1]: populations and biogeocenoses, researches in biological society theory, ecological modeling. Biological systems, like reserves ecosystems and populations of different species, have a complex structure and processes inside them are difficult to describe using mathematics.

Developing a universal algorithm of modeling ecological and biological systems will simplify process of describing complex dynamic systems and provide engine for performing modeling.

II. MATHEMATICAL SCHEMAS FOR MODELING

Computer modeling, as a field of science and engineering activity, connected to theory and practice of computing experiment. Complicated dynamic systems are special kind of mathematical models, and computer modeling – is a modern form of mathematical modeling, new technology of obtaining knowledge about objects.

Main tasks of mathematical modeling are:

- to find such mathematical representation of a object (such object also called mathematical model), so it will be equivalent to a real object;
- to research this mathematical model and determine main characteristics of model and real object.

Type of mathematical model depends on the nature of real object, research goals and desirable accuracy. Every mathematical model describe corresponding object with finite approximation level [2].

In analytical modeling processes inside models described using functions and logical expressions. The most complete research of system functionality can be achieved if exact dependencies between system characteristics, start parameters and variables are known. However, those dependencies could be determined only for relatively simple models. As model complication level increases, analytical method faces problems, sometimes unsolvable.

In imitational modeling implemented algorithm reproduces how real object behave in time. Basic processes in objects are imitated, saving their logical structure and sequence in time. This approach allows determining system state in particular moments of time and estimating system characteristics.

There is a combined approach, which integrates advantages of analytical and imitational methods. In combined models the main operating process of an object divides to several sub-

T. Burak, Elitrans Ltd., Minsk, Belarus (e-mail: timburik@gmail.com).

M. Lukashevich, Belarussian State University of Informatics and Radioelectronics, Minsk, Belarus (e-mail: lukashevich@bsuir.by).

processes. For every sub-process then represented as model: analytical model if possible, imitational otherwise. This combined approach allows covering new types of systems, which cannot be researched using just analytical method or just imitational method separately [3].

Classification of basic mathematical modeling schemas includes following approaches:

A. Deterministic-continuous models

Deterministic-continuous models are described as one or several differential equations. If system is distributed, then functions describing processes inside system depend on several variables. In this case partial differential equations are used.

B. Deterministic-discrete models

Deterministic-discrete models are the subject of automata theory. According this theory, models represented as automaton, which processes discrete portion of information and changes its state in discrete moments of time. Sub-state machine is separate subclass of automaton with finite number of states.

C. Stochastic-discrete models

Stochastic-discrete models are also separate subclass of automaton – nondeterministic automata. The main difference is that nondeterministic automaton transition function has stochastic component and value of this function is basically a probability distribution function for transition.

D. Stochastic-continuous models

Stochastic-continuous models, or queuing models, are the object of queuing theory. In queuing theory a model is constructed so that queue lengths and waiting time can be predicted [4].

III. MODELING IN BIOPHYSICS AND ECOLOGY

Biophysics is an interdisciplinary study about fundamental basics of structure, functioning and development of living systems. Biophysics use experiments along with mathematical modeling to describe processes in living systems with different levels of organization. Unlike physical processes, processes in biological systems are hard to describe using mathematical equations [5]. Therefore in modeling of biological processes they are mathematically simplified and abstracted. In most cases difficulties in describing biological models exclude the possibility of using analytical modeling methods.

According to [6], modeling process of ecological and biological systems has following features:

- All biological systems are complex, spatially structured systems consisting of many components. Two approaches could be used in modeling such systems. The first is to distinguish key characteristics of system as a whole and determine how these characteristics change in time. Second approach is to consider in detail every component of system and determine the way they interact with each other.
- One of the most important features of biological systems is their ability to autoreproduce. It means that equations in biological models should have autocatalytic elements, which determine population stability and its ability to grow.
- Biological systems are open. They always pass through themselves energy and matter flows. In practice it means that biological and ecological systems are not in state of thermodynamic and energetic equilibrium.
- Biological objects have complex multilevel system of self-regulating. It means that biological components are connected to each other using positive and negative feedback loops. In models feedback loops described using nonlinear equations, which determine the

occurrence of complex kinetic modes, including oscillation mode.

Book [7] analyzes different modeling approaches in history of theoretical ecology. The conclusion is that majority of mathematical models in ecology and biology are either inadequate and shouldn't be used in practice, or trivial and useless in practical experiments. However system approach in modeling gives more accurate results due to using expert functions.

IV. MODELING METHODOLOGY

Basic mathematical modeling schemas are simple and clear, but they have small application area. Most practical problems require working with complex dynamic systems. In this case basic modeling schemas cannot be used. One of the approaches for modeling complex dynamic systems introduced in the papers of J. Forrester, the founder of system dynamics [8]. This approach combines features of basic schemas and can be used as a simple and flexible tool in modeling of complex dynamic systems.

The main idea of system approach is that model represented as a set of main characteristics. Changes of model characteristics are driven by feedback loops [9]. *Feedback loop* is the closed chain of interaction between parameters. Such self-regulating mechanism better describes processes in dynamic systems.

System with feedback loops described using two kinds of variables: *stocks* and *flows*. Stock L is a numerical value of significant model characteristic at a certain moment of time. Flow D_L describes how value of stock changes during interval Δt . Equation (1) shows how value of stock L could be determined:

$$L(t_{i+1}) = L(t_i) + \Delta t \cdot \sum_j D_{Lj} \quad (1)$$

where Δt is time interval between moments t_{i+1} and t_i ; D_{Lj} are flows for stock L .

Assume $t_0, \dots, t_i, t_{i+1}, \dots, t_n$ are discrete moments of time, which corresponded to modeling iterations (index i is a serial number of iteration), and $t_{i+1} - t_i = \Delta t \forall i \in [1, n]$. If Δt will be sufficiently small, equation (1) transforms to following equation (2):

$$\frac{L(t_{i+1}) - L(t_i)}{\Delta t} = \frac{\Delta L}{\Delta t} = L' = \sum_j D_{Lj} \quad (2)$$

Thereby model is represented as deterministic-continuous model using system of differential equations.

Depending on whether or not stochastic variables are used in equations, system approach of J. Forrester could be used to describe deterministic and stochastic models.

Stock L is described by its value at the initial moment of time $L(t_0)$ and the set of flows D_{Lj} , which determines how value of stock L will change during modeling. Stocks with empty set of flows are constants.

To simplify the way of describing formulas for flows temporary variables are used. Temporary variables are basically intermediate calculations for flows and other temporary variables. Also, temporary variables could be used as additional source of information about model behavior during modeling. In model temporary variables set as functions of model stocks and other temporary variables (eq. 3):

$$Tmp(t_i) = f(IL(t_i), IT(t_i)) \quad (3)$$

where $IL = \{L_0, \dots, L_m\}$ – certain set of system stocks, which temporary variable Tmp depends on; $IT = \{Tmp_0, \dots, Tmp_k\}$ – certain set of temporary variables, which temporary

variable Tmp depends on.

Eco-biological systems are complex and consist of many interacting components, so it is necessary to provide ability to divide complex system into smaller sub-systems. Division will simplify process of describing model and provide its hierarchical structure. Lets define object Obj as structural unit of model, structural equivalent of system component. Every object is a sub-model, which interacts with other objects. Decomposition of complex systems into separate components makes process of describing model easier. Hierarchical structure of a model illustrated in figure 1.

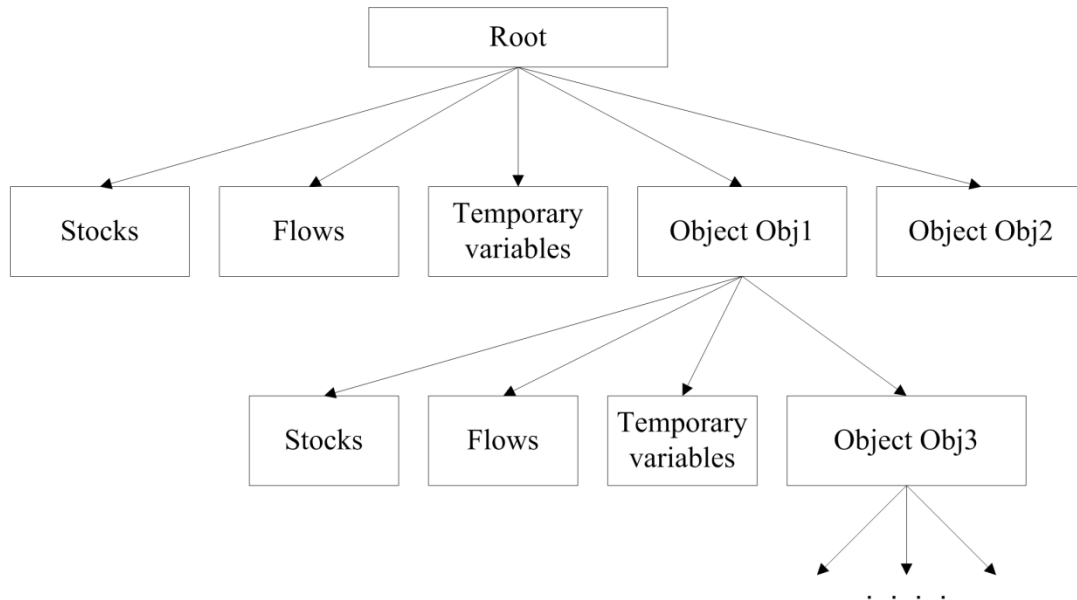


Fig. 1 Model structure

Modeling process for complex eco-biological models can be divided into three steps: model describing, model tuning and performing experiments on the model. Following sequence of actions could be useful for model describing:

- Complex system should be divided into components, i.e. system decomposition should be performed. Obtained components specify the set of model objects. If components themselves are complex systems, process of decomposition should be repeated for them. Thus, the hierarchical structure of model will be obtained.
- It is necessary to determine main parameters of model and each component, which will determine system state in certain moments of time and show system dynamics in time. These parameters specify the set of model stocks.
- For every stock we should determine factors, which influence its value. Factors should be analyzed to determine dependency function between factors and variation of stock value. This dependency formula specifies a flow for certain stock.
- Finally, to simplify calculations and model describing, we could introduce temporary variables into model structure.

As a result of actions listed above we will get model of complex eco-biological system with hierarchical structure. Before using this model for experiments and researches it is necessary to check if model is valid. To do this we should perform a testing modeling on time period, where precise state of model is known. Results of testing modeling we compare to actual data about system and make conclusion: is this model accurate enough or not.

If modeling results are not accurate enough – it should be tuned. Methods for tuning model include: correction of model constants and coefficients, correction of dependency formulas for

flows and change of model structure.

Model tuning can be performed in several iterations, until needed accuracy of model will be achieved. After model is described and tuned it is ready for using in experiments and researches.

V. PROGRAM IMPLEMENTATION

Program modeling is a process of getting sequence of model states in time. Let's define S_M as model state in certain moment. S_M is a set of values of all model stocks L_i and temporary variables Tmp_j as shown in equation (4):

$$S_M(t_i) = \{L_0(t_i), \dots, L_N(t_i), Tmp_0(t_i), \dots, Tmp(t_i)\} \quad (4)$$

where N – amount of model stocks; K – amount of temporary variables.

Modeling process is shown in figure 2. At the beginning program performs model initialization: set start values for stocks and calculate values of temporary variables (step A). After that, program saves current model state $S_M(t_i)$ (step B). Using values of stocks and temporary variables from $S_M(t_i)$ new model state $S_M(t_{i+1})$ is calculated (step C). It means that using values of stocks and temporary variables from previous iteration we calculate values of stocks and temporary variables for next iteration. Steps B and C are the one modeling iteration. Finally, iteration counter check if program completed required amount of iterations, and return program flow to step B if not.

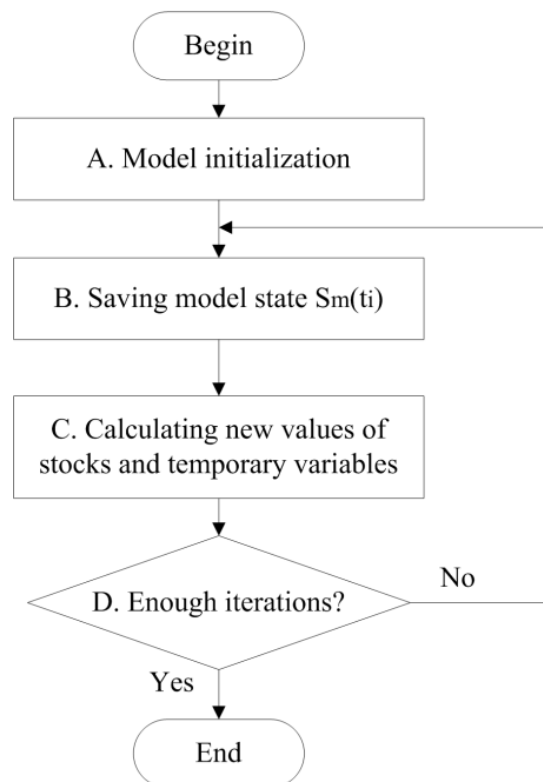


Fig. 2 Modeling process

Right now graphical user interface for modeling software is under development. Graphical interface will use “visual programming” technology, which minimize programming skills requirements for using this software.

VI. MODELING RESULTS

Modeling methodology described in this paper was used in modeling of lemmings population. Used model “vegetation – lemmings - arctic foxes” described in work [10]. Modeling results shown in figures 3-5.

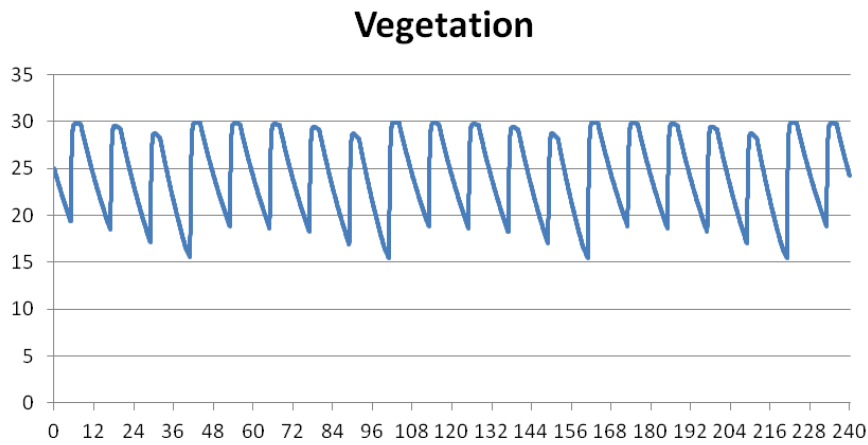


Fig. 3 Vegetation level, quintals per hectare

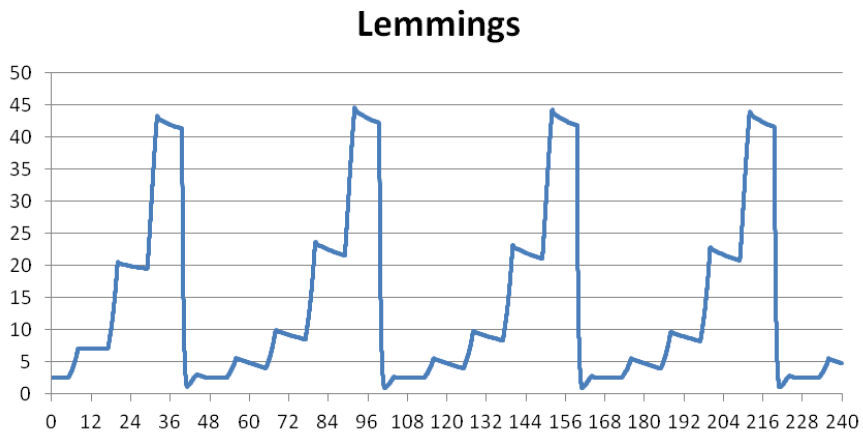


Fig. 4 Lemmings population, specimens per hectare

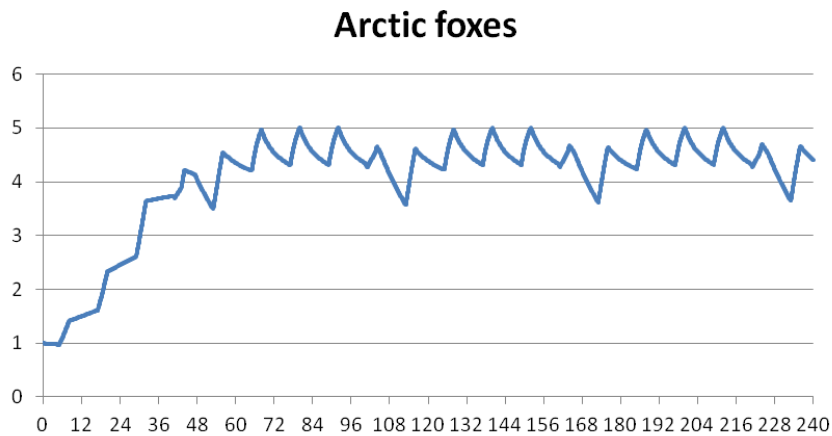


Fig. 5 Arctic foxes population, specimens per hectare

VII. CONCLUSION

Developed algorithm of describing models is universal for complex ecological and biological systems. Modeling algorithm considers specialties of eco-biological systems and shows adequate and accurate results in practice.

REFERENCES

- [1] Mathematical modeling in biology. / Academy of science, Scientific council on the biosphere; ed. A. M. Molchanov — M., “Science” publishing, 1975. — 156 p.
- [2] Sovetov B. Y., Yakovlev S. A., System modeling: University textbook — 3-e ed., — M.: “High school” publishing, 2001. — 343 p.
- [3] Buslenko N. P. Modeling of complex systems. — M.: “Science” publishing, 1988. — 355 p.
- [4] Gnedenko B. D., Kovalenko I. N. Introduction into queueing theory. — M.: “Science” publishing, 1987. — 432 p.
- [5] Rizchenko G. Y., Rubin A. B. Mathematical models of biological productional processes. — M., Moscow State University publishing, 1993. — 302 p.
- [6] Rizchenko G. Y. Mathematical models in biophysics and ecology. — Moscow-Izhevsk: Institute of Computer Science, 2003. — 184 p.
- [7] Tatubalin V.N., Barabasheva Y.M., Grigoryan A.A. and others. Mathematical modeling in ecology: historical and methodological analysis. — M.: “Science” publishing, 1999. — 208 p.
- [8] Forrester, Jay W. Principles of Systems. (2nd ed.). — MA: Pegasus Communications, Waltham, 1968. — P. 391.
- [9] Forrester, Jay W. World Dynamics. — M.: AST, 2006. — 384 p.
- [10] Trashev R.V., Lulyakin O.P., Sarancha D.A. and others. Complex research method on an example of lemmings population modeling. — M., Computing center of A.A.Dorodnitsin, Russian Academy of Science, 2014. — 116 p.



This publication is the result of the project implementation:
 TEMPUS CERES: Centers of Excellence for young REsearchers.
 Reg.no.544137-TEMPUS-1-2013-1-SK-TEMPUS-JPHES

