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Computer research of nonlinear stochastic models with migration flows

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The problems of the design methods extension and computer research of nondeterministic finite-dimensional population models describing migration flows are studied. The significant difficulties arise in the construction of high dimension dynamic models in the course of analytical research. Computer research allows not only to obtain the results of numerical experiments to search for trajectories and estimate the parameters of deterministic models, but also to reveal the effects caused by stochasticization. The model parameters are estimated and local phase portraits are constructed for the initial four-dimensional migration-population model. The transition from the vector ordinary differential equation to the corresponding stochastic differential equation is performed. The structure of the stochastic model is described on the basis of applying the method of constructing self-consistent stochastic models. As a tool for the study of population-migration models, a software package is used to solve numerically the differential equations systems using modified Runge–Kutta methods. The software package allows numerical experiments based on the implementation of algorithms for generating trajectories of multidimensional Wiener processes and multipoint distributions and algorithms for solving stochastic differential equations. The comparative analysis of the computer research results obtained for stochastic models is carried out. The properties of migration-population systems in deterministic and stochastic cases are characterized. The comparison of the results obtained for the three-dimensional and four-dimensional cases is carried out. The effects inherent in models with migration flows are revealed. The obtained results can be applied to the problems of modeling and forecasting the behavior of multidimensional systems describing the migration flows.

Key words and phrases: computer modeling, nonlinear models of migration flows, stochasticization of one-step processes, symbolic representation algorithms, symbol computing libraries.

1. Introduction

The construction and study of the models with migration are devoted to the work of various authors (see, for example, [1–3]). In [2–6] migration flows in deterministic population is considered. The analysis of distributed multidimensional population models taking into account cross-migration is carried out in papers [7–10]. Migration mechanisms can be described by both linear and non-linear functions, and lead to different effects [2, 11]. In [3, 5, 11, 12] the issues of qualitative behavior and sustainability of population-migration models are studied. In [13–15] a qualitative analysis of a three-dimensional non-deterministic model with migration is performed. To study the model, a combination of known methods of synthesis and analysis of models and a method for constructing stochastic self-consistent models are used [16]. In [12] a methodological support is developed for the analysis and synthesis of multidimensional nonlinear dynamic models describing migration flows taking into account the effects of broadband parametric and additive noise. The stability of stationary states is studied and the effects obtained for stochastic models are interpreted. The model examples show a comparison of the migration-population systems properties in deterministic and stochastic cases and the effects due to stochastic broadband perturbations are revealed.

When modeling population-migration systems, various software tools are used that present wide possibilities for building computer models and carrying out computational experiments. However, many software products do not contain libraries for numerical and symbolic calculations and do not have sufficient computational complexity. In this regard, in the study of the population-migration systems models, the application of mathematical packages and general-purpose programming languages [17–19] is relevant. In [20] sufficient conditions are proposed for the uniform stability of the equilibrium states of a four-dimensional non-linear model of population dynamics. In [21] the Maxima mathematical package is used to study the stability of this model. One of the instrumental software tools for studying population-migration models is a software package for the numerical solution of differential equations systems using modified Runge – Kutta methods. The specified complex was developed in [22, 23]. The software package allows numerical experiments based on the implementation of algorithms for generating trajectories of multidimensional Wiener processes and multipoint distributions and algorithms for solving stochastic differential equations.

The several types of four-dimensional models with migration flows are studied in this paper. A comparative analysis of the computer research results obtained for three-dimensional and four-dimensional stochastic models with migration flows is carried out. A comparison is made of the qualitative properties of four-dimensional models, taking into account changes in migration rates, as well as intraspecific and interspecific interaction coefficients. The properties of the models in the deterministic and stochastic cases are characterized. As a tool for the study of the models, a software package in the Python language using the NumPy and SciPy libraries is used.

2. Deterministic Migration Models

A nonlinear model is considered that is described by a system of ordinary differential equations of the form:

$$\begin{aligned}
 \dot{x}_1 &= x_1 - x_1^2 - p_{13}x_1x_3 - p_{14}x_1x_4 + \beta x_2 - \gamma x_1, \\
 \dot{x}_2 &= x_2 - x_2^2 + \gamma x_1 - \beta x_2, \\
 \dot{x}_3 &= x_3 - p_{31}x_1x_3 - x_3^2 - p_{34}x_3x_4, \\
 \dot{x}_4 &= x_4 - p_{41}x_1x_4 - p_{43}x_3x_4 - x_4^2.
 \end{aligned} \tag{1}$$

The following notation is used in (1): x_1 , x_3 and x_4 is the population density of competing species in the area of the forma x_1 (area 1), x_2 is the population density

in the area of the form x_2 (area 2), $p_{13}, p_{14}, p_{31}, p_{34}, p_{41}, p_{43} > 0$ are the coefficients of species competition in the area of 1, $\beta > 0$ and $\gamma > 0$ are the coefficients of the migration of species between two areas, while area 2 is a refuge and $\beta \neq \gamma$.

In the model (1) the first two equations describe the dynamics of one type taking into account migration processes. The first equation sets the dynamics in the first area, the second one sets the dynamics in the second area. The third and fourth equations describe the dynamics of the second and third types, interacting as competitors with the first type in the first area. Previously, we studied the three-dimensional model (two species, the first species migrated to another area, and in the first area it competed with the second type).

In the case when $p_{13} = p_{31}$, $p_{14} = p_{41}$, $p_{34} = p_{43}$, the model (1) takes view

$$\begin{aligned} \dot{x}_1 &= x_1 - x_1^2 - p_{13}x_1x_3 - p_{14}x_1x_4 + \beta x_2 - \gamma x_1, \\ \dot{x}_2 &= x_2 - x_2^2 + \gamma x_1 - \beta x_2, \\ \dot{x}_3 &= x_3 - x_3^2 - p_{13}x_1x_3 - p_{34}x_3x_4, \\ \dot{x}_4 &= x_4 - x_4^2 - p_{14}x_1x_4 - p_{34}x_3x_4. \end{aligned} \tag{2}$$

At the same migration rates $\beta = \gamma = \varepsilon$ from (2) we get a model of the form

$$\begin{aligned} \dot{x}_1 &= x_1 - x_1^2 - p_{13}x_1x_3 - p_{14}x_1x_4 + \varepsilon(x_2 - x_1), \\ \dot{x}_2 &= x_2 - x_2^2 + \varepsilon(x_2 - x_1), \\ \dot{x}_3 &= x_3 - x_3^2 - p_{13}x_1x_3 - p_{34}x_3x_4, \\ \dot{x}_4 &= x_4 - x_4^2 - p_{14}x_1x_4 - p_{34}x_3x_4. \end{aligned} \tag{3}$$

In this paper, deterministic models (1)–(3) and their stochastic generalizations are studied.

A three-dimensional model that describes two types of dynamics, the first species migrating to another area, and in the first area competing with the second type, has the form:

$$\begin{aligned} \dot{y}_1 &= y_1 - y_1^2 - p_{13}y_1y_3 + \beta y_2 - \gamma y_1, \\ \dot{y}_2 &= y_2 - y_2^2 + \gamma y_1 - \beta y_2, \\ \dot{y}_3 &= y_3 - y_3^2 - p_{13}y_1y_3, \end{aligned} \tag{4}$$

where y_1 and y_3 are the density of populations of competing species in the area of the form y_1 (area 1), y_2 is the population density in the area type y_2 (area 2), $p_{13} > 0$ is the coefficient of competition of species in the area 1. The results of the analysis of the (4) model and the generalized stochastic model are presented in [13–15]. The model (4) is a generalization of the model considered in [3], in the case when the migration rates are different.

The numerical experiment for the model (4) is carried out with the help of the developed software for the study and numerical solution of systems of ordinary and stochastic differential equations using the Runge–Kutta method [22, 23]. The library is written in Python using the NumPy and SciPy modules. The models (1)–(3) and their stochastic generalizations are studied using this software package.

For the numerical experiment of the deterministic model, the following sets of parameters are chosen: the initial values $y_1(0) = 0.5$, $y_2(0) = 1.0$, $y_3(0) = 0.5$ for the three-dimensional model and $x_1(0) = 0.5$, $x_2(0) = 1.0$, $x_3(0) = 0.5, x_4 = 0.7$ for a

four-dimensional model, the values of the parameters $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$, $\beta = 1.5$, $\gamma = 0.2$.

Fig. 1 presents solution trajectories for (2) and (4) models with the specified initial values and parameter values in the time interval $[0,40]$. The effect of an additional competitor on the migration flow is shown. The introduction of an additional competitor corresponding to the phase variable x_4 , leads to a decrease in both the density of the migrating population in both areas and the density of the competitor corresponding to the variable x_3 .

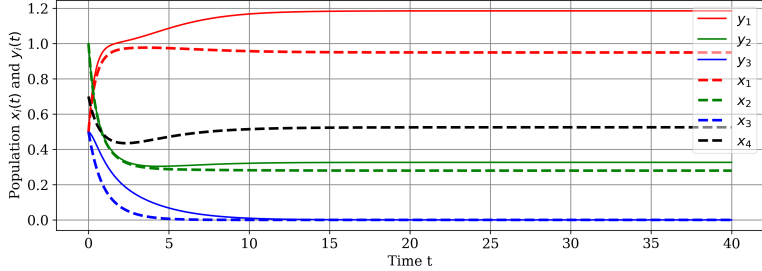


Figure 1. Model solution trajectories (2) and (4) with
 $(y_1(0), y_2(0), y_3(0)) = (0.8, 0.1, 1.0)$, $(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.8, 0.1, 1.0, 1.0)$,
 $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$, $\beta = 1.5$, $\gamma = 0.2$.

With the values of the parameters $p_{13} = 0.9$, $p_{14} = 0.4$, $p_{34} = 0.8$, $p_{34} = 0.6$, $p_{41} = 0.5$, $p_{43} = 0.7$, $\beta = 0.25$, $\gamma = 0.3$ in the model (1) there are the following equilibria: $P_1(0, 0, 0, 0)$, $P_2(0, 0, 0, 1)$, $P_3(0, 0, 1, 0)$, $P_4(0, 0, 0.69, 0.517)$, $P_5(0.63, 0.949, 0.4957, 0)$, $P_6(0.75, 0.98, 0.043, 0.595)$. Here P_1, P_5 are unstable nodes, $P_2 - P_4$ are saddles, P_6 is a stable node.

Consider the models (1) and (2) with the same set of migration velocity values for these models, but with different sets of intraspecific and interspecific interaction coefficients. Solution trajectories for the model (1) with the values of the parameters $p_{13} = 0.9$, $p_{14} = 0.4$, $p_{31} = 0.8$, $p_{34} = 0.6$, $p_{41} = 0.5$, $p_{43} = 0.7$ and the trajectories of solutions for the model (2) with $p_{13} = 1$, $p_{14} = 0.6$, $p_{34} = 0.7$ in the time interval $[0, 25]$ is presented in fig. 2. For models (1) and (2) the initial values are $(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.3, 0.7, 1.1, 0.8)$, values of migration speeds $\beta = 0.25$, $\gamma = 0.3$. In fig. 2 a record of the form $x_i(1)$, $i = 1, 2, 3, 4$, indicates the trajectory corresponding to the phase variable x_i for the model (1), a record of the form $x_i(2)$ denotes the trajectory corresponding to the phase variable x_i for the model (2).

As a result of a comparative analysis of the solution trajectories of (1) and (2) presented in fig. 2:

- 1) in the model (2) the population of x_4 is dying out, the population density of x_1 is increasing, and the population density of x_3 is decreasing;
- 2) for the models (1) and (2) favorable conditions are created in the second area, and the population density of x_2 increases;
- 3) in the model (2) competition intensified, which led to the extinction of the x_4 population and the improvement of living conditions for the x_1 and x_3 populations.

For the values of the parameters $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$, $\varepsilon = 0.3$ in model (3) there are the following equilibrium positions: $P_1(0, 0, 0, 0)$, $P_2(0, 0, 0, 1)$, $P_3(0, 0, 1, 0)$, $P_4(0, 0, 0.42, 0.42)$, $P_5(1, 1, 0, 0)$, $P_6(0.76, 0.94, 0, 0.62)$. Here $P_2 - P_5$ are saddles, P_1 is an unstable node, P_6 is a stable node.

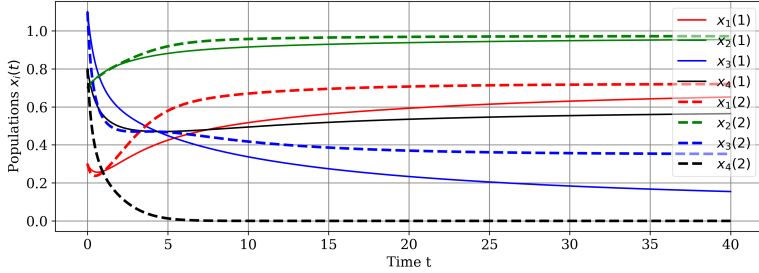


Figure 2. Model solution trajectories (1) and (2) with
 $(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.3, 0.7, 1.1, 0.8)$, $\beta = 0.25$, $\gamma = 0.3$.

Consider the models (2) and (3) taking into account the coincidence of the intraspecific and interspecific interaction for these models. Note that in the model (2) in the general case $\beta \neq \gamma$, and in the model (3) $\beta = \gamma$. Solution trajectories for models (2) and (3) with the values of the parameters $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$ and the initial values $(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.5, 1, 0.8, 1)$ in the time interval $[0, 25]$ are presented in fig. 3. For the model (2) the values of migration speeds $\beta = 1.5$, $\gamma = 0.2$, for the model (3) the value of migration speed $\varepsilon = 0.3$. In fig. 3 the record of the form $x_i(3)$ denotes the trajectory corresponding to the phase variable x_i for the model (3).

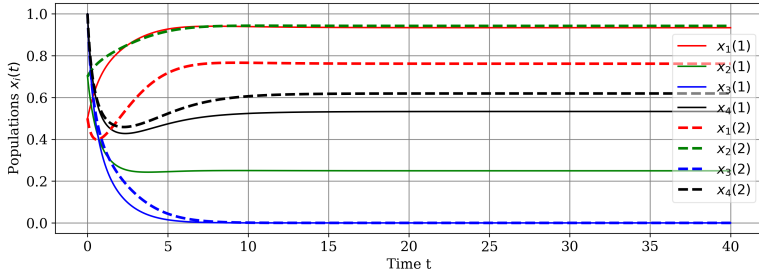


Figure 3. Model solution trajectories (2) and (3)
 $(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.5, 1, 0.8, 1)$, $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$, $\beta = 1.5$,
 $\gamma = 0.2$, $\varepsilon = 0.3$.

As a result of a comparative analysis of the solution trajectories of the (2) and (3) models shown in fig. 3, the following conclusions are obtained:

- 1) in the model (3) the population density x_4 increased insignificantly, and the population density x_1 decreased, while the population x_3 in both models is rapidly dying out;
- 2) as the migration rate increases, the model (3) in the second area creates more favorable conditions than in the model (2), so the population density x_2 increases significantly.

For a series of parameter sets, stationary states of the model (3) are found. It is established that for the values of the parameters $p_{13} = 1.2$, $p_{14} = 0.5$, $p_{34} = 1.4$, $\beta = 1.5$, $\gamma = 0.2$ in the model (2) the following stationary states exist: $P_1(0, 0, 0, 0)$, $P_2(0, 0, 0, 1)$,

$P_3(0, 0, 1, 0)$, $P_4(1.18, 0.29, 0, 0)$, $P_5(0, 0, 0.42, 0.42)$, $P_6(0.93, 0.25, 0, 0.53)$. In addition, the system is linearized in the vicinity of stationary states and the stability on the first approach is investigated. For the model (2) the projections of the phase portraits (x_1, x_2) are shown in fig. 4. The projections of the phase portraits (x_1, x_2) in the vicinity of equilibrium positions are shown in fig. 5. The projections of the phase portraits (x_1, x_3) are shown in fig. 6.

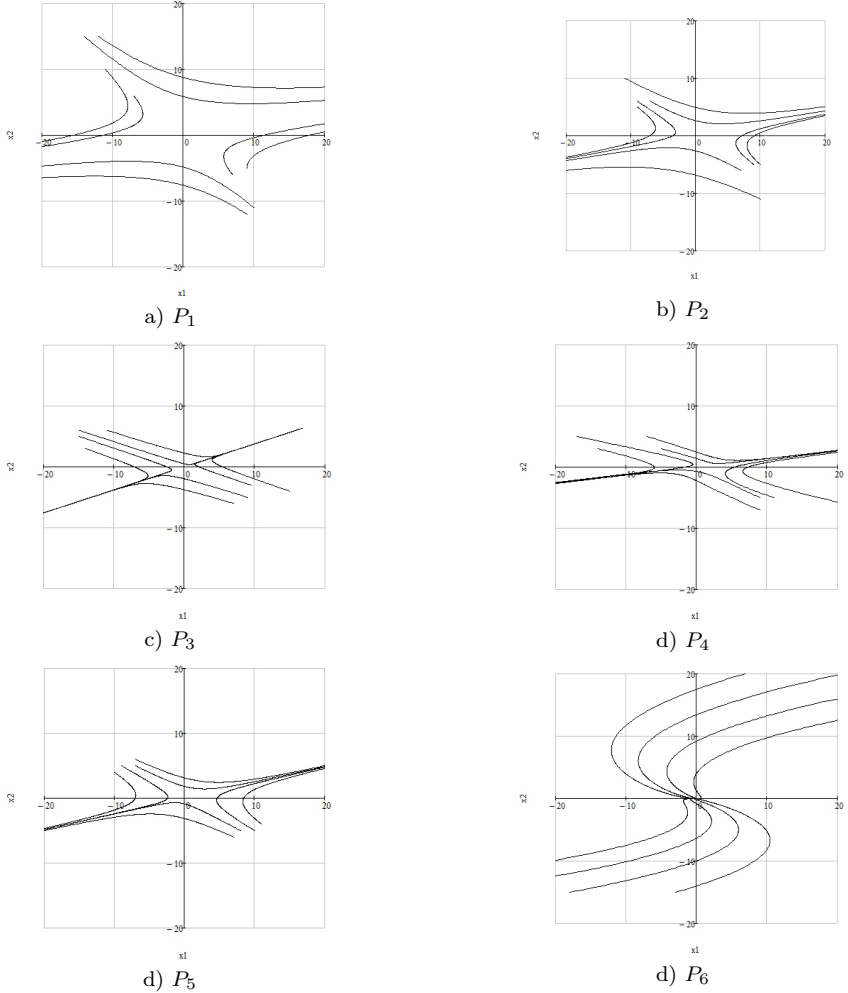


Figure 4. Phase portraits for the model (2).

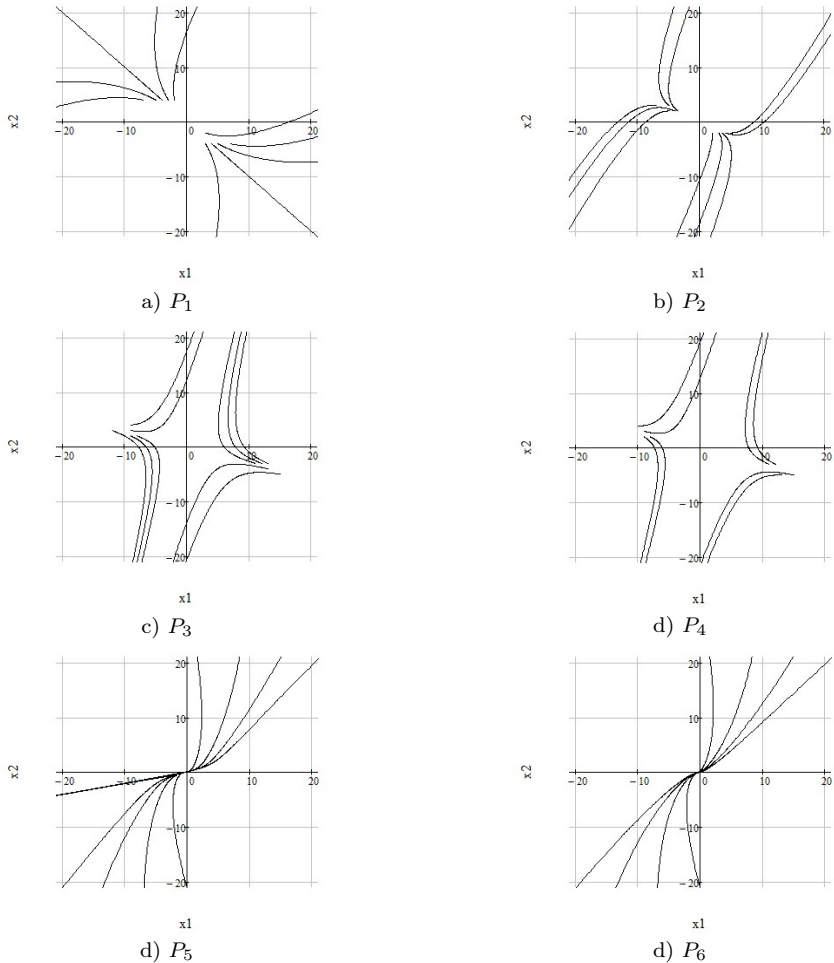


Figure 5. Phase portraits of the projections (x_1, x_2) for the model (1) in the vicinity of the equilibrium positions P_1 – P_6 .

3. Stochastic Migration Models

Questions of constructing and studying a stochastic model for a three-dimensional system with regard to migration are considered in the works [13–15]. In this paper, stochastization of (1)–(3) models is carried out using the method of constructing self-consistent stochastic models [16]. The basis of this method is combinatorial methodology. This method involves recording the system under study as an interaction scheme, i.e. a symbolic record of all possible interactions between elements of the system. For this, the

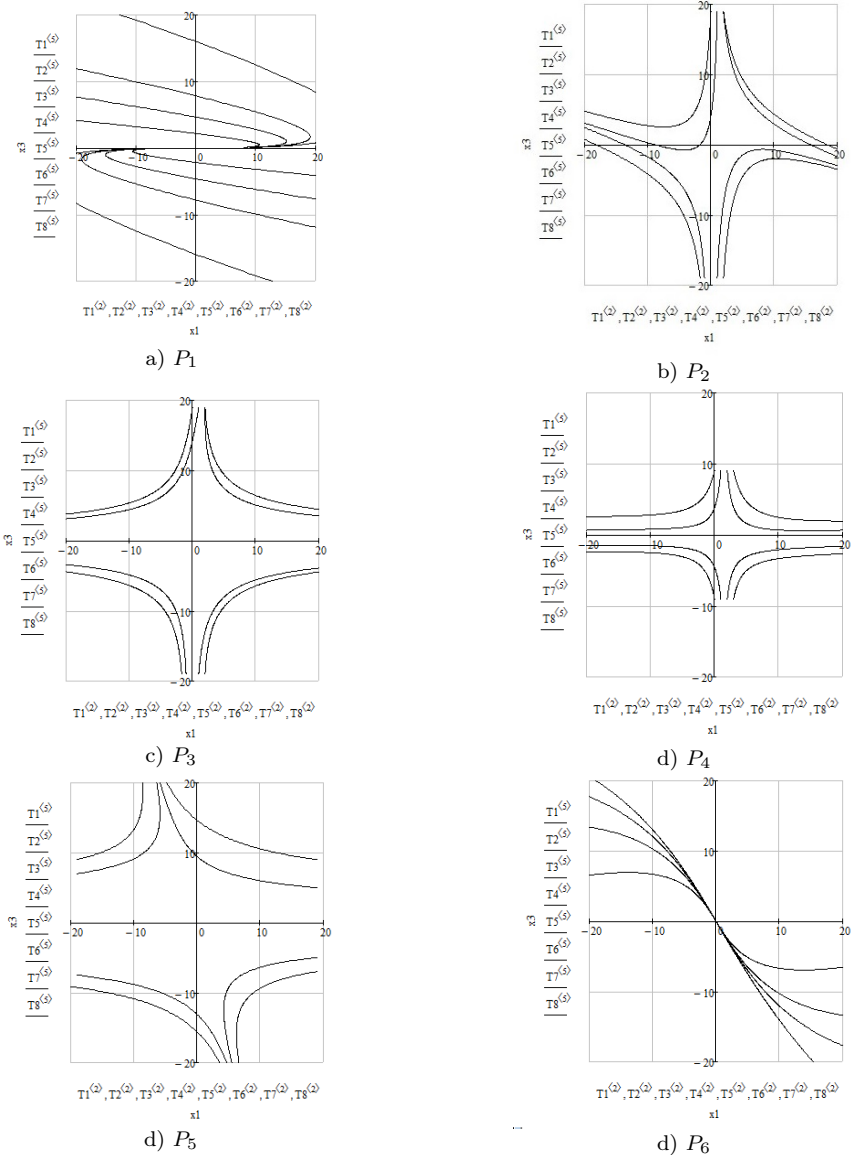


Figure 6. Phase portraits for the model (3).

system state operators and the system state change operator are used. Then we can get the drift and diffusion coefficients for the Fokker–Planck equation, which allows to write the equation itself and its equivalent stochastic differential equation in the Langevin form.

However, an increase in the dimension and complexity of the system under study leads to the complexity of the analytical conclusion of the necessary coefficients of the Fokker–Planck equation. As a solution to this problem, a software implementation is developed for obtaining the coefficients of the Fokker–Planck equation from interaction schemes using a symbolic computation system. This software implementation is a modification of the stochastization method for one-step processes in the computer algebra system described in [24]. This implementation is introduced as a module into a software package developed earlier for the numerical study of deterministic and stochastic models [22].

The following is the algorithm for obtaining the symbolic notation of a stochastic differential equation (Algorithm 1).

Algorithm 1. Getting the system of differential equations from the interaction scheme

Initial parameters: interaction scheme.

Result: system of differential equations in the form of Langevin.

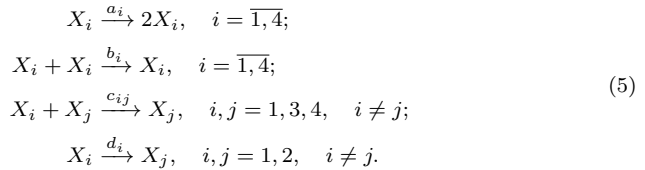
Start:

1. Getting the system state operators from the interaction scheme.
2. Getting the change of the system state.
3. Getting the transition intensities.
4. Record the coefficients of the Fokker–Planck equation.
5. Record the system of differential equations.

end

To implement the described algorithm, SymPy [17], computer computing system is used, which is a powerful symbolic computation library for the Python language. In addition, the output data obtained using the SymPy library can be transferred for numerical calculations using the NumPy [19] library and SciPy [18].

To obtain a stochastic model corresponding to the models (1)–(3), it is necessary to write the interaction scheme, which is as follows:



The values of the coefficients for each of the models are given in the table 1.

The first line corresponds to the natural reproduction of the species in the absence of other factors, the second line symbolizes intraspecific competition, and the third one is interspecific competition. The last line corresponds to the description of the species migration process from one area to another. Then, expressions for the coefficients of the Fokker–Planck equation are obtained for this interaction scheme using the developed software (fig. 7).

Further, the coefficients are transferred to the appropriate module of the software complex for the numerical solution of the constructed stochastic differential equation. For the numerical experiment of the obtained stochastic model, the parameters are chosen, the same as for the numerical analysis of the deterministic model (3). Fig. 8 presents the trajectories of average values for 100 realizations for the specified initial values and parameter values in the time interval $[0, 40]$.

A numerical experiment showed the closeness of trajectories for stochastic and deterministic cases. Similarly to the deterministic case, the mean values trajectories of different implementations of the stochastic differential equation solutions go to the

Table 1

Coefficients for the interaction scheme (5)

	Model (1)	Model (2)	Model (3)
a_i	$a_i = 1, i = \overline{1, 4}$	$a_i = 1, i = \overline{1, 4}$	$a_i = 1, i = \overline{1, 4}$
b_i	$b_i = 1, i = \overline{1, 4}$	$b_i = 1, i = \overline{1, 4}$	$b_i = 1, i = \overline{1, 4}$
c_{ij}	$c_{13} = p_{13}, c_{14} = p_{14}, c_{31} = p_{31}, c_{34} = p_{34}, c_{41} = p_{41}, c_{43} = p_{43},$	$c_{13} = c_{31} = p_{13}, c_{14} = c_{41} = p_{14}, c_{34} = c_{43} = p_{34}$	$c_{13} = c_{31} = p_{13}, c_{14} = c_{41} = p_{14}, c_{34} = c_{43} = p_{34}$
d_i	$d_1 = \gamma, d_2 = \beta$	$d_1 = \gamma, d_2 = \beta$	$d_1 = d_2 = \varepsilon$

```
In [36]: f = drift_vector(X, P_sl, K_minus, N, M)
         G = diffusion_matrix(X, P_sl, K_minus, N, M)

In [37]: f
Out[37]: [-ex1 + ex2 - p13x1x3 - p14x1x4 - x1^2 + x1
           ex1 - ex2 - x2^2 + x2
           -p13x1x3 - p34x3x4 - x3^2 + x3
           -p14x1x4 - p34x3x4 - x4^2 + x4]

In [38]: G
Out[38]: [ex1 + ex2 + p13x1x3 + p14x1x4 + x1^2 + x1    -ex1 - ex2    p13x1x3    p14x1x4
           -ex1 - ex2    ex1 + ex2 + x2^2 + x2    0    0
           p13x1x3    0    p13x1x3 + p34x3x4 + x3^2 + x3    p34x3x4
           p14x1x4    0    p34x3x4    p14x1x4 + p34x3x4 + x4^2 + x4]
```

Figure 7. The coefficients of the equation of Fokker–Planck

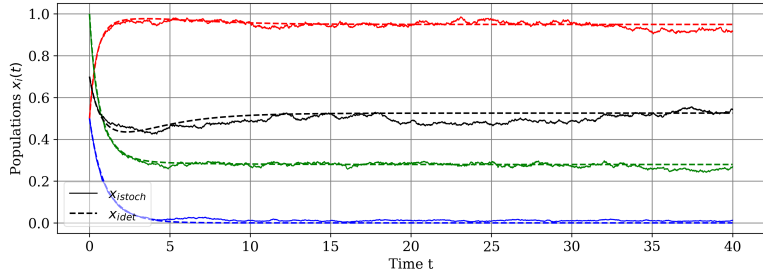


Figure 8. Model Solution Trajectories (5) with

$(x_1(0), x_2(0), x_3(0), x_4(0)) = (0.8, 0.1, 1.0, 1.0), p_{13} = 1.2, p_{14} = 0.5, p_{34} = 1.4, \beta = 1.5,$
 $\gamma = 0.2.$

stationary mode, retain the character and values of the stationary state are weakly distinguished.

A series of numerical experiments is carried out using different sets of model parameters. For each set, we analyzed the stationary states and constructed the trajectories of solutions. Taking into account the characteristic cases, the peculiarities of the influence

of an additional competitor on the dynamics of the migrating population are revealed and the effects of stochastization of one-step processes are described.

4. Conclusions

A computer study of nonlinear models with migration flows made it possible obtain the results of numerical experiments on trajectory search and parameter estimation in the case of high dimensionality of models, as well as to reveal effects due to stochastization. The estimation of the influence of an additional competitor type on the dynamics, stability and level of migration in the multidimensional model is obtained. A comparative analysis of computer simulation results showed that with an increase in the rate of migration in the second area, more favorable conditions are created, which leads to a significant increase in the number of the second population. At the same time, competition in the first area is increasing, which leads to the extinction of one of the population. The comparison of the results obtained for the three-dimensional and four-dimensional cases. The software package developed in the Python language using the NumPy and SciPy libraries is demonstrated sufficient efficiency for computer studies of multidimensional nonlinear migration models. Numerical experiments using problem-oriented software show the closeness of the trajectories types for stochastic and deterministic cases. The results obtained can be applied to the problems of computer modeling of ecological, demographic and socio-economic systems.

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