Article

Three different ways for estimating Green Oak Leaf Roller dynamics type: OLS, MEP, and Almost-Bayesian approaches

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Abstract
The generalized discrete logistic model (GDLM) of population dynamics was used for fitting of the known empirical time series on the green oak leaf roller (*Tortrix viridana* L.) fluctuations in European part of Russian Federation (Korzukhin and Semevsky, 1992). The model was assumed to demonstrate satisfactory data approximation if and only if the set of deviations of the model and empirical data satisfied several statistical criterions (for fixed significance levels). Distributions of deviations between theoretical (model) trajectories and empirical datasets were tested for symmetry (with respect to the ordinate line by Kolmogorov–Smirnov, Mann – Whitney U-test, Lehmann – Rosenblatt, and Wald – Wolfowitz tests) and the presence or absence of serial correlation (the Swed–Eisenhart and “jumps up–jumps down” tests). Stochastic search in a space of model parameters show that the feasible set (set of points where all used tests demonstrate correct/required results) is not empty and, consequently, the model is suitable for fitting of empirical data. It is also allowed concluding that observed regime of population dynamics isn’t cyclic (if length of cycle is less than 1500 years) and can be characterized by the fast decreasing autocorrelation function (with further small fluctuations near zero level). Feasible set allows constructing almost-Bayesian estimations of GDLM parameters. For the situation when model parameters are stochastic variables algorithm of calculation of model trajectories is presented.

Keywords discrete logistic model; parameter estimation; ordinary least squares; method of extreme points; analysis of deviations; almost-Bayesian approach.

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1 Introduction

One of the most important problems in modern ecology is a problem of identification of population dynamics type for existing time series (Isaev et al., 1984, 2001). Solution of this problem can give us a scientifically-based background for forecast, understanding of situation when we have to use one or other method for optimal population dynamics management (and what kind of methods we must use for it), and methods for solution of some other important ecological problems.

Determination of population dynamics type can be provided by two different ways. We can use various biological tests (Isaev et al., 1980, 1984; Berryman, 1981, 1990) which allows using information of qualitatively different types. We can also use mathematical models of ecosystem dynamics (Berryman, 1992; McCallum, 2000; Tonnang et al., 2009a, b, 2010; Nedorezov, 2012a, b, 2016), and compare existing time series with values generated by these models (Turchin et al., 2003; Nedorezov, 2014).

For various mass species of forest insects (and, in particular, for green oak leaf roller (*Tortrix viridana* L.); Korzukhin and Semevsky, 1992; Rubtsov, 1983; Rubtsov and Shvytov, 1980; Nedorezov and Sadykova, 2010; Nedorezov et al., 2010), we have (rather) big time series from various locations, and for analyses of these datasets it is possible to use ecological models with several (visible and invisible) variables (Isaev et al., 1984, 2001; Myers, 1988, 1993; Turchin, 2003; Baltensweiler, 1964, 1978; Baltensweiler et al., 1977; Baltensweiler and Fischlin, 1988). But before applying of complex multi-component models describing population /ecosystem dynamics we must be sure that we cannot obtain sufficient description of population dynamics with simpler models (Lyapunov and Bagrinovskaya, 1975). In particular, as it was demonstrated in various publications (see, for example, Rubtsov, 1983; Isaev et al., 1980, 1984, 2001) population dynamics of green oak leaf roller can be characterized as an outbreak proper (or pulse eruptive outbreak in Berryman's classification; Berryman, 1981, 1990) or as permanent outbreak. But these dynamic regimes contain several non-trivial stationary states of system (in positive part of phase space) and respectively can be realized within the framework of rather complicated mathematical models. But before use of difficult models we have to be sure that population dynamics cannot be described by simple models which have one non-trivial equilibrium.

In current publication for fitting of known time series (Korzukhin and Semevsky, 1992) on the dynamics of green oak leaf roller generalized discrete logistic model (GDLM) was used (Maynard Smith, 1968, 1974). Estimations of model parameters were provided by several different statistical approaches: Ordinary Least Squares (OLS) (Draper and Smith, 1981; Bard, 1973; Demidenko, 1981; Lawson and Hanson, 1986), Method of Extreme Points (MEP) (Nedorezov, 2012a, b, 2014, 2015), and almost-Bayesian approach. The last approach was called as "almost-Bayesian approach" because it was assumed that parameters of the GDLM are stochastic variables. Bayes theorem wasn't used, and a'priori density functions of parameters were not considered: determinations of model parameter's distributions were based on elements of *feasible set* (which was constructed for MEP approach) and presentation of joint density function as product of marginal density and conditional density functions (for initial value of population size and model parameters).

Feasible set is a set of points from a space of model parameters (plus initial value of population size; for GDLM dimension of this space is equal to three) which correspond to model trajectories with specific features. These specific features are following: several statistical criterions give correct results for set of deviations (between model trajectories and empirical time series) for fixed significance levels. Set of deviations must have symmetric distribution (with respect to origin); density function must have monotonic behavior of branches for negative and positive values of deviations; there are no serial correlations in a sequence of deviations. In other words, for every point of feasible set we can conclude that respective values can be used as estimations of model parameters and used statistical criterions don't allow concluding that model isn't suitable for fitting of empirical time series.

Provided calculations show that OLS-estimations belong to "non-biological zone" of space of model parameters, and it doesn't allow determining of population dynamics type and present a real forecast of population size changing in time. Searching of MEP-estimations of model parameters was provided within the boundaries of "biological zone" of space of model parameters (definition of "biological zone" and "non-biological zone” are presented below). Several points with extreme properties were found; on a qualitative level all extreme points correspond to one and the same dynamic regime: it isn’t cyclic fluctuations of population size (when length of a cycle is less than 1500 years), and it can be characterized by fast decreasing of auto-correlation function.

For model with “almost-Bayesian” estimations of parameters algorithm of generating of model trajectory is presented. Initial steps of generating process are illustrated by figures with density functions and by method of obtaining of values of model parameters (Mikhailov, 1974; Ermakov, 1975).

2 Model Description

Ecological studies employ a relatively small number of basic population dynamics models, which serve as a kind of blocks used in a construction of more complex multicomponent models (Maynard, 1968, 1974; Svirezhev and Logofet, 1978; Svirezhev, 1987; Nedorezov and Utyupin, 2011; Kostitzin, 1937; Pielou, 1977; Berezovskaya et al., 2005; Karev et al., 2008, and others). The very first of such basic models was the discrete logistic model (Nedorezov, 2012a):

$$x_{k+1} = \begin{cases} ax_k(b - x_k), & x_k \le b \\ 0, & x_k > b \end{cases} \tag{1}$$

Here, x_k is a population size (or population density) at time moment k, $k = 0,1,2 \ldots$. Parameter b is a maximum value of population size; in (1) it is assumed that if $x_k > b$ at time moment k than for all $m > k$ we have $x_m \equiv 0$. Product ab is a maximal value of birth rate (which is defined as relation of sizes of population of two nearest generations). Parameters a, b, and initial value of population size x_0 are non-negative amounts, $a, b, x_0 \ge 0$.

If inequality $ab \le 4$ is truthful trajectories of model (1) are non-negative and bounded for all $0 \le x_0 \le b$. If inequalities $ab > 4$ and $0 < x_0 < b$ are observed for model parameters possibility for model trajectory to intersect limits of the domain $\{x: x < b\}$ is appeared; in this situation identification of population dynamics type is practically impossible: behavior of model trajectory will correspond to regime of population extinction. In other words, in a space of model parameters domain $\{(a, b): ab > 4\}$ can be defined as “non-biological zone”. Below domain $\{(a, b): ab \le 4\}$ will be called as “biological zone”.

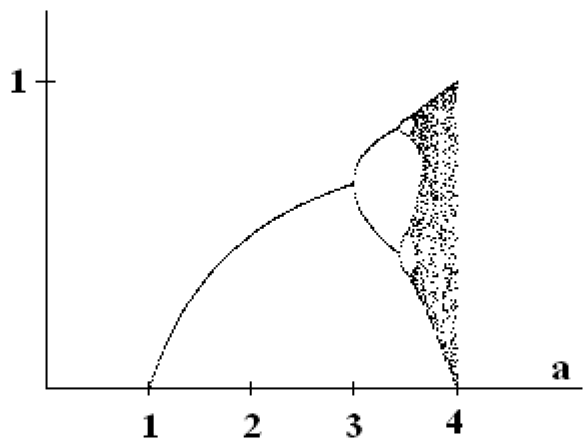

Fig. 1 Bifurcation diagram of model (1). Parameter $b = 1$.

Model (1) has very rich set of dynamical regimes (Fig. 1). If $ab < 1$ there is the regime of population asymptotic extinction (in figure 1 this domain is $[0,1]$). If inequalities $1 < ab < 3$ are truthful there is the regime of stabilization of population size at non-zero level for all initial positive values of population size,

$0 < x_0 < b$. If $3 < ab < 4$ cyclic dynamical regimes of all lengths can be observed (Maynard, 1968, 1974; Nedorezov, 2012a; Nedorezov and Utyupin, 2011).

3 Statistical Criterions

In publication several different ways for analysis of correspondence of empirical time series and model trajectories were used. Ordinary least squares (OLS) method (Bard, 1974; Draper and Smith, 1981) was used in traditional way. Parameters of model (1) were determined in a result of minimization of squared deviations between empirical time series and model trajectories (*global fitting*). After that deviations between empirical time series and model trajectories were tested for Normality, equivalence of average to zero, and existence/absence of serial correlation. If we can conclude (i.e. we cannot reject the respective Null hypothesis) that distribution of set of deviations corresponds to Normal distribution (it was checked with Lilliefors test, Shapiro – Wilk test and some other tests; Shapiro and Wilk, 1965; Shapiro et al., 1968; Lilliefors, 1967, 1969; Bolshev and Smirnov, 1983; Anderson and Darling, 1952, 1954), after that we can use tests for checking existence/absence of serial correlation (for this reason Durbin – Watson test was used; Draper and Smith,1981). In a situation when distribution of deviations doesn't correspond to Normal there are no reasons to check existence/absence of serial correlation: in such conditions we have to conclude that model doesn't correspond to considering datasets.

It is well-known that criterions can give qualitatively different result: some tests can demonstrate that Null hypothesis (for example, about Normality of deviations) cannot be rejected, and some other criterions can demonstrate that Null hypothesis must be rejected. In this situation we will follow the "principle of spoon of tar": it is well-known that spoon of tar can make foul a barrel of honey. In other words, result of application of statistical criterions doesn't correspond to our target (we get "bad result").

Non-traditional way – method of extreme points (MEP) (Nedorezov, 2012a, 2015, 2016) – was applied to estimation of model parameters too. MEP is based on qualitatively different approach to estimating of model parameters (than it is observed for OLS). At first step of determination of MEP-estimations we must find elements of *feasible set*.

As it was pointed out above feasible set is a set of points from a space of model parameters (plus initial value of population size which is assumed to be unknown too) which correspond to model trajectories with special properties. These properties are following: used statistical criterions described below give required results for sets of deviations (between model trajectories and empirical time series). Set of deviations must have symmetric distribution (with respect to origin); density function must have monotonic behavior of branches for negative and positive values of arguments; there is no serial correlation in a sequence of deviations. For every point of feasible set we can conclude that respective values can be used as estimations of model parameters, and for every point used statistical criterions don't allow concluding that model isn't suitable for fitting of empirical time series. After determination of elements of feasible set, we have to find points with extreme properties: these points correspond to sets of deviations when one or other property (or several properties) are observed in its maximum realization.

When we use Ordinary Least Squares approach to estimating model parameters we try to realize the following steps. Let $g(a, b, x_0, k)$ be a solution of Eq. (1), $g(a, b, x_0, 0) = x_0$, and $\{x_k^*\}$, $k = 0,1, \dots, N$, be a considering sample where N is sample size. At first step we must determine the basic ideology of analysis. Below we'll use global fitting (Wood, 2001 a, b): real (empirical) trajectory we'll approximate by artificial (model) trajectory. It means that model parameters are estimated at minimization of the following functional form:

$$Q(a, b, x_0) = \sum_{k=0}^{N} (x_k^* - g(a, b, x_0, k))^2 \to \min_{a,b,x_0} Q \qquad (2)$$

It is easy to find in literature other variants of loss-function (2): this form can be constructed for birth rates (birth rate is defined as relation of two nearest values of population sizes), it is possible to use absolute values of deviations, squared deviations may have constant or dynamic weights etc. (see, for example, Nedorezov, 2012a, 2018a, b; Wood, 2001a, b; Mvalusepo et al., 2011). It means that there are no rules for determination of kind of loss-function. It can be marked as one of serious problems of OLS approach.

For example, in literature one can find other types/modifications of functional form (2). If we want to take into account stronger influence of small values of initial sample onto final result (on parameter estimations), functional form (2) with weights can be applied:

$$Q(a,b,x_0)=\sum_{k=0}^{N} w_k\left(x_k^*-g(a,b,x_0,k)\right)^2 \to \min_{a,b,x_0} Q$$

In this expression weights w_k are non-negative values for all k, $w_k \geq 0$, $w_0+\cdots+w_N=1$. But now criterion for selection of weights w_k doesn't exist. The only recommendation can be present: in such occasion we have to have bigger values of weight for smaller deviation.

One more way for modification of functional form (2) is as following:

$$Q(a,b,x_0)=\sum_{k=0}^{N} \left|x_k^*-g(a,b,x_0,k)\right|^{\gamma} \to \min_{a,b,x_0} Q$$

In this expression γ is positive number, $\gamma > 0$.

Abundance of types of loss-functions allows concluding that now we have no criterions for selection of functional forms of the type (2). If for obtained estimations of parameters one of used statistical criterions give negative result (in particular, Null hypothesis about correspondence of distribution of set of deviations to Normal distribution, serial correlation is observed in sequence of residuals etc.) it gives a background for conclusion that model cannot be used for fitting of time series. In other words, final conclusion about suitability or non-suitability of model for fitting of considering time series we make using one point of a space of model parameters. Use of loss-functions for finding estimations of model parameters is one of the basic limitations of OLS. It becomes extra serious problem in a situation when we have to use several correlated time series (Rosenberg, 2010; Gilpin, 1973; Gilpin and Ayala, 1973; Tonnang et al., 2009a, b, 2010; Nedorezov, 2014).

As it was pointed out above after estimation of model parameters following hypotheses must be checked: about equivalence of average of residuals to zero; about Normality of deviations (Kolmogorov – Smirnov, Lilliefors, and Shapiro – Wilk tests were used; Bolshev and Smirnov, 1983; Shapiro et al., 1968; Lilliefors, 1967), about absence of serial correlation in sequences of residuals (Draper and Smith, 1981; Bard, 1973). If Null hypotheses cannot be rejected, we can conclude that good correspondence between model and empirical datasets is observed. Below we will call it as traditional approach. On the other hand, requirements on Normality of deviations are rather strong. Thus, we can modify it and check the following properties of samples: symmetry of distribution with respect to origin; density functions must be unimodal with monotonic branches. Hypotheses about monotonic behavior of branches of density functions were checked with Spearman correlation coefficient of ranks (Bolshev and Smirnov, 1983; Nedorezov, 2012a, b, 2014, 2015). Like in previous case it is important to check existence/absence of serial correlation. For checking of absence/existence of serial correlation in sequence of deviations Durbin – Watson test, test "jumps up – jumps down", and some other tests were used (Draper and Smith, 1981; Bard, 1973; Hollander and Wolfe, 1973; Likes and Laga, 1985; Hettmansperger, 1987).

Note that use of Method of Extreme Points (MEP) (Nedorezov, 2012b; Nedorezov and Utyupin, 2011) doesn't assume using of any loss-functions. For obtaining of MEP-estimations of model parameters we have to construct feasible set of points Ω^* in a space $\Omega = \{(a, b, x_0): a, b, x_0 \geq 0$. Set Ω^* must be constructed by the following way: at the beginning we have to choose a set of statistical criterions which must be used for checking of properties of sets of deviations between theoretical/model values and respective values of initial time series. We have also to fix significance level for all criterions. After that we must find points in a space Ω which correspond to sets of deviations when all used statistical criterions give desired results.

If feasible set is empty, $\Omega^* = \emptyset$, we get a background for conclusion that model isn't suitable for fitting of considering time series. When Ω^* isn't empty for approximation of time series we must choose points with extreme properties (for example, we can choose points with maximum *p-value* for one or another statistical criterion).

In current paper 5% significance level was fixed for all used criterions. For every selected point of space of model parameters set of respective deviations was checked on symmetry with respect to origin (it was provided with tests of homogeneity of two samples: Kolmogorov – Smirnov, Mann – Whitney, Lehmann – Rosenblatt, and Wald – Wolfowitz tests were used). Monotonic behavior of branches of density function was checked with Spearmen rank correlation coefficient (Bolshev and Smirnov, 1983; Lakin, 1990). For analysis of absence/existence of serial correlation in sequences of deviations Swed – Eisenhart test and test "jumps up – jumps down" were used (Draper and Smith, 1981; Hollander and Wolfe, 1973; Likes and Laga, 1985; Hettmansperger, 1987).

4 OLS-estimations of Model Parameters

Minimizing of loss-function (2) allowed obtaining following estimations of model (1) parameters: $x_0 \approx 0.086465$, $a \approx 0.090102$, $b \approx 54.236778$; for these estimations we have $Q(a, b, x_0) \approx 1215.035$. This point of space of model parameters belongs to zone where origin is global stable equilibrium; when time step $k = 30$ population size $x_k = 65.12392$, and after that step population size becomes equal to zero for all $k \geq 31$.

Analysis of deviations shows that with 5% significance level hypothesis about equivalence of average to zero cannot be rejected. At the same time probability that distribution of deviations corresponds to Normal distribution is following: $p < 0.1$ (Kolmogorov – Smirnov test), $p < 0.01$ (Lilliefors test), $p = 0.0116$ (Shapiro – Wilk test). Thus with 1% significance level hypothesis about Normality of deviations must be rejected (we follow the principle of "spoon of tar").

For weaker testing conditions we have following results. Testing of symmetry of distribution of deviations: probability of event that distribution is symmetric is equal to $p = 0.584645$ (Wald – Wolfovitz test), $p = 0.033261$ (Mann – Whitney U-test). It allows concluding that with 5% significance level hypothesis about symmetry must be rejected, and consequently OLS-estimation doesn't belong to feasible set Ω^*.

Thus, obtained results allow concluding that with OLS-estimations model (1) cannot give sufficient approximation of time series. Regime of population extinction is observed in model at 31 time step; distribution of deviation doesn't correspond to Normal (respective hypothesis must be rejected with 1% significance level) and so on. In Fig. 2 there are real trajectory and model trajectory obtained for pointed out above values of parameters.

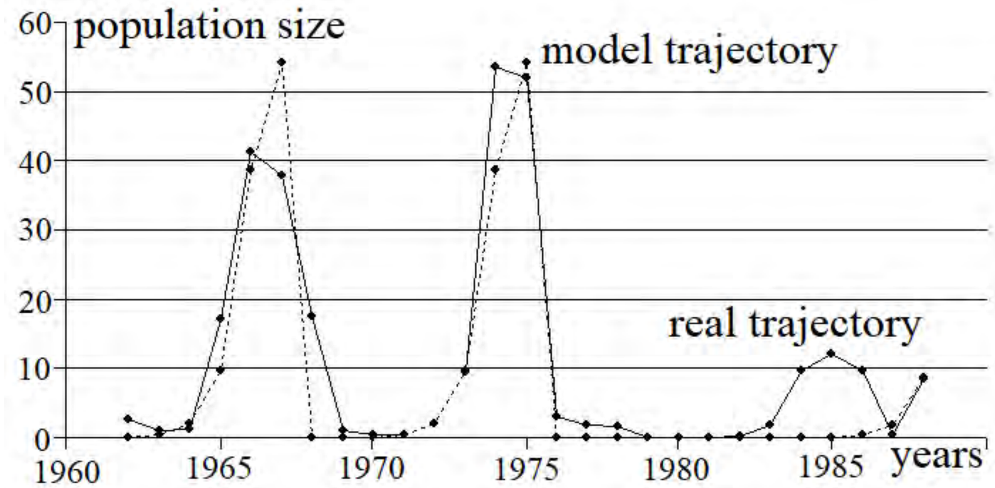

Fig. 2 Time series of fluctuations of green oak leaf roller (real trajectory, solid line) and trajectory of discrete logistic model (1) (broken line) obtained for parameters when minimum value of functional form (2) is observed.

5 MEP-estimations of Model Parameters

In Fig. 3 there are projections of 120000 points of feasible set Ω^* onto coordinate planes. All points were found at pure stochastic search in the domain $[0,102] \times [0,3] \times [0,180]$. Outside of this domain points of feasible set were not detected. As we can see on Fig. 3 big number of points of feasible set Ω^* are within the boundaries of "biological zone" of space of model parameters where inequalities $ab \leq 4$ and $x_0 \leq b$ are truthful. Highest concentration of points (Fig. 3) is observed near bifurcation curve $ab = 4$. It indicates that with a big probability population dynamics of green oak leaf roller corresponds to cyclic regime with a big length of cycle.

Analysis of elements of feasible set shows that 0.15% of all points are in zone between bifurcation curves $ab = 2$ and $ab = 3$. It means that with rather small probability we can observe a regime of fading fluctuations (with asymptotic stabilization of population size at non-zero level). About 79.52% of points are in zone between bifurcation curves $ab = 3$ and $ab = 4$. It means that with rather big probability we observe a regime of periodic fluctuations for population. More than 20% of points belong to non-biological zone ($ab > 4$). Points of feasible set (Fig. 3c) in the zone $ab < 2$ were not detected. It means that estimations of probabilities of regimes of monotonic stabilization of population size at non-zero level and population extinction are equal to zero.

For points of set Ω^* it was obtained that minimum value for Kolmogorov – Smirnov test ($d = 0.25064$) was observed at $x_0 = 26.16194$, $a = 0.11327$, $b = 35.31373$ ($ab = 3.999978$). For these estimations minimum value (0.019231) was also observed for Lehmann – Rosenblatt test. For $t = 0.26$ probability $K(t)$ of Kolmogorov distribution is close to zero (Bolshev and Smirnov, 1983), and respectively with significance level which is close to one, we cannot reject Null hypothesis about symmetry of distribution of deviations. Lehmann – Rosenblatt test shows that this hypothesis cannot be rejected with significance level 0.997. It means that Null hypothesis about symmetry of distribution *must be accepted*. Close result was obtained for Mann – Whitney test: $U = 60$ with critical level 45 when sample size is equal to 26.

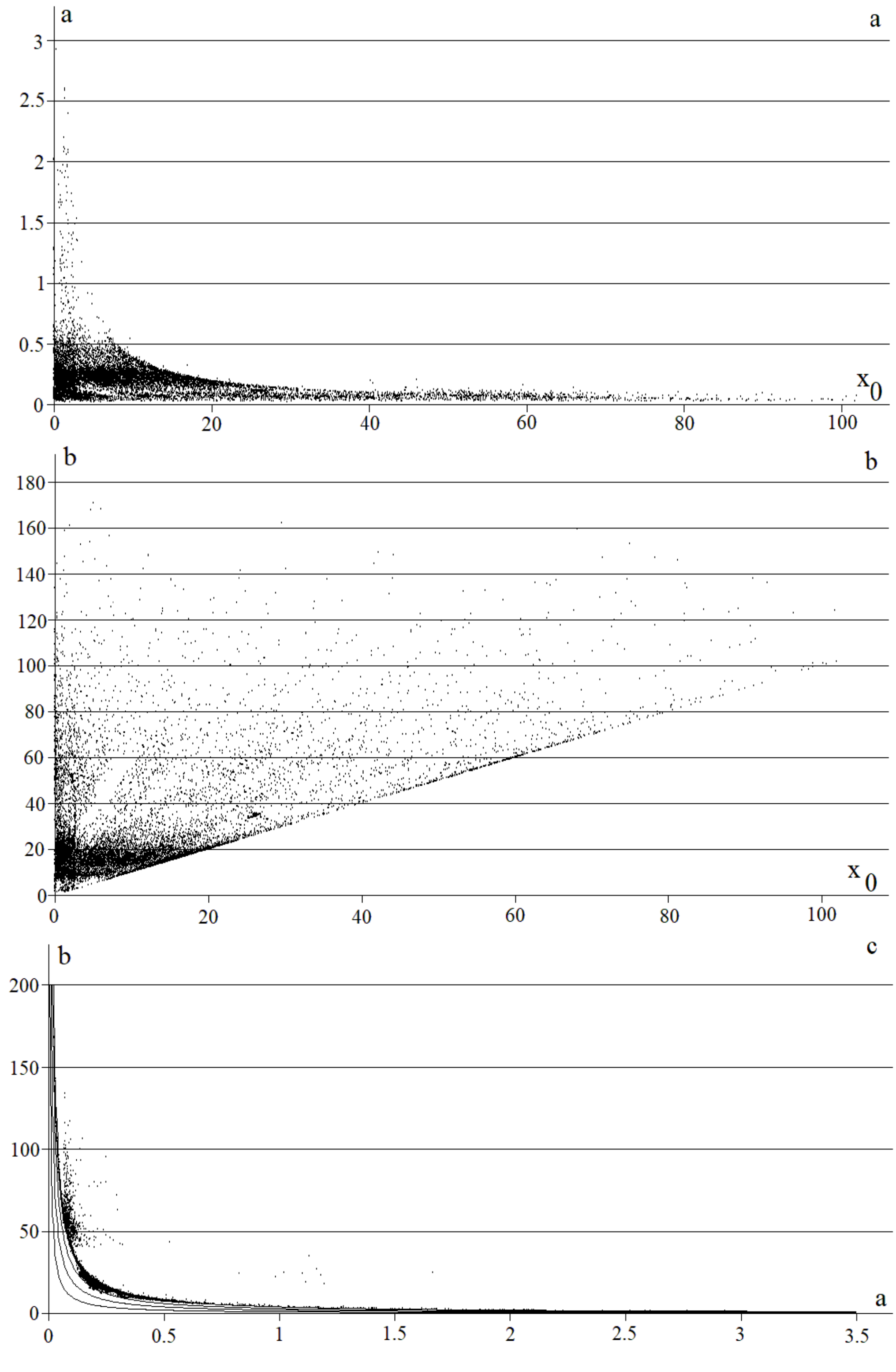

Fig. 3 Projections of 15000 points of feasible set Ω^* onto coordinate planes. a – projection onto plane (x_0, a); b – projection onto plane (x_0, b); c – projection onto plane (a, b) and bifurcation curves $ab = 1$, $ab = 2$, $ab = 3$, and $ab = 4$.

Checking of monotonic behavior of branches of density function of deviations can be provided in two possible variants. If sample size is rather big then we can check pointed out property for deviations $\{e_k^+\}$ and $\{-e_k^-\}$ separately where

$$e_k = x_k^* - g(a, b, x_0, k).$$

Deviation e_k^+ is positive value of deviation e_k, and respectively e_k^- is a negative one. If sample size is small, then we can check pointed out property for set $\{e_k^+\} \cup \{-e_k^-\}$. Let's consider a situation when $\{e_k^+\}$ is sufficient big sample, $k = 1, \ldots, m$. And let $\{e_k^{+*}\}$ be a sample of ordered positive deviations:

$$e_1^{+*} \leq e_2^{+*} \leq \cdots \leq e_m^{+*}.$$

Monotonic decreasing of density function means that bigger values (in sample) must be observed with smaller probabilities. Respectively, for lengths of intervals

$$[0, e_1^{+*}], [e_1^{+*}, e_2^{+*}], \ldots, [e_{m-1}^{+*}, e_m^{+*}]$$

we have to have the similar order (in ideal situation). Rank 1 will correspond to shortest interval $[0, e_1^{+*}]$, biggest rank $m$will correspond to biggest interval $[e_{m-1}^{+*}, e_m^{+*}]$. Ideal case we must compare with real situation which is determined by sample $\{e_k^{+*}\}$. For this reason, we have to calculate Spearmen rank correlation coefficient ρ (and/or Kendall correlation coefficient τ) and check Null hypothesis $H_0: \rho = 0$ with alternative hypothesis $H_1: \rho > 0$. For selected significance level Null hypothesis must be rejected. Note we have stronger result in a case when we can reject Null hypothesis with smaller significance level.

For pointed out parameters we have $p - value = 0.02052$ for Spearmen rank correlation coefficient, and $p - value = 0.02325$ for Kendall correlation coefficient τ. Thus, Null hypotheses must be rejected for both coefficients with 3% significance level.

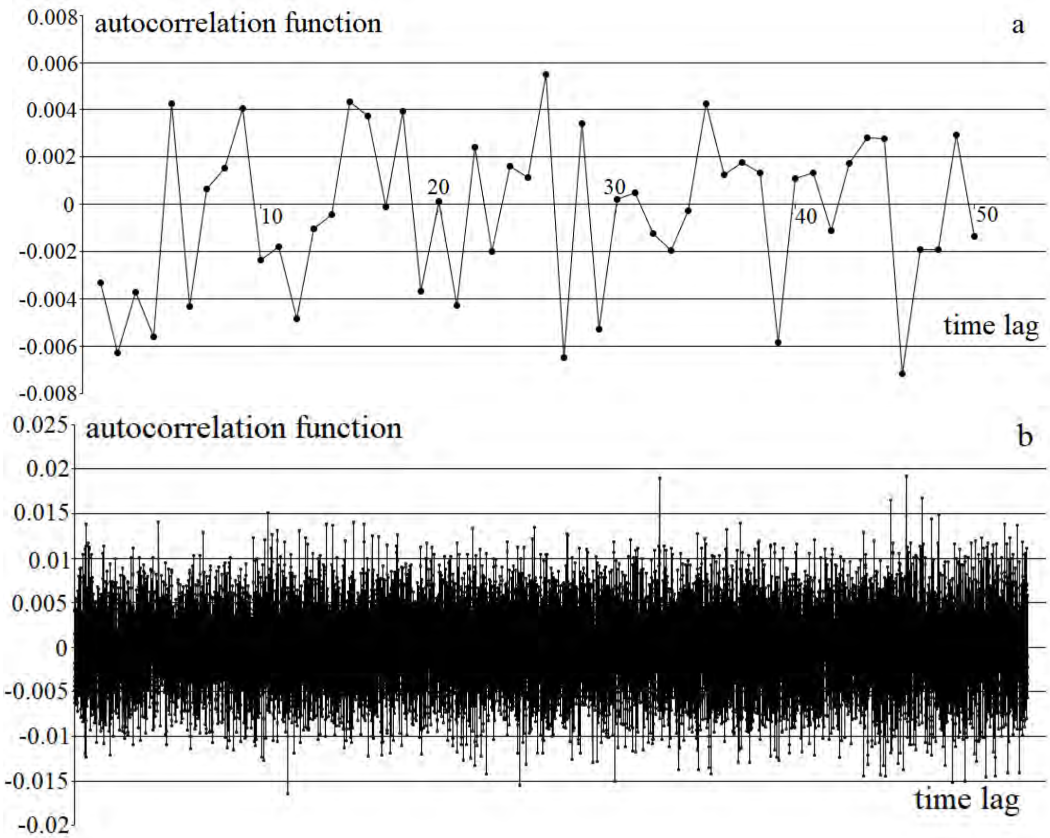

Fig. 4 Behavior of autocorrelation function. a – first 50 steps; b – 1500 steps.

Analysis of behavior of auto-correlation function $r(k)$ shows that for $0 < k < 15000$ all values of this function belong to close interval $[-0.02, 0.02]$ (Fig. 4). It allows concluding that if observed process is cyclic, the length of cycle is bigger than 1500 years. Moreover, fast decreasing of values of this function (Fig. 4a)

$(r(0) = 1)$ and further fluctuations in narrow limits near zero level (Fig. 4b) is typical behavior for processes which forget their history very fast (for example, like pure stochastic processes). In Fig. 5 considering time series and model (1) trajectory obtained for pointed out parameters are presented.

For points of feasible set Ω^* (Fig. 3) it was obtained that maximum value for Mann – Whitney test $U = 119$ was observed for $x_0 = 0.529402$, $a = 0.299619$, $b = 13.234814$ (note this point belong to "biological zone" of space of model parameters, $ab = 3.9654$). For these parameters we have $p - value = 0.1838$ (Kolmogorov – Smirnov test), $p - value = 0.06028$ (Lehmann – Rosenblatt test). Thus with 6% significance level Null hypothesis about symmetry cannot be rejected; but we must note that amount of $p - value$ is very close to critical threshold.

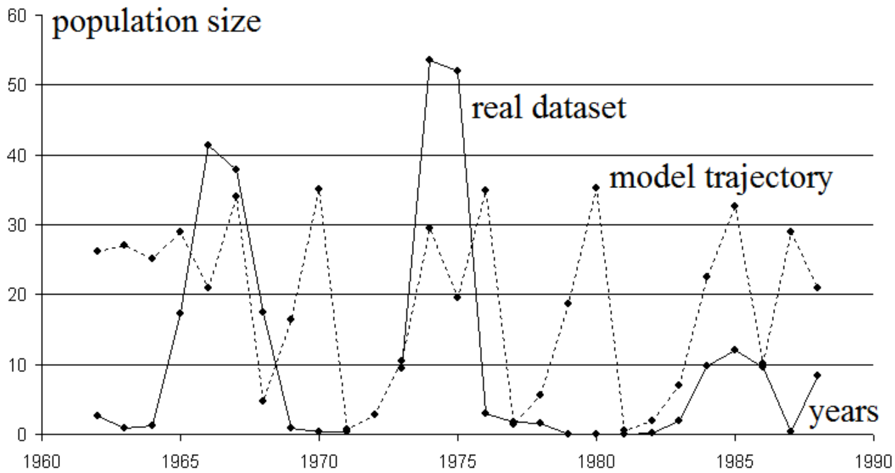

Fig. 5 Time series of fluctuations of green oak leaf roller (solid line) and trajectory of model (1) (broken line) obtained for parameters when maximum amounts of $p - value$ are observed for Kolmogorov – Smirnov and Lehmann – Rosenblatt tests.

Spearmen rank correlation coefficient $\rho = 0.6178$ with $p - value = 0.0004933$. Kendall correlation coefficient $\tau = 0.4277$ with $p - value = 0.0009166$. Taking it into account *we must accept hypothesis about monotonic behavior of branches of density function*.

Analysis of behavior of auto-correlation function $r(k)$ shows (Fig. 6) that for arguments $8 < k \leq 15000$ all values of this function belong to close interval $[-0.08074, 0.0685]$. Like in a previous case if observed process is cyclic length of this cycle must be bigger than 1500 years. In Fig. 7 considering time series and model (1) trajectory obtained for pointed out parameters are presented.

For set Ω^* (Fig. 3) maximum value of Spearmen rank correlation coefficient $r = 0.888547$is observed for the following estimations of model parameters: $x_0 = 0.573105$, $a = 0.217602$, $b = 18.18987$ (this point belong to "biological zone" of space of model parameters, and$ab = 3.958159$). For obtained parameters $p - value = 0.1226$ for Kolmogorov – Smirnov test, $p - value = 0.20171$ for Lehmann – Rosenblatt test, $p - value = 0.218743$ for Wald – Wolfovitz test, and $p - value = 0.293265$ for Mann – Whitney test. Thus with 12% significance level hypothesis about symmetry of deviation's distribution cannot be rejected.

For Spearmen rank correlation coefficient we have $p - value = 8.367 \cdot 10^{-7}$. Kendall correlation coefficient $\tau = 0.7169231$ with $p - value = 5.988 \cdot 10^{-9}$. Considering presented results for deviations we have to accept hypothesis about monotonic behavior of branches of density function.

Analysis of behavior of auto-correlation function $r(k)$ shows (Fig. 8) that for arguments $11 < k \leq 15000$ all values of this function belong to close interval $[-0.038, 0.035]$. Like in previous cases if observed process is cyclic length of this cycle must be bigger than 1500 years.

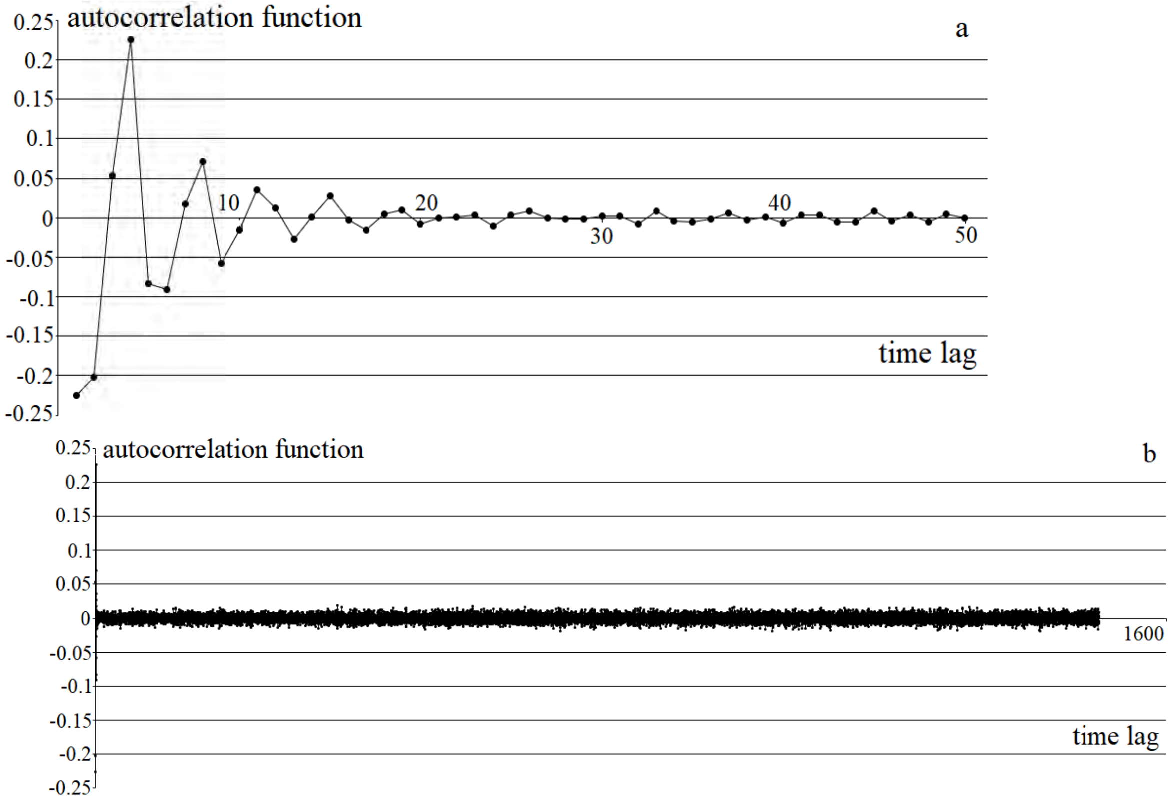

Fig. 6 Behavior of autocorrelation function when Mann – Whitney test has maximum value: a – first 50 steps; b – 1500 steps.

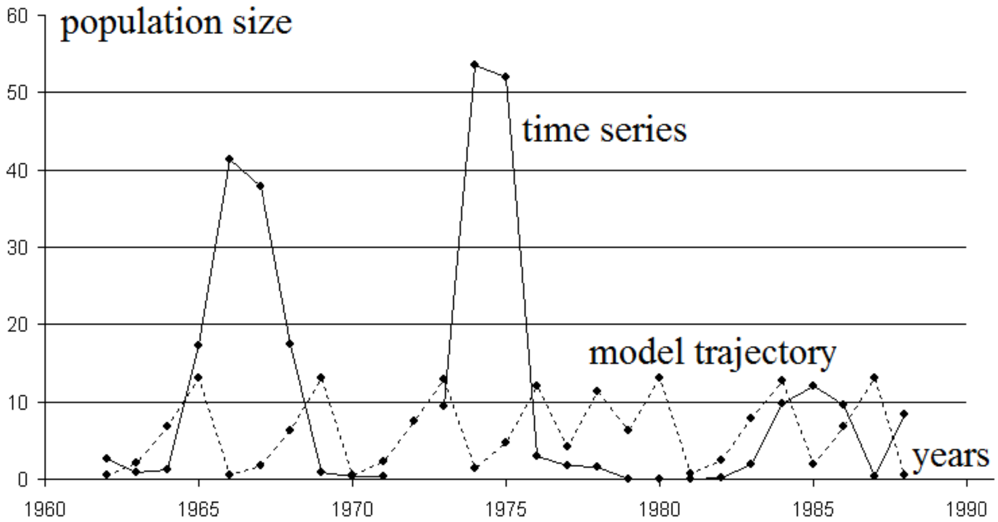

Fig. 7 Time series of fluctuations of green oak leaf roller (solid line) and trajectory of discrete logistic model (1) (broken line) obtained for parameters when maximum amounts for $p - value$ are observed for Mann – Whitney test.

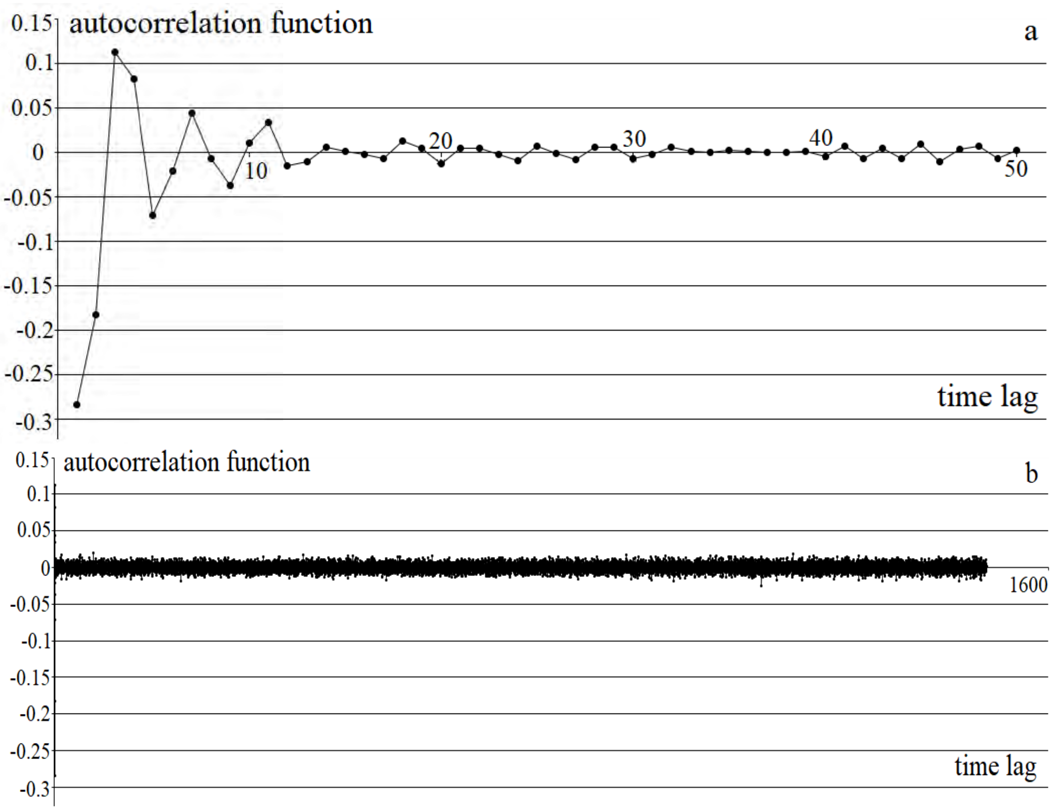

Fig. 8 Behavior of autocorrelation function when Spearmen correlation coefficient has maximum value: a – first 50 steps; b – 1500 steps.

6 Almost-Bayesian Approach to Parameter Estimations

In this chapter we'll consider one more approach to estimating of model parameters. It can be called as "Almost-Bayesian Approach" because it is assumed that parameters of model (1) are stochastic variables (with unknown distribution). Within the framework of Bayesian approach, we must assume that every model parameter has prior density; after that we have to use existing initial sample for determination of a posteriori density functions for all parameters.

It is well-known that selection of type of prior densities for parameters is a serious problem of Bayesian approach. On the other hand, if we have feasible set Ω^* we have no necessity to use any prior densities: we can use joint density for variables, $f(z_1, z_2, z_3)$. Argument z_1 can correspond to first variable, x_0; argument z_2 can correspond to second variable, a; and argument z_3 can correspond to third variable, b. This joint density $f(z_1, z_2, z_3)$ can be presented in the following form:

$$f(z_1, z_2, z_3) = f_1(z_1) f_2(\, z_2/z_1) f_3(z_3/z_1, z_2).$$

In this expression $f_1(z_1)$ is a marginal density of distribution of x_0. Respectively, $f_2(\, z_2/z_1)$ is a conditional density function for second variable, a, for known value of x_0. Finally, $f_3(z_3/z_1, z_2)$ is conditional density function for third variable, b, for known values of x_0 and a. If we know these functions, we can present the following algorithm for calculation of trajectories of model (1) which has following steps:

Step 1. Generate value of x_0 with $f_1(z_1)$.

Step 2. Generate value of parameter $a f_2(\, z_2/x_0)$.

Step 3. Generate value of parameter b with $f_3(z_3/x_0, a)$.

Step 4. After step 3 we can calculate value of population size x_1 using equation (1).

Step 5. Generate value of parameter a with $f_2(\, z_2/x_1)$.

Step 6. Generate value of parameter b with $f_3(z_3/x_1, a)$

Step 7. After step 6 we can calculate value of population size x_2 using equation (1) and so on.

After that we can compare model trajectory with initial time series. But there is a serious problem: we haven't function $f(z_1, z_2, z_3)$. On the other hand, we can consider elements of feasible set Ω^* as stochastic points obtained with joint density $f(z_1, z_2, z_3)$. Thus, we can try to restore densities pointed out above using elements of set Ω^*. For example, for density $f_1(z_1)$ we can use first arguments of all elements of feasible set. It is possible to point out a lot of various methods for determination of $f_1(z_1)$ (see, for example, Parzen, 1962; Aivazyan et al., 1989; Gubarev, 1985; Vasiliev and Melnikova, 2009); below we'll use well-known k-nearest neighbors algorithm in all considering cases. After determination of density function $f_1(z_1)$ (additionally we'll assume that argument is greater than zero: all parameters of model and initial population size cannot be negative; but use of k-nearest neighbors algorithm for density estimation is based on assumption that with positive probabilities we can obtain big and small values of variables) we can determine initial population size using von Neuman algorithm (Ermakov, 1975; Mikhailov, 1974).

After that we have a possibility to find value of parameter a. For this purpose, we have to choose an interval $[x_0 - \delta_0, x_0 + \delta_0]$ which contains sufficient number of points of feasible set (it must be sufficient for obtaining a good estimation of density function of stochastic variable a, $f_2(\,z_2/x_0)$). Note, that we cannot exclude a situation when for fixed value x_0 we haven't points from Ω^*. After determination of subsample of Ω^* we can construct density function using the same k-nearest neighbors algorithm, and with the help of von Neuman algorithm we can get value of parameter a. After that we can repeat this procedure again for obtaining of value of parameter b.

For determination of value of initial population size 15000 points of feasible set were used. In figure 9 there is a function which is proportional to density function (for obtaining of density function we have to divide pointed out function onto respective integral). In figure 10 there are two conditional densities which were obtained for $x_0 = 14.6378$.

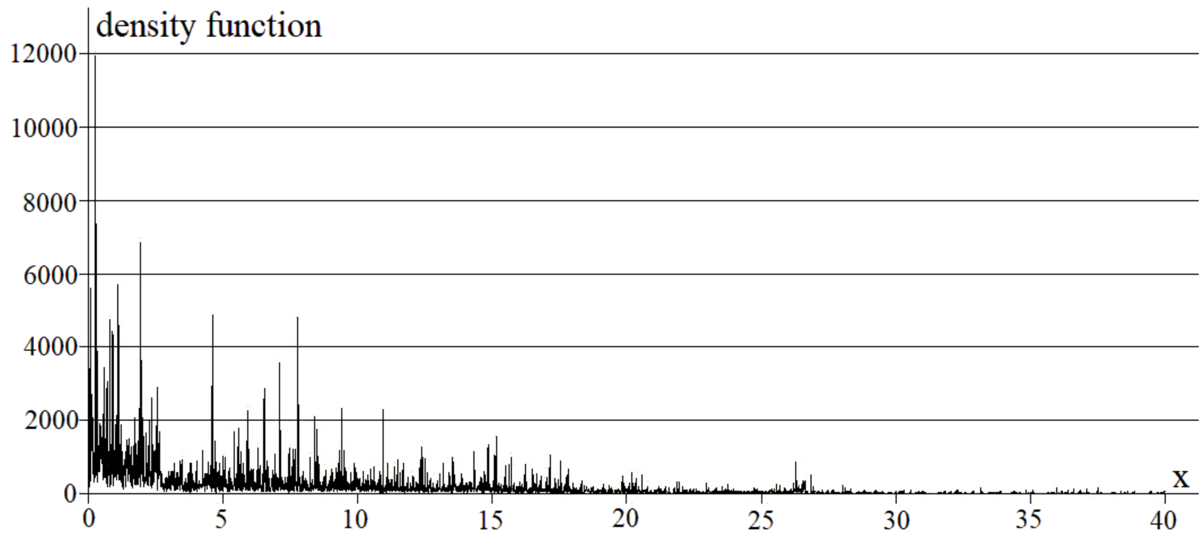

Fig. 9 Function which is proportional to density function of x_0.

Remark. It is important to note that one or other assumption (on a method for estimation of density function) leads immediately to appearance of additional conditions. For example, use of k-nearest neighbors algorithm means that we assume a'priori that our distribution is unbounded – with positive probability we can get negative and big positive values of stochastic variable. On the other hand, we know that all parameters of considering model (1) are non-negative. And it was taken into account in all situations when we used determined algorithm for estimation of density function (fig. 9) for x_0 and density functions for other model parameters. In various situations (for example, when we use Parzen's windows for density fitting) we have to use variants of loss-functions (Parzen, 1962). The following principle for fitting of density function looks rather interesting: in a situation when we have a scalar sample and we have no idea about properties of density function (in other words, sample is a total information we have) width of Parzen's window must be equal to value when Null hypothesis about equivalence of artificial sample (generated by Monte Carlo methods) and initial sample can be rejected with smallest probability (with Kolmogorov – Smirnov test, Lehman – Rosenblatt test etc.). For this reason, we have to generate a lot of artificial samples and for every sample we have to check respective Null hypothesis.

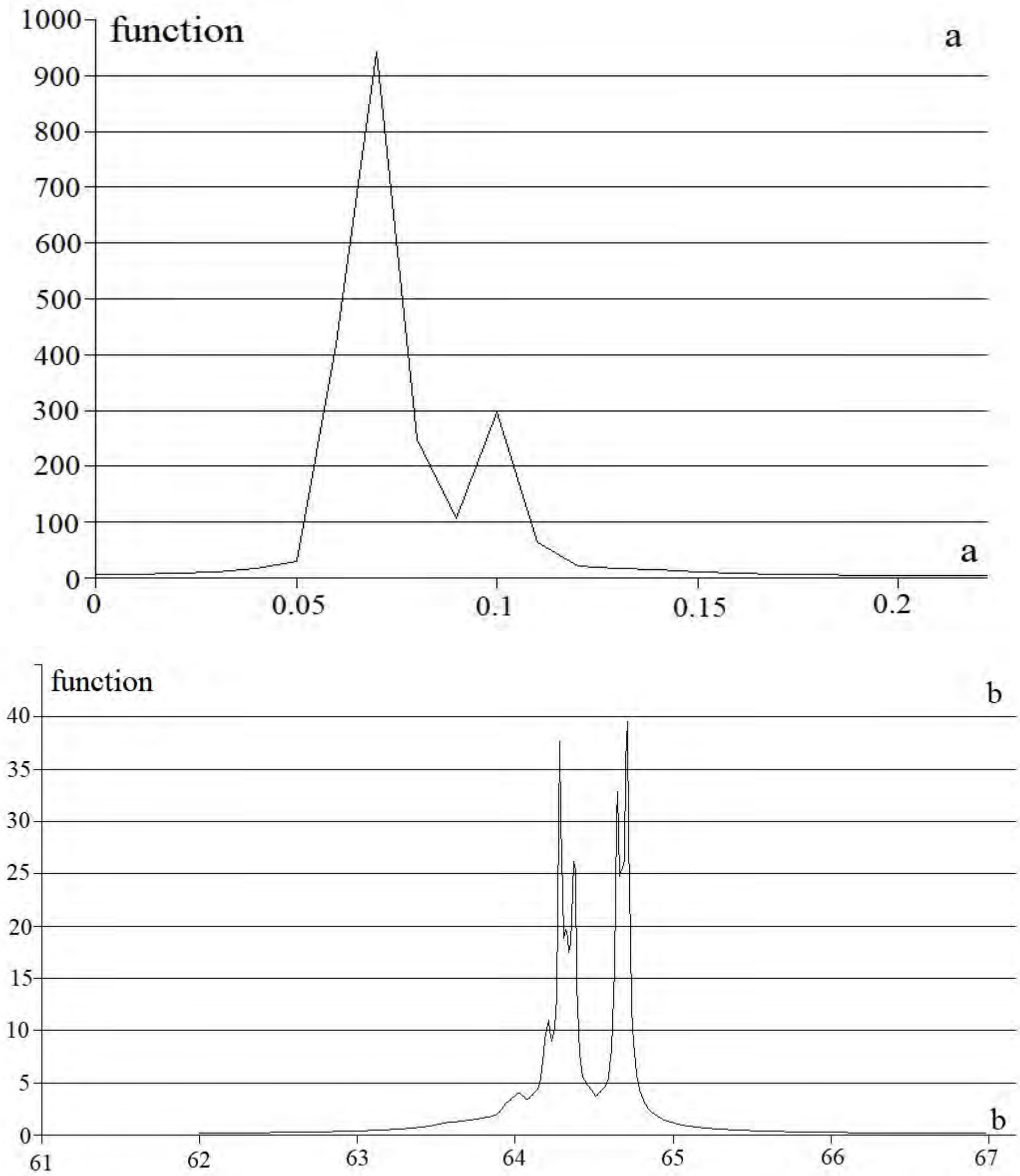

Fig. 10 Conditional densities (after dividing on respective integrals; fragments) for parameter a (with condition $x_0 = 14.6378$) (a), and for parameter b (with conditions $x_0 = 14.6378$ and $a = 0.08$) (b).

In Fig. 11 there are several trajectories of model which were obtained with the help of algorithm described above. A solid black curve is average for 10 stochastic trajectories of model.

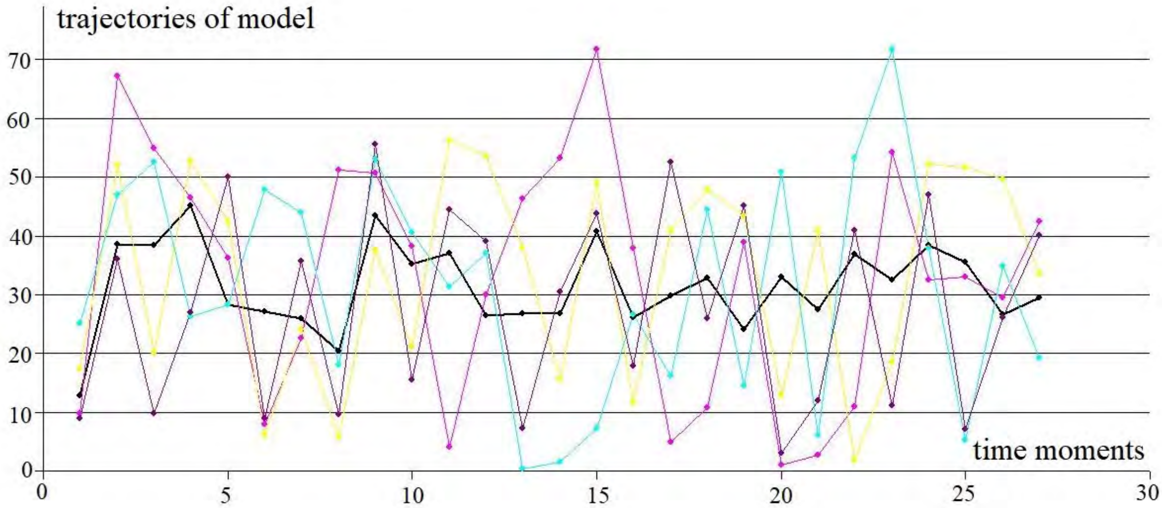

Fig. 11 Behavior of trajectories of model and average trajectory (solid black curve).

7 Conclusion

Provided analysis of fluctuations of green oak leaf roller population (Korzukhin, Semevsky, 1992) with generalized discrete logistic model showed that estimations of model parameters obtained with Ordinary Least Squares method belong to “non-biological zone”. Use of this approach gives us a background for conclusion that model doesn’t allow obtaining sufficient approximation for considering time series. Deviations between theoretical/model values and empirical numbers don’t correspond to several common requirements which must be observed if we check a “good” correspondence between model and existing dataset. For example, hypothesis about Normality of set of deviations must be rejected with 1% significance level.

Use of Method of Extreme Points (MEP) allowed presenting several points of space of model parameters which are suitable for fitting. All presented points belong to “biological zone”, and deviations between theoretical/model trajectories and real dataset are satisfied to set of statistical criterions. In other words, analysis of deviations doesn’t allow concluding that model isn’t suitable for fitting of considering time series.

It is interesting to note that all variants of dynamic regimes which are observed for MEP-estimations of model parameters, correspond (on a qualitative level) to one and the same population size behavior. This is not a cyclic regime with cycle length in 1500 years or less. Moreover, in all situations fast decreasing of values of auto-correlation function (calculated for model trajectories) with further small fluctuations near zero level is observed.

Use of feasible set from the space of model parameters allows constructing modification of model (1) when parameters and initial population size are stochastic variables. It can be called as almost-Bayesian approach to estimation of model parameters (but Bayes’ theorem wasn’t used for determination of distributions of parameters). Projection of feasible set onto coordinate line corresponding to initial population size can be used for fitting of marginal density function of x_0. Set of points which can be obtained in a result of separation of feasible set by rather narrow stripe (near value x_0) can be used for fitting of conditional density for one of model parameters and so on. Finally, it allows obtaining of model trajectory with stochastic parameters. One of problems which exists in such situation is following: difference between model trajectory and existing time series can be rather big (and we cannot conclude that there is a good correspondence between these trajectories).

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