

Article

Modeling and analysis of some methods of entomological data collection

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Abstract

In current publication the stochastic model of individual migrations within the limits of closed domain and processes of data collections using in entomology are considered. The behavior of data variation with respect to changing of population size is analyzed. In particular, it was shown that dependence of standard deviations has a non-linear character under the population density increasing. It was also shown that confidence level to datasets of population density which were obtained with traditional methods and under the low value of population density must be extremely low.

Keywords population dynamics; stochastic mathematical model; data collection.

1 Introduction

Estimations of model parameters of mathematical models of population dynamics are among the main items for creating forecasts of population size changing in time, for finding optimal methods of population management, and for solution of many other important problems. In many cases the process of model parameters estimation starts with the words “Let’s consider a time series of population density (or population size) changing in time...” $\{x_k^*\}$, $k = 0, \dots, N$, where $N + 1$ is a sample size. Also this investigation starts with the words “Let’s consider the following mathematical model with unknown parameters which describes the population density changing”:

$$\frac{dx}{dt} = F(t, x, \alpha). \quad (1)$$

In equation (1) $x(t)$ is a population density at time t ; α is a vector of unknown model parameters; F is non-linear function which satisfies to a set of known limits (Nedorezov and Utyupin, 2011; McCallum, 2000; Brauer and Castillo-Chavez, 2001; Bjornstad et al., 1999; Kendall et al., 1999, 2005; Tonnang et al., 2009, 2010; Nedorezov, 2011a; Turchin, 2003 and others). Of course, model (1) may be of other type (for example, it can be a system of recurrence equations; Isaev et al., 2009; Ivanchikov and Nedorezov, 2011; Nedorezov and Sadykova, 2005, 2008, 2010, and other) but the problem will be the same: for existing time series $\{x_k^*\}$ values of model (1) parameters α must be determined. It is important to note, that in various cases initial value of population density $x_0 = x(0)$ must also be determined using existing datasets. Even in the case when we have experimental datasets, initial value x_0 is known and doesn’t need to be determined (Nedorezov, 2011b).

It is possible to point out a lot of various approaches to the problem of estimation of model parameters (see, for example, Pawitan, 2001; McCallum, 2000; Wood, 2001a, b). Least squares method is one of the basic methods and it is widely used in practice (Hudson, 1970; Gubarev, 1985; Nedorezov and Sadykova, 2005, 2008, 2010; Nedorezov et al., 2008; Demidenko, 1981). The use of least squares method assumes that we have to find the global minimum for squared deviations between theoretical (model) values (which must be obtained with model (1)) and empirical dataset $\{x_k^*\}$. For example, we have to find the global minimum for the following functional form:

$$Q(\alpha, x_0) = \sum_{k=0}^N (x_k^* - x(t_k, \alpha, x_0))^2 . \quad (2)$$

In (2) $x(t_k, \alpha, x_0)$ is the respective theoretical value (for *global fitting* it is a solution of equation (1); Wood, 2001a, b) which is obtained with equation (1) for concrete values of model parameters α and initial value of population density x_0 .

There are some additional assumptions for models which are assumed to be suitable for fitting of considering time series. In particular, it is assumed that deviations between theoretical and empirical values must correspond to Normal distribution with zero average. In this case the natural question arises: what is the base for the assumption that deviations between theoretical and empirical values must have Normal distribution? And additional question is: what is the base for the assumption that all deviations have one and the same Normal distribution? The answer is obvious: there are no real bases (which are determined by the biology of investigated object) for both these assumptions.

Requirement about the equivalence of arithmetic average to zero (in this situation we must talk about requirement but not about assumption) is obvious – in a set of measurements the systematic errors cannot be observed. It is also understandable that distribution of deviations must be a symmetric function (with respect to origin), and realization of bigger deviation must have smaller probability. From these two obvious requirements we can't conclude that distribution of deviations is Normal. We have also to say that assumption about normality of deviations is in contradiction with common sense: for example, if we estimate the weight of larva in milligrams we cannot have a mistake in several tons with positive probability in principle. We can't also to have a negative value of weight (with positive probability also).

In current publication we analyze other important problem – we consider the base of assumption about the equivalence of distributions of deviations. It is obvious a priori that if local population size is equal to zero for every number of measurements (for every number of trial areas or number of “casts of frame”) the average will be equal to zero, and sample variation will be equal to zero too. Increase of population density leads to the respective increase of average and sample variation. And we have to take it into account in expression (2) if we want to have all deviations $x_k^* - x(t_k)$ are equally distributed.

In a situation when small deviations (especially in the case when population density is small enough) play the similar role like big deviations (i.e. small deviations have the same contribution to the estimations of model (1) parameters) researchers use so-called weights $\{w_k\}$. Expression (2) transforms into the following form:

$$Q(\alpha, x_0) = \sum_{k=0}^N w_k (x_k^* - x(t_k, \alpha, x_0))^2 . \quad (3)$$

Weights $\{w_k\}$ have the following properties:

$$w_k = \text{const} \geq 0, \sum_{k=0}^N w_k = 1.$$

The use of these weights $\{w_k\}$ leads to appearance of new set of questions. For example, how can we choose amounts of weights for making parameter estimations better? Unfortunately, up to current moment we have no criterions for the weights selection. Introduction weights into the formula (2) looks like a good wish only. It is very important to note that solution of this problem (the problem of finding of the best weights for the expression (3)) is outside of the domain of model parameter estimations, analyses of properties of initial sample, or analyses of deviations between theoretical and empirical datasets. Solution of this problem can be found in the domain of modeling and analyses of existing methods of information collection, field methods of estimation of population density. It has strong correlation with modeling and analyses of migration processes in populations and types of interaction of individuals with each other.

In current publication we give possible values of the weights $\{w_k\}$ when migration processes in a local population are organized rather simple. It is assumed that movements of individuals from one place to another (within the boundaries of finite domain on a plane) are stochastic, and depend on the relations between population sizes in neighboring plots. It is also assumed that population size is constant (thus, every time *real population density* is well-known), and “methods of data collection” (within the framework of considering model) can be identified with a method of “casting of the frame” (which is used, for example, for the estimation of insect population density on the field) or with a method of “excision of squared meter of forest floor in autumn”.

For considered model it was found that for low value of population density the confidence level of obtained results (estimations of population density) must be extremely low (even in the cases when “frame casts” several times, or several plots of forest floor are used for obtaining estimations). It was also obtained that dependence of standard deviations on the real population density changing has non-linear character; but in the case when population density is small enough it can effectively be approximated by linear function.

2 Description of the Model

Let N be a total population size. We'll assume that $N = \text{const}$ during the time of providing of computer experiments (for estimation of population density). And let Z_{nm}^2 be an integer rectangular lattice on the plane R^2 :

$$Z_{nm}^2 = \{(i, j) : 1 \leq i \leq n, 1 \leq j \leq m\}.$$

Additionally we'll assume that local population size is determined in knots (i, j) of the lattice Z_{nm}^2 . Denote it as $x_{ij}(t)$ for $(i, j) \in Z_{nm}^2$ at time moment t . For all time moments $t, t = 0, 1, 2, \dots$, the following relation is truthful:

$$\sum_{i=1}^n \sum_{j=1}^m x_{ij}(t) = N.$$

It means that there are no migrations outside the domain Z_{nm}^2 .

Definition. We'll call two knots $(i_1, j_1), (i_2, j_2) \in Z_{nm}^2$ as neighboring knots if and only if the following relation is truthful:

$$|i_1 - i_2| + |j_1 - j_2| = 1.$$

Within the framework of model it will be assumed that migration processes from the knot (i, j) can be observed to neighboring knots only. About the behavior of migrants we'll assume that for all values of local population sizes there is the quota δ , $\delta = const > 0$, $\delta < 1$, of individuals which migrate to neighboring knots with equal probabilities (in other words, behavior of these individuals doesn't depend on current situations in Z_{nm}^2). Let's also assume that probabilities of migration of all other individuals to neighboring knots (the quota of these individuals is equal to $1 - \delta$) depend on a distribution of individuals in neighboring knots of the lattice Z_{nm}^2 .

All knots of the lattice Z_{nm}^2 can be divided with respect to local population size on to three qualitatively different types. Denote as D_1 and D_2 , $D_1 < D_2$, two critical levels which determine the optimal interval of population size; respectively, we'll assume that if in knot (i, j) the population size $x_{ij}(t)$ satisfies to the following inequalities $D_1 \leq x_{ij}(t) \leq D_2$ from this knot we can observe stochastic migrants only (total number of stochastic migrants is about $\delta x_{ij}(t)$). In this situation the number of non-migrated individuals is about $(1 - \delta)x_{ij}(t)$.

If the following inequality is truthful $x_{ij}(t) < D_1$, all individuals try to leave this knot (they migrate to neighboring knots). Let

$$y_{ij}(t) = \frac{1}{x_{ij}(t) + \varepsilon}. \quad (4)$$

In (4) ε is a positive parameter which corresponds to sensitivity of migrants to local population sizes in neighboring knots of lattice. Sensitivity decreases with the increase of parameter ε . If the value of this parameter is big enough all probabilities become equal. Decrease of parameter ε leads to increase of sensitivity to local population sizes.

For every knot (i, j) which doesn't belong to the boundary of lattice Z_{nm}^2 we'll assume that probability p_{i-1j} of migration of every individual to knot $(i-1, j)$ is determined by the following formula:

$$p_{i-1j} = \frac{y_{i-1j}(t)}{y_{i-1j}(t) + y_{i+1j}(t) + y_{ij-1}(t) + y_{ij+1}(t)}. \quad (5)$$

The similar formulas can be presented for all other (three) probabilities. It is obvious, for example, if $i = 1$ and $1 < j < m$ knot (i, j) belongs to the boundary of lattice Z_{nm}^2 , and the respective probability (5) is equal to zero; probability p_{i+1j} is determined by the following formula:

$$p_{i+1j} = \frac{y_{i+1j}(t)}{y_{i+1j}(t) + y_{ij-1}(t) + y_{ij+1}(t)}. \quad (6)$$

The use of formulas (5) and (6) means that the probability for individuals to migrate to any knot increases with decrease of the local population size in considering knot. If knot (i, j) is in corner of the lattice (let, for example, $i = 1, j = 1$) probability p_{i+1j} (6) will have the following form:

$$P_{i+1j} = \frac{y_{i+1j}(t)}{y_{i+1j}(t) + y_{ij+1}(t)}. \quad (7)$$

Presentation of probabilities in the forms (5)-(7) means that in population there is no mechanism for the supporting of the optimal population density (within the limits D_1 and D_2). Thus, all optimal groups will disappear in time (in a result of existence of “crazy migrants” $\delta x_{ij}(t)$). But described above model can be modified. Let’s assume that we have three various weights: weight q_1 is for knots where local population size is less than $D_1 \leq x_{ij}(t) \leq D_2$; weight q_2 is for optimal zone when $D_1 \leq x_{ij}(t) \leq D_2$; weight q_3 is for third zone where local population size is greater than level D_2 . All weights q_j are non-negative, $q_j \geq 0$. In modified model probabilities were calculated with the formulas like (5)-(7): it was assumed that probability is proportional to the weight of the respective knot and inversely proportional to the sum of weights of the neighboring knots.

Finally, in the situation when we have very high local population size, $x_{ij}(t) > D_2$, the considering system is out of the optimal zone, and in this situation we’ll also assume that individuals try to leave this knot. But for this situation we’ll have one more probability – the probability for staying in this knot. This probability will be calculated by the following formula:

$$P_{ij} = \frac{y_{ij}(t)}{y_{ij}(t) + y_{i-1j}(t) + y_{i+1j}(t) + y_{ij-1}(t) + y_{ij+1}(t)}. \quad (8)$$

Remark. Probabilities which are determined by the formulas (4)-(8) have strong dependence on the value of parameter ε . For example, if in one neighboring knot local population size is equal to zero, and in all other neighboring knots we observe one or more individuals, then the probability of individual’s migration to empty knot becomes close to one even for $\varepsilon \approx 10^{-3}$.

3 Results of Modeling

For the computer modeling of migration processes it was assumed that total population size N is constant; thus, theoretical population density μ was known and equal to $\mu = N/nm$. Below we present results of modeling for the quadratic lattice Z_{nm}^2 with $m = n = 100$. Initial population state was modeled in the following manner: every individual with equal probabilities could appear in every knot of the lattice. After determination of initial situation the process of individual’s migrations was started (with respect to formulas (5)-(8)). During the time T (number of time steps, for providing calculations it was assumed that $T = 200$) was run free. It is important moment because we have to have on the lattice the situation which is determined by the population migration process only, and doesn’t depend on the initial state of population.

After that the process of data collection was started: in four stochastic points of the lattice the local population size was fixed (it looks like four times of casts of the frame). After that model run free during the next T time steps; after that we had the process of data collection again and so on. This procedure was repeated 1000 times. For obtained values of local population sizes standard deviations from the *real population density* were calculated:

$$s_1^2 \left(\frac{N}{nm} \right) = \frac{1}{999} \sum_{k=1}^{1000} \left(x_{1,k}^* - \frac{N}{nm} \right)^2,$$

$$s_2^2\left(\frac{N}{nm}\right) = \frac{1}{999} \sum_{k=1}^{1000} \left(\frac{x_{1,k}^* + x_{2,k}^*}{2} - \frac{N}{nm} \right)^2,$$

$$s_3^2\left(\frac{N}{nm}\right) = \frac{1}{999} \sum_{k=1}^{1000} \left(\frac{x_{1,k}^* + x_{2,k}^* + x_{3,k}^*}{3} - \frac{N}{nm} \right)^2,$$

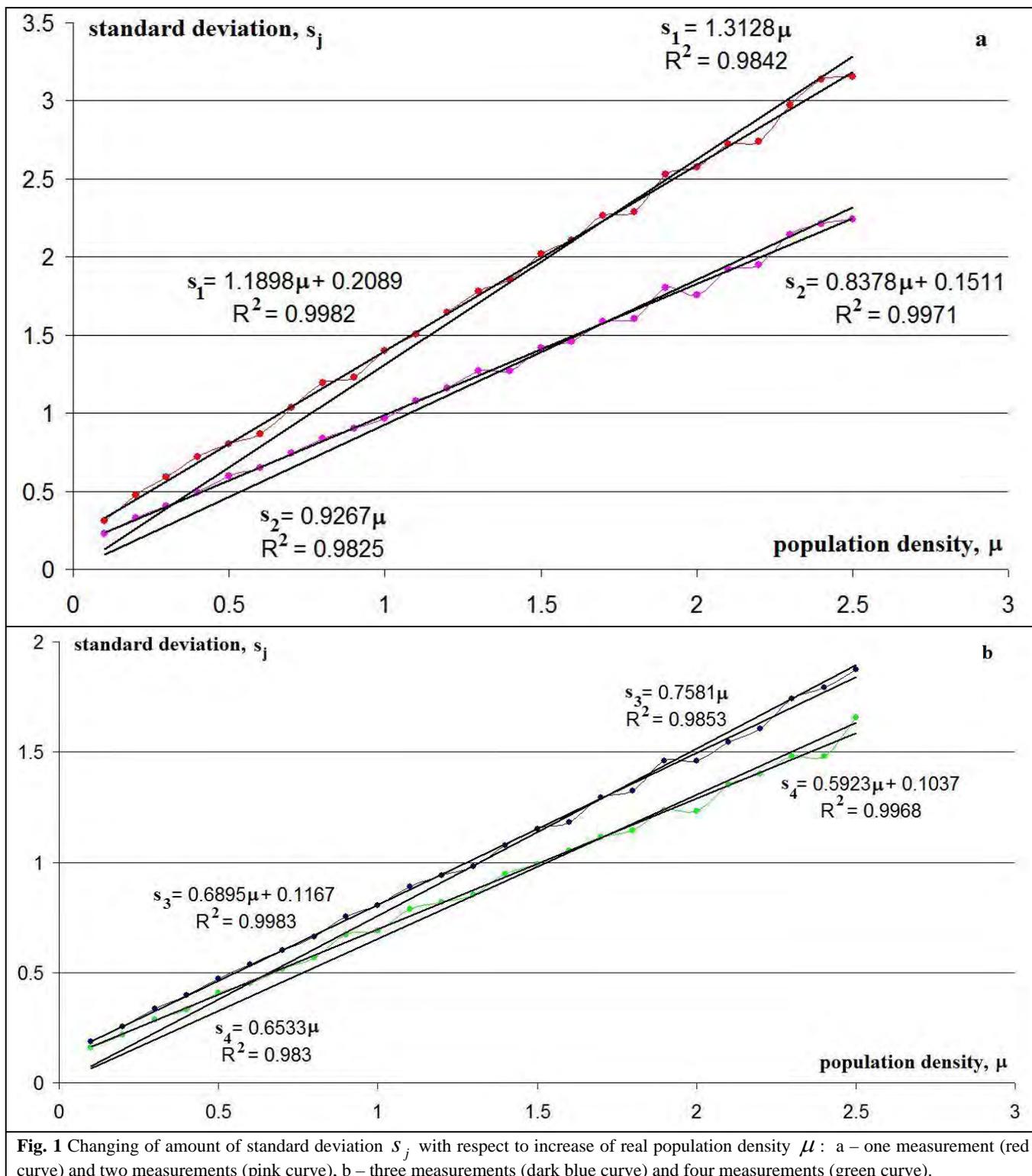
$$s_4^2\left(\frac{N}{nm}\right) = \frac{1}{999} \sum_{k=1}^{1000} \left(\frac{x_{1,k}^* + x_{2,k}^* + x_{3,k}^* + x_{4,k}^*}{4} - \frac{N}{nm} \right)^2.$$

In these formulas $x_{j,k}^*$ is element number k from the sample number j , $j = 1, 2, 3, 4$. It is important to note that weights $\{w_k\}$ in the expression (3) must be inversely proportional to s_j ; in such a situation every bracket in expression (3) will be normalized stochastic variable with zero average and variance which is equal to one. Some results of modeling with parameters $D_1 = 10$, $D_2 = 30$, $\varepsilon = 0.1$, $\delta = 0.1$ and low value of population density ($N \leq 2.5nm$) are presented on Fig. 1.

As we can see on Fig. 1, if population density μ is small enough the standard deviation of observations near real density corresponds to linear function: coefficient R^2 is close to one (it is observed for all four considering cases; in this situation there are no influence of boundary conditions or existence of knots with qualitatively different types of migration processes onto the character of existing migration processes – really we have a homogeneous stochastic population process). It is obvious that linear function *must intersect the origin* because for $\mu = 0$ all standard deviation s_j must be equal to zero too. But if we use for the approximation a linear function without free element of equation we have bad results (Fig. 1): a big number of values (for example, on the interval $\mu \in [0, 1.25]$) belong to one part of straight line (points have bigger values of ordinates). Thus, we have to take it into account at the selection process of finding weights for the equation (3).

Presented results of modeling (Fig. 1) allow us to conclude that increase of the number of trials leads to the decrease of amount of free element of linear function (it is obvious, that asymptotically amount of this coefficient must converge to zero under the increasing of number of trials); at the same time we can observe the decrease of the coefficient of incline of straight line at the increase of number of trials (but asymptotically this coefficient doesn't converge to zero). Decrease of the coefficient of incline of straight line means that differences of the weight coefficients w_j in (3) will decrease at the increase of number of trials.

On the bigger intervals of changing of the density μ the qualitatively different picture can be observed (Fig. 2), and there are no possibilities to give a good approximation for the datasets by straight lines. After the monotonic increasing (up to the value $\mu \approx 10$) we can observe the decrease of dispersion; it means that on the corresponding interval of changing of population density practically we have no changing in estimations of dispersion. It is interesting to note that decreasing of dispersion is observed for all considering four variants (Fig. 2).



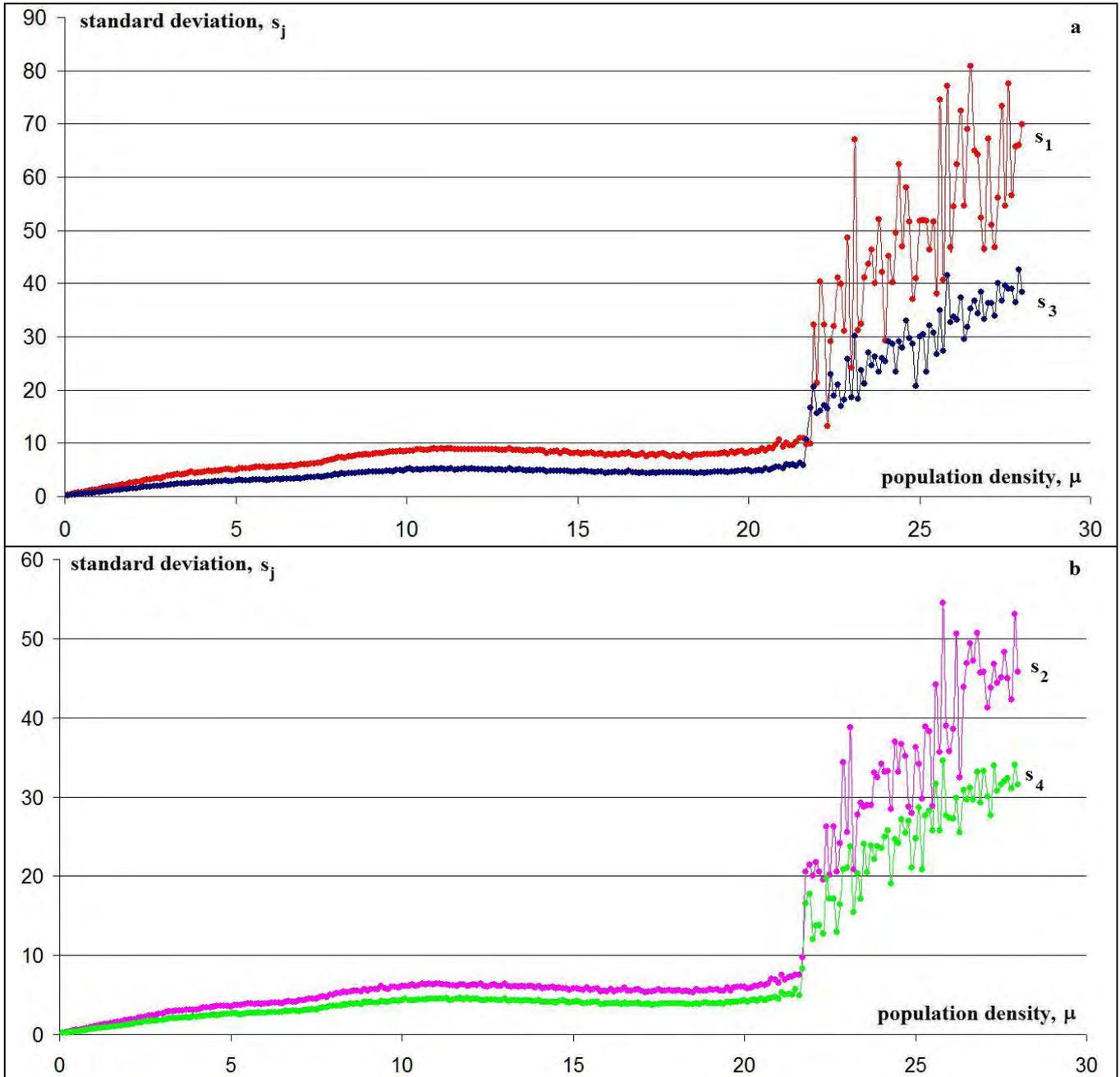


Fig. 2 Changing of amount of standard deviation s_j with respect to increase of real population density μ : a – one measurement (red curve) and three measurements (dark blue curve) (pink curve), b – two measurements (pink curve) and four measurements (green curve).

Further increasing of population density (up to the values when boundary conditions have strong influence onto dynamics of migration processes; Fig. 2) leads to the situation when standard deviations have strong increasing (after the value $\mu = 21.7$). In this situation we can observe big fluctuations of estimations. It means, in particular, that in such situations we have problems as with finding of confidence domains for population density as for finding weight coefficients for expression (3). Nevertheless, we cannot exclude the possibility that for finding good estimations for standard deviations we have to have more than 1000 observations.

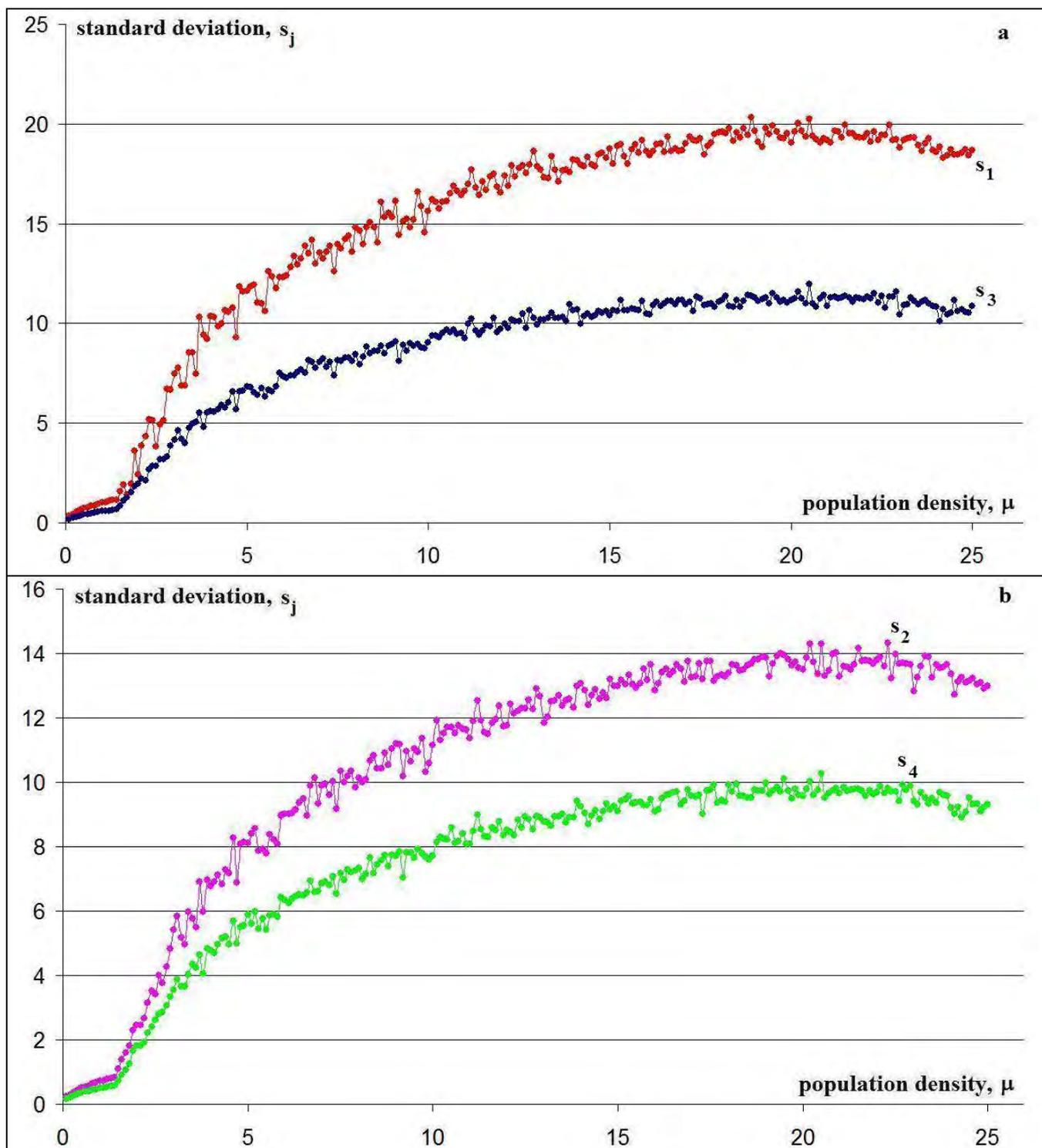


Fig. 3 Changing of amount of standard deviation s_j with respect to increase of real population density μ (within the framework of modified model): a – one measurement (red curve) and three measurements (dark blue curve) (pink curve), b – two measurements (pink curve) and four measurements (green curve).

On the Fig. 3, there are the results of modeling and estimation of standard deviation for the cases when migration processes are organized in other manner then in the previous considered case. It is assumed that

coefficients of the migrations (probabilities of transmissions of individuals from one knot of the lattice to neighboring knots) depend on the weights q_j which describe the attractiveness of various knots for migrants.

For realization of stochastic process on the computer it was assumed that weight $q_1 = 1$ if the local population size is less than D_1 ; weight $q_2 = 10$ if the local population size belong to optimal zone $[D_1, D_2]$; weight $q_3 = 0.2$ if local population size is greater than D_2 . It is important to note that in considering variant the mechanism for supporting of optimal population density is observed.

As we can see from the presented results of computer modeling (Fig. 3), up to the amount $\mu = 1.5$ (approximately) the linear increase of standard deviation with respect to increase of population density is observed. Like in the previous case, we cannot exclude the following explanation for observed behavior of standard deviation: existing situation is homogenous, and there are no influence of optimal zones onto migration processes or influence of zones with local population density over the level D_2 . In other words, initial linear growth of standard deviation corresponds to migrations of “crazy” individuals only.

Increase of local population size leads to the situation when laws of migration become more complicated, and it has strong influence onto amounts of standard deviations. In particular, it leads to more intensive increase of estimations and increase of dispersion of estimates itself. Note, that in considering situation like in the previous one, it is possible to point out intervals where increase of population density leads to decrease of standard deviation (Fig. 3).

4 About Errors of Estimations for Small Values of Population Density

On the considering lattice $Z_{100,100}^2$ transect with eight points (1,1), (10,10), (20,20), (30,30), (40,40), (50,50), (60,60), (70,70) was chosen. It was assumed that local population size could fixed simultaneously in all points of transect. Between two times of measurements of local population sizes in transect's points model was run free during 500 time steps (in other words, every individual of considering population could intersect domain $Z_{100,100}^2$ from one boundary to another 5 times with positive probability). It was also assumed that total population size N is constant, and quota δ of density-independent migrants is high enough, $\delta = 0.4$.

For every point of transect local population size was fixed 1000 times, and for every time moment (of population size fixation) for all transect's points average was calculated. After that the hypothesis $H_0 : \mu = N/10000$ was checked with alternative hypothesis $H_1 : \mu \neq N/10000$. For checking of the hypothesis the standard Student' t-criterion was used with confidence level 0.05. Finally, quota of cases when hypothesis H_0 must be rejected was calculated. Results of modeling and calculations are presented on Fig. 4 for $N = 1000, 2000, 3000, 4000, 5000$.

On Fig. 4 there are the averages of quotas of mistakes (hypothesis H_0 is truthful and cannot be rejected) for 1000 trials plus-minus standard errors for respective values of real population density μ . As we can see, if population density is small enough the probability of event that value of *real population density* doesn't belong to 95% confidence interval, is greater than 0.5. Note, that close results was obtained with significance level 0.01.

Thus, we have the following conclusion. Even in a case when migration processes are very simple organized (which we have in considering model) estimations of population density along the transect which includes eight points, correspond to nothing in 50% cases (Fig. 4). Increasing of population density in to two times leads to strong decreasing (more than in two times) of number of mistaken results – in 21.8% cases only

the value of real population density is out of the respective confidence interval. If we increase the value of density in three times there is 11.9% of mistaken results only (i.e. we have the decreasing of number of mistaken results more than in three times).

Remark. It seems that in considering case we have a paradox situation: with the probability $p \approx 0.512$ value of real population density is out of the interval where it must be with the probability 0.95 (for $\mu = 0.1$; Fig. 4). But answer is obvious: for small value of population density in initial samples we have a big number of zero values. Thus, there are no reasons to talk about Normality of elements of samples. And, consequently, standard (parametric) methods of the estimation of boundaries of confidence intervals and checking of hypotheses don't work in this occasion.

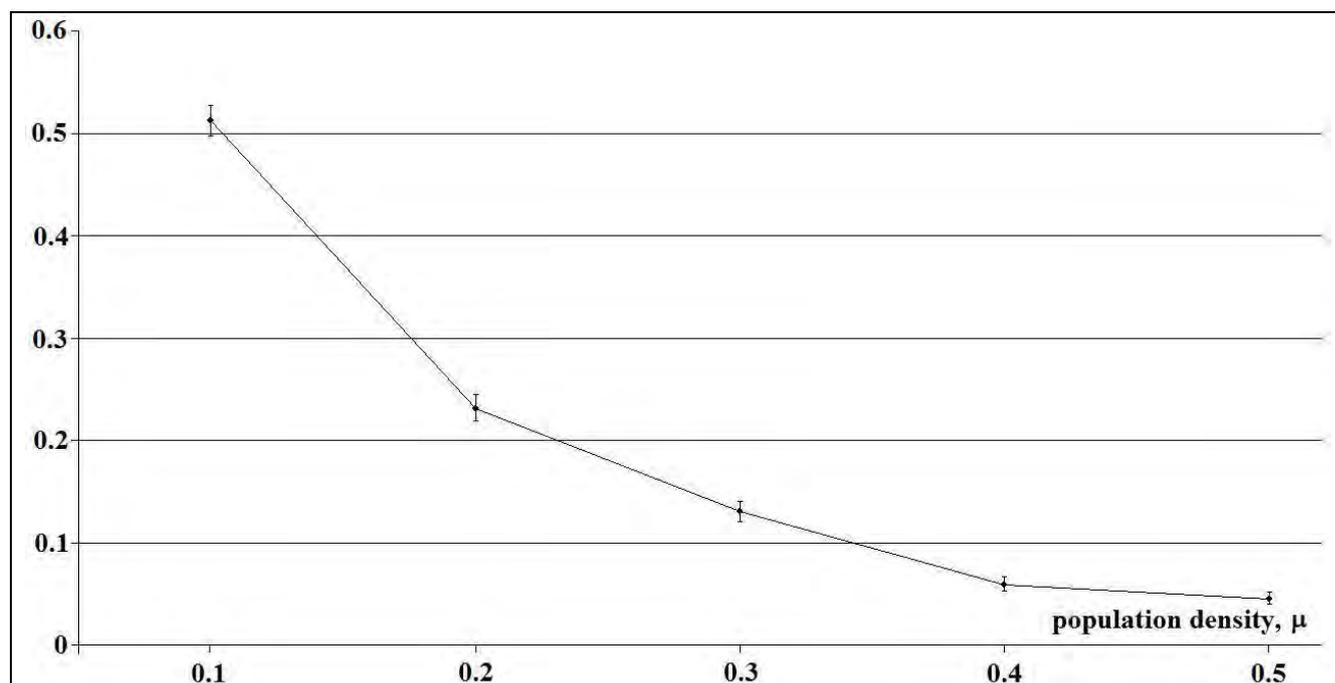


Fig. 4 Estimations of quotas of errors (averages were calculated for 1000 measurements for transects with 8 points of observations) plus – minus standard errors for every value of real population density μ .

5 Conclusion

Considered in paper stochastic model of the processes of data collection looks like well-known method of “casting of the frame” or some methods of estimation of forest insect population densities in boreal zone. Within the framework of basic model (when migration processes are determined by the local population sizes) the existence of optimal zone for individuals was postulated. At the same time mechanisms of supporting of optimal population density were absent. Existence of optimal zone had strong influence onto intensities of migration processes from the respective knot to neighboring knots. The pure stochastic migrants could be observed from the knots with optimal local population size.

Within the framework of modified model it was assumed that migration processes depends on the conditions of knots. Condition of the knot had been determined with respect to interval of population size. Knot had a highest weight if population size was in optimal interval. Knot had smaller weight if population size was less than in optimal zone. Finally, knot had smallest weight if population size was bigger than in optimal zone. Thus, in modified model we have the mechanism supporting optimal local population size.

The basic question we tried to solve with the help of computer experiments was following: what is the character of the dependence of standard deviation of estimation of population density (average of local population size in a knot) on real population density? It is obvious that for all computer experiments we knew real population density. It is also obvious that amount of standard deviation will increase monotonously with respect to population density. But what's the law of this increasing?

This is very actual problem for the solution of other important problem – for estimation of ecological model parameters. Least square method is frequently used technique for the estimation of model parameters. The use of this method requires finding of global minimum for the squared deviations between theoretical (model) results and empirical datasets (2) and (3). If global minimum is found deviations have to be analyzed, and basic properties of the set of deviations must be determined.

It is well-known problem: if we use least square method without the respective weights in the expression of minimized functional form (2), we have a situation when small values in initial sample have no influence on parameter's estimations. In other hand, up to current moment there are no real recommendations for the process of selection of the weights. Moreover, it is well-known too, that set of deviations is a set of stochastic values with different distributions. In spite of it we can check some important properties of this set – for example, we can check the equivalence of average to zero or symmetry of a sample. But analysis of some other properties (like existence/absence of serial correlation with Durbin – Watson criteria) meets with insuperable difficulties.

Provided calculations showed that in some cases (see Fig. 1) standard deviation changes practically linear (with $R^2 > 0.98$) at increase of population density (but it is observed for strong rarefied populations only). Let $y = ax + b$, where y is a standard deviation, x is a population density, a, b are the coefficients of straight line which are determined (in particular) by the number of trials for the estimation of population density. When we use mathematical model (for example, of the type (1)) for the approximation of biological datasets, we can assume that for every fixed set of parameters model gives us real value of population density (of course, this assumption isn't truthful – this is a substitution of unknown value of real density on known value obtained with the help of model). If so, criterion (3) can be presented in other form when all elements of the sum have one and the same characteristics: they have zero average and unit dispersion:

$$Q(\alpha, x_0) = \sum_{k=0}^N \frac{C}{ax(t_k, \alpha, x_0) + b} (x_k^* - x(t_k, \alpha, x_0))^2 .$$

In this expression value of coefficient C can be determined from the condition that total sum of all weights must be equal to one. Taking into account that we have to find a global minimum of this functional form, without changing of the final results we can put $C = b = 1$. In more general case (see Fig. 2 and 3) one can try to use piece-linear function or linear function in a combination with fractional-linear function (in a term of fraction). In cases when interval of changing of population density includes values corresponding to over-concentrated populations, even in simplest situations considered in current publication it is very difficult to give a good recommendation.

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