

**Restoration of phase portrait structure for the dynamics of a forest pest,  
the pine looper moth (*Bupalus piniarius* L.)**

**L.V. Nedorezov**

Research Center for Interdisciplinary Environmental Cooperation RAS, Saint-Petersburg, Russia  
E-mail [l.v.nedorezov@gmail.com](mailto:l.v.nedorezov@gmail.com)

**Abstract.** In this paper we consider the method for the restoration of phase portrait structure of population dynamics and apply this method for analysis of experimental data on the population dynamics of pine looper moth (*Bupalus piniarius* L.). The method is based on the results of phenomenological theory of forest insect population dynamics (Isaev et al., 1984, 2001; Nedorezov, 1986) and includes the elements of statistics, cluster analysis and knowledge of trajectory's behavior of system of ordinary differential equations. Using the method allows determination of such important features of phase plane as the value of stable level, structure and boundaries of the stable zone, behavior of the threshold curve which separates the stable and outbreak zones and coordinates of “point of escape” etc.

### **1. Introduction**

A lot of various publications is devoted to analysis of pine looper moth population dynamics (Schwerdtfeger, 1941, 1944, 1957, 1968; Klomp, 1966; Isaev et al., 1984, 1997, 2001; Nedorezov, 1986, 2012; Nedorezov, Nekljudova, 2000; Kendall et al., 2005; Palnikova, Sviderskaya, Soukhovolsky, 2002 and many others). These publications are devoted to general analysis of existing datasets, identification of population dynamic types, constructing of phase portraits for various particular cases, and to modeling and forecast of population size changing.

Within the framework of phenomenological theory of forest insect dynamics (Isaev et al., 1984, 2001; Isaev, Nedorezov, Khlebopros, 1979, 1980) pine looper moth was classified as eruptive species with dynamics corresponding to an outbreak proper. Note that classification of insects was based on analysis of non-parametric model (model of Kolmogorov type) of predator-prey system dynamics, obtained dynamic regimes were ranked, and insects were classified with respect to their maximal possibilities. An outbreak proper, permanent outbreak and fixed outbreak have maximal ranks (among all other types of population dynamics). All these types of population dynamics belong to group of dynamic regimes which characterize eruptive species.

Further development of phenomenological theory was realized in several directions. First of all, there were attempts to construct parametric model (of general type) which have all necessary dynamic regimes (Khlebopros et al., 1979, 1980), and models which describe dynamics of concrete species (Nedorezov, 1981; Nedorezov, Nekljudova, 2000). Development of this direction has a serious problem: if we have a model with rather big number of parameters and variables which gives good approximation of existing time series, may be, we have nothing. We have no reasons to say that we have a good result if we did not prove that we cannot give good approximation with poorer model (with smaller number of parameters and variables). Current state of this direction is following: we try to apply simplest mathematical models (like Verhulst, Gompertz, Kostitzin etc. models) for description of dynamics of some important species of forest and agricultural pests (in particular, *Tortrix viridana* L., *Zeiraphera diniana* Gn., *Lymantria dispar* L. etc.). And it is interesting to note that in some cases we got good results in application of primitive mathematical model (for example, discrete logistic model) to known time series (see, for example, Nedorezov, 2012, 2015; Nedorezov, Sadykova, 2015).

Other direction of phenomenological theory development was correlated with checking of completeness of insect classification with methods of cluster analysis. It was provided for big number of empirical trajectories and for various types of encoding of these trajectories (Nedorezov, 1986, 2013a). Obtained results are close to original classification; but this problem cannot be solved totally because empirical time series are very short (very big part of existing empirical trajectories), datasets are presented in various units, time series for “uninteresting species” (non-outbreak species, indifferent species) are absent etc.

May be, the next direction is most of interest: this is the problem of identification of phase portrait structure (Nedorezov, 1989, 1999; Nedorezov, Utyupin, 2011). For every species we have to have analog of “passport” which gives information about population dynamic types, about critical levels, and specificity of domains when and where we can use one or other protected methods. It becomes extremely important in a situation when we do not know a law of population dynamics, when we cannot find or construct mathematical model which can give good approximation of time series and obtain reliable prediction.

Phase portrait contains various its elements: stable and unstable stationary states, special surfaces (separatrixes) which divides zones of attractions of one or other attractors etc. If we have a mathematical model we can estimate model parameters using various statistical methods. For estimated values of model parameters we can easily find structure of phase space (in a result of analytical or numerical analysis of model). But if we have not a model problem becomes very difficult. In any sense this situation is close to other problems in statistics: if we know (or if we can

assume) that elements of sample have concrete distribution we can estimate parameters of this distribution; if we have no idea about a law we can restore density function using various statistical methods (Gubarev, 1985).

Before restoration of phase portrait we have to demonstrate that observed time series do not correspond to simple strong cycles. It can be realized with standard statistical methods: in details it was described in our publications where it was also applied to some well-known time series (Nedorezov, 2013b, 2013c, 2013d). In particular, it was applied to analysis of considering in current publication time series on pine looper moth population dynamics.

Main goal of current publication is following: to determine basic elements of phase portrait of pine looper moth population dynamics in Germany (Schwerdtfeger, 1941, 1944, 1957, 1968).

## 2. Idea of method

The basic idea of the method of the restoration of phase portraits structure is the following: to combine our knowledge about the behavior of theoretical trajectories, methods of cluster analysis and mathematical statistics. The phase portrait of an outbreak proper on Figure 1 was obtained as a result of analysis of mathematical model which describes the interaction between phytophagous insects and their entomophagous (Isaev et al., 1984, 2001).

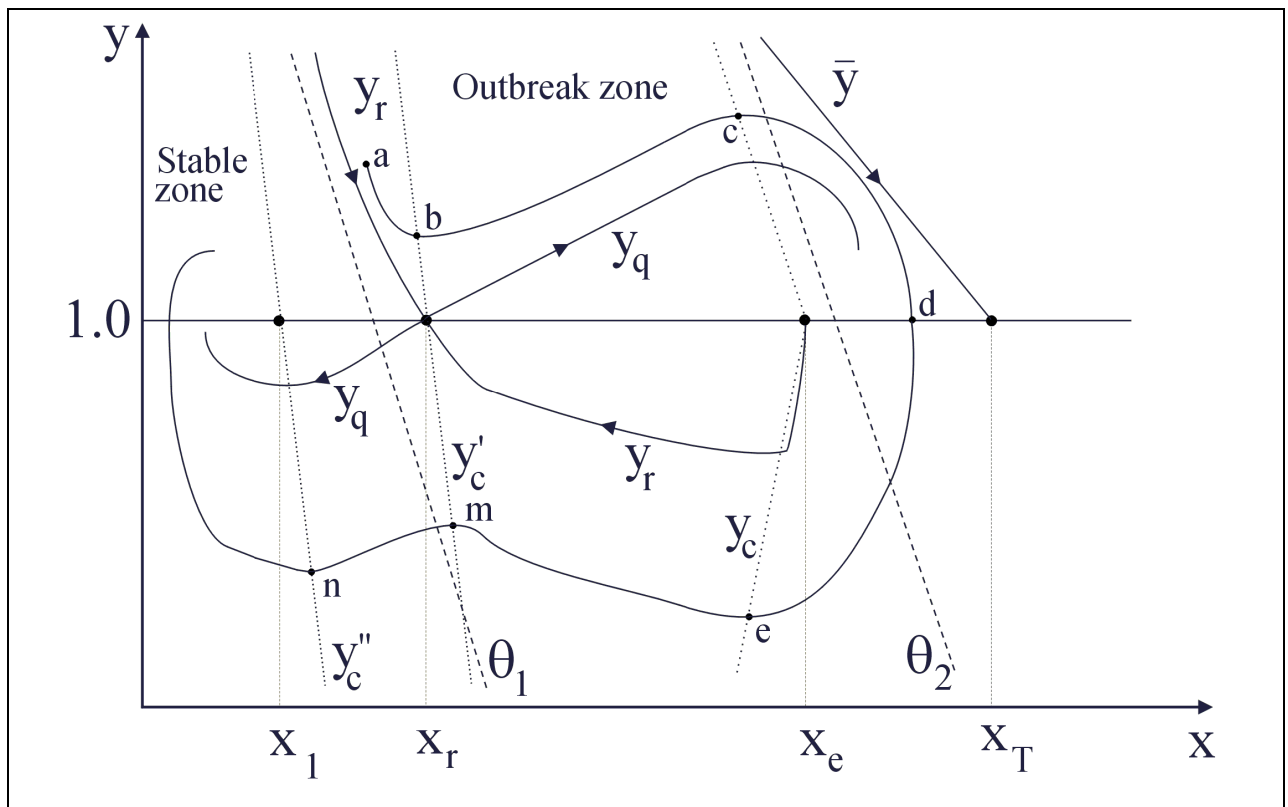


Fig. 1. Phase portrait of an outbreak proper. Details are in the text.

Phase portrait is presented on the plane “population density – birth rate”.  $x_k$  is a population density at moment  $k$ . Birth rate is determined as relation of two nearest values of population densities:

$$y_k = \frac{x_{k+1}}{x_k}.$$

It is well-known that all stationary states of system belong to strait line  $y = 1$ . If birth rate is greater than 1,  $y > 1$ , population density increases; if there is the inverse relation,  $y < 1$ , population density decreases. Point  $x_1$  is global stable equilibrium. In phase portrait we have no other stable attractors. Thus, if we check population density changing during a long time interval, biggest cluster of points must be concentrated near this stable point  $x_1$ . Within the boundaries of zone of stability (near point  $x_1$ ; fig. 1) we have to observe “ring” moving of empirical trajectory. Below we will divide between two types of moving of trajectory: “ring” moving which can be observed around any attractor, and moving with determined direction of changing of population density for all parts of trajectory in cluster.

Point of escape  $x_r$  is a saddle point:  $y_r$  is incoming separatrix and  $y_q$  is outgoing separatrix of this saddle (fig. 1). In upper part of phase plane ( $y > 1$ ) separatrix  $y_r$  divides zone of stability and outbreak zone. As we can see an outbreak trajectory  $abcd\dots$  at initial period of outbreak goes to saddle point  $x_r$ . This dynamic effect was found for big part of outbreak species (Isaev et al., 1984, 2001). At that moments speed of movement of system decreases: in a result of it we can get concentration of empirical points near saddle point  $x_r$ . But it will be a cluster with points with determined direction: from left part of phase plane to right. At the same time we may have big fluctuations of population size within the limits of zone of stability (fig. 1): these trajectories can be close to point of escape  $x_r$ , and respective decrease of speed of system moving can be observed too. As it was pointed out above it can lead to appearance of cluster of points near  $x_r$ . This cluster can be close to cluster which contains points of type “b” of outbreak trajectory.

Finally, if population dynamics corresponds to the outbreak proper (fig. 1) we have to have biggest cluster of points near stable level  $x_1$ . Taking into account that number of outbreak trajectories and trajectories corresponding to big fluctuations within the limits of stable zone are not so big, big (but smaller) cluster must be observed near point of escape  $x_r$ .

Maximum of population size can be observed near saddle point  $x_r$  (fig. 1). Near this point we also have a decreasing of speed of system moving and, respectively, sometimes we may have cluster organized by points of “d” type (points with maximum values of population size). This

cluster can be formed by points of outbreak trajectories only. It means that this cluster must be smaller than two previous clusters.

Minimum value of population size on peak phase of outbreak is  $x_c$ . This point (fig. 1) is unstable knot or focus (“repeller”): it means that all trajectories go out of this point. In other words, we cannot have any clusters near this point, and concentration of empirical points in this zone must have minimum value.

On phase portrait we have some important curves like  $\theta_1$  and  $\theta_2$  (boundaries of zone of inertia regulative mechanisms action),  $y_c$ ,  $y_c'$  and  $y_c''$  (curves of maximum and minimum values of birth rate  $y$ ),  $\bar{y}$  (upper limit of phase portrait) which cannot be determined without using of mathematical model. But in all situations before determination of detailed features of phase portrait we have to solve the problem with identification of dynamic type of population. There exists a lot of methods from very simple and up to very difficult.

### 3. Time series

We used the known data of Schwerdtfeger (1957, 1968) on fluctuations of the density of pine moth (*Bupalus piniarius* L.) in the pine forests near the town of Letzingen in Germany. The data are freely available online in the NERC database (Centre for Population Biology, Imperial College, 1999, no. 3759). The data are presented as “the number of caterpillars in the litter per one square meter in December”. In total, there are 58 values ( $N = 58$ , initial sampling volume), and the data for 1911 and 1912 are absent. Empirical trajectories are presented in Figure 2 on the plane  $(x_k, x_{k+1})$  – “population density at time  $k$  – population density at time  $k+1$ ” – in logarithmic scales.

### 4. Very simple method

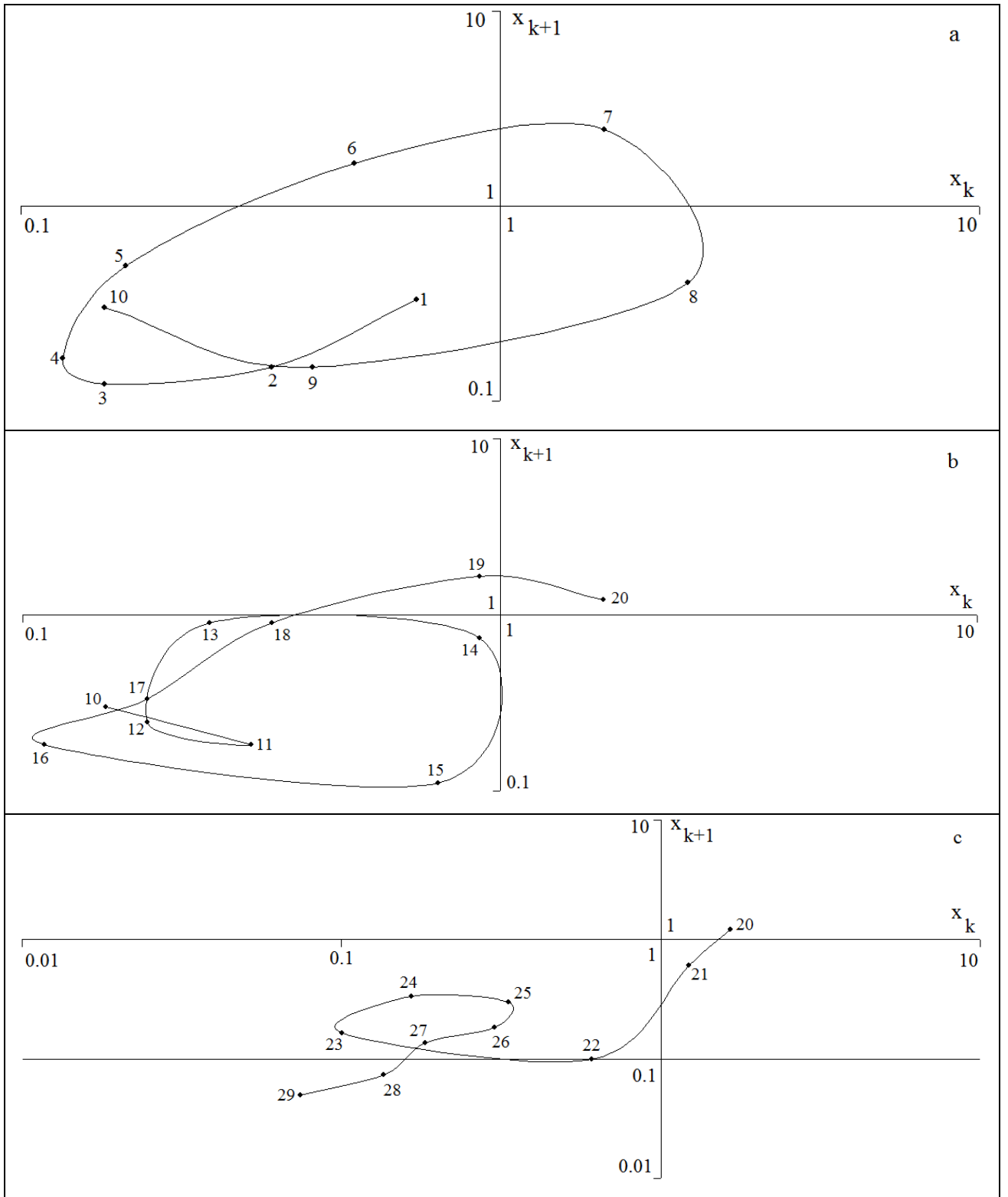
In book by Lakin (1990) it is possible to find very simple method for grouping of existing dataset (Starges method). For scalar sample  $\{z_k\}$ ,  $k = 1, 2, \dots, m$ , we have to determined a relation of scope of the sample and number of intervals we want to have:

$$\lambda = \frac{z_{\max} - z_{\min}}{K}.$$

$z_{\max}$  is a maximum value in the sample  $\{z_k\}$ , and  $z_{\min}$  is a minimum value in the sample.  $\lambda$  is a length of interval.  $K$  can be determined as follows (approximately):

$$K = 1 + 3.322 \lg(m).$$

Left boundary of intervals (which must cover all points of sample  $\{z_k\}$ ) may be determined as



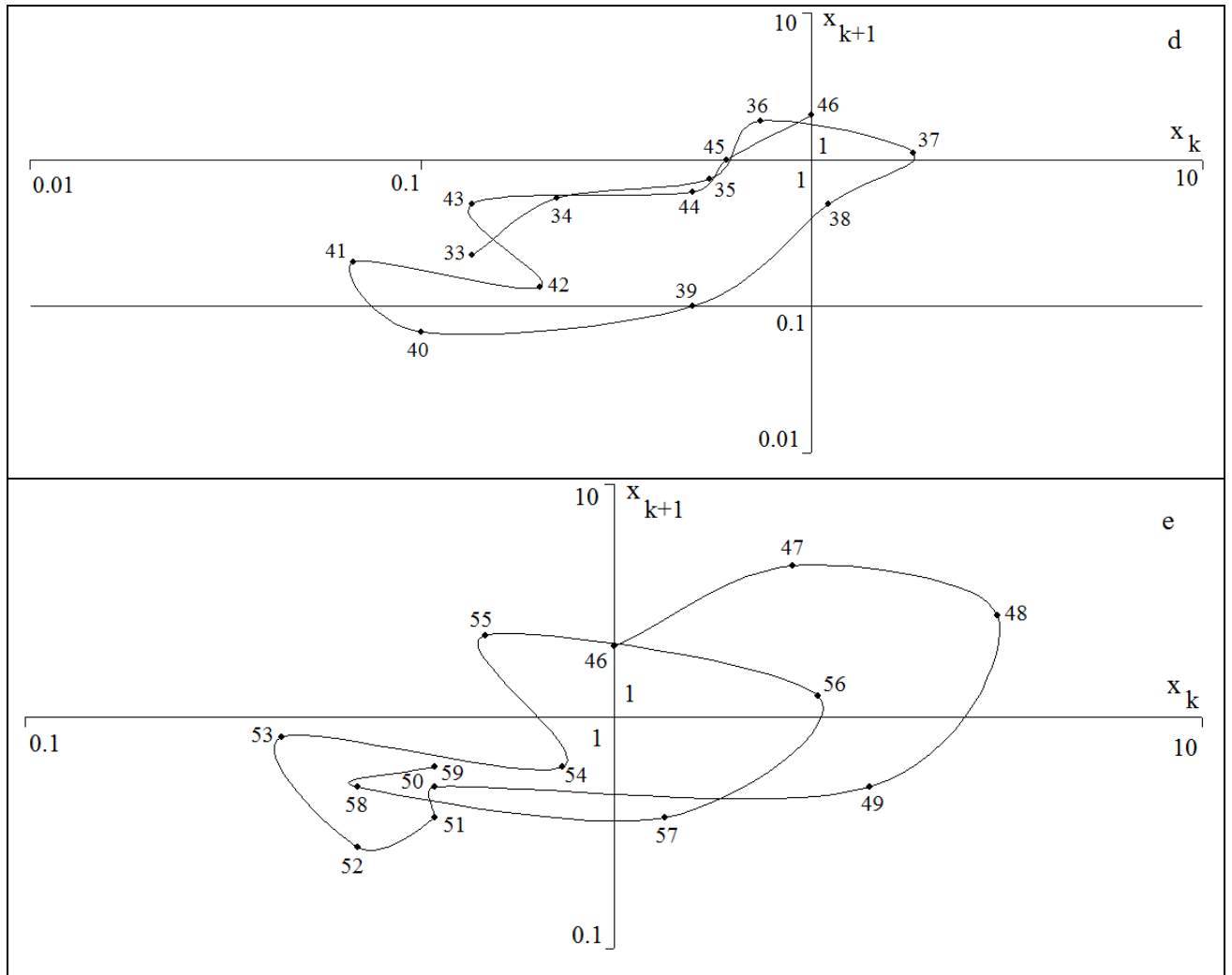


Fig. 2. Empirical trajectory of pine looper moth population dynamics (in logarithmic scales): a – point 1 corresponds to 1881/1882, point 10 corresponds to 1890/1891; b – point 20 corresponds to 1900/1901; c – point 29 corresponds to 1910; d – point 33 corresponds to 1913/1914; e – point 59 corresponds to 1939/1940.

$$z_L^1 = z_{\min} - \frac{\lambda}{2}.$$

It means that point  $z_{\min}$  will be a mid point of first interval. Process of determination of boundaries of intervals can be described by the formula  $z_R^1 = z_L^2 + \lambda$ . The right boundary of last interval must satisfy to condition  $z_R^j > z_{\max}$ . Determination of numbers of points in every pointed out intervals allows constructing a histogram.

In considering case we have the sample  $\{(x_k, x_{k+1})\}$ : it is more comfortable to use phase plane  $(x_k, x_{k+1})$  – “population density at time  $k$  – population density at time  $k+1$ ” – than phase plane “population density  $x$  – birth rate  $y$ ” because we don’t need to divide onto zero (sometimes estimations of population density can be equal to zero), we can use obvious metrics on this phase

space (in particular, Euclidian distance), all stationary states of system belong to bisectrix  $x_{k+1} = x_k$  etc.

Separately for abscissas and ordinates of sample we can apply Starges' method, and divide the plane onto system of rectangles. For every rectangle we can calculate number of points of sample, and finally it will allow obtaining estimation of two-dimensional density function (fig. 3).

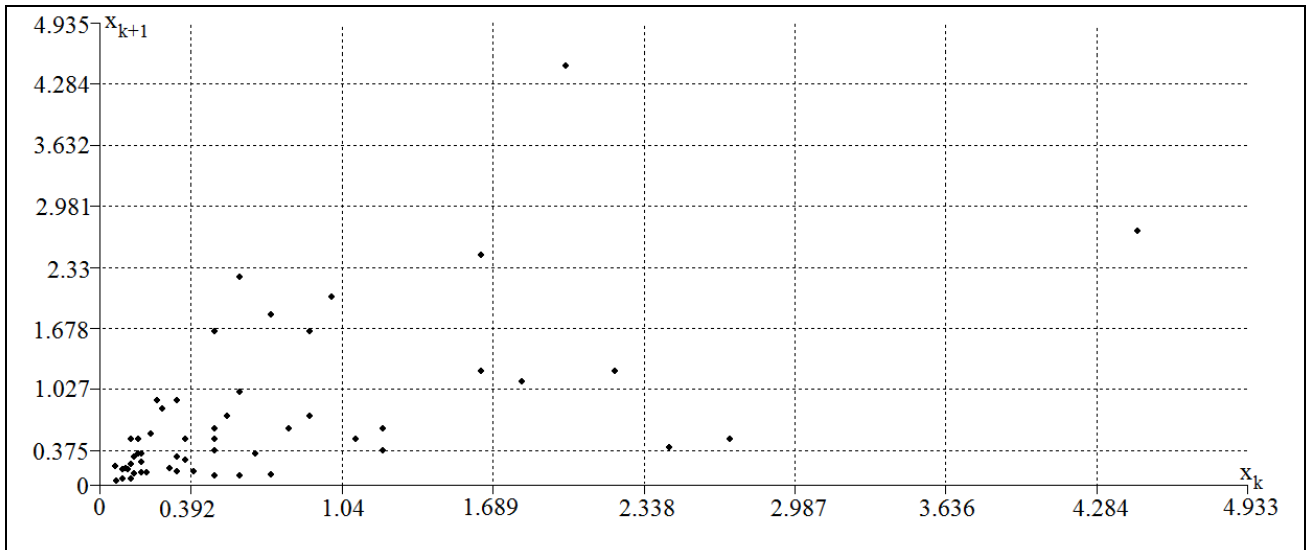


Fig. 3. Distribution of empirical points on the plane.

As we can see on figure 3, biggest cluster is in the left part of plane, in rectangle  $[0,0.392] \times [0,0.375]$  (20 points). In rectangle  $[0,0.392] \times [0.375,1.027]$  we have 7 points, in rectangle  $[0.392,1.04] \times [0,0.375]$  – 6, in rectangle  $[0.392,1.04] \times [0.375,1.027]$  – 7, in rectangle  $[0.392,1.04] \times [1.678,2.33]$  – 3. In all other rectangles we have 0,1 or 2 points. Such distribution of points gives us an argument for conclusion that population dynamics corresponds to outbreak proper (Isaev et al., 1984, 2001). May be, we have other type of population dynamics: prodromal type with wide phase portrait and one point of system stabilization. Other hypotheses about correspondence of pine looper moth population dynamics to permanent outbreak, or fixed outbreak, or reverse outbreak we have to reject.

### 5. Estimation of values of stationary states

Very simple method we used in previous chapter doesn't allow determination of coordinates of stationary states. For this reason we have to use other methods (Gubarev, 1985). As it was pointed out above on the phase plane  $(x_k, x_{k+1})$  all stationary states are on straight line  $x_{k+1} = x_k$ . Thus, we can try to estimate positions of stationary states analyzing value of density



along this straight line. For estimation of values of density function we used method of  $k$ -nearest points (neighbors): value of density is proportional to the following amount (Gubarev, 1985):

$$f(x) = \frac{D}{\sum_{m=1}^k \rho_m} .$$

In this expression  $\rho_m$  is Euclidian distance between point  $x$  on straight line  $x_{k+1} = x_k$  and one of  $k$  nearest points determined by considering sample. Constant  $D$  is determined from condition that integral of density function must be equal to 1.

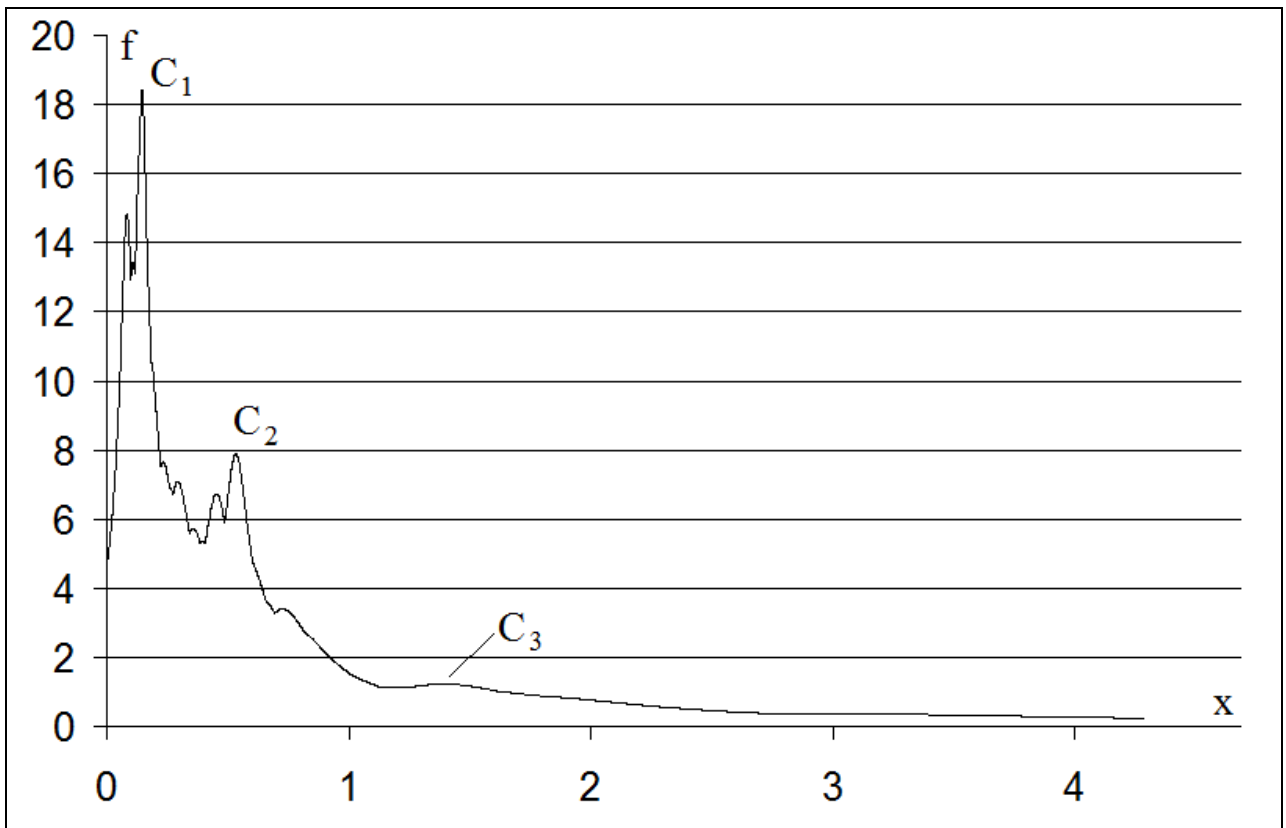


Fig. 4. Dependence of function  $f$  on  $x$  for  $k = 3$ .

In Figure 4 there are results of calculations for  $k = 3$ . As we can see in this figure biggest maximum  $C_1$  of density function  $f$  is observed in the zone of low value of population density (for  $x = 0.146$  function  $f(x) = 18.4015$ ). This amount 0.146 can be used as estimation of stable level  $x_1$  (fig. 1). Local maximum  $C_2$  can be interpreted as cluster of points which was organized near saddle point (point of escape)  $x_r$  (fig. 1). Thus,  $x_r \approx 0.533$ ,  $f(x_r) \approx 7.8768$ . One more cluster (theoretically) can be observed near saddle point  $x_r$ . But it is necessary to take into account that point's density in this part of phase plane is extremely small. We can accept as preliminary

hypothesis that maximum  $C_3$  corresponds to pointed out stationary state. If so,  $x_T \approx 1.392$ ,  $f(x_T) \approx 1.2258$ .

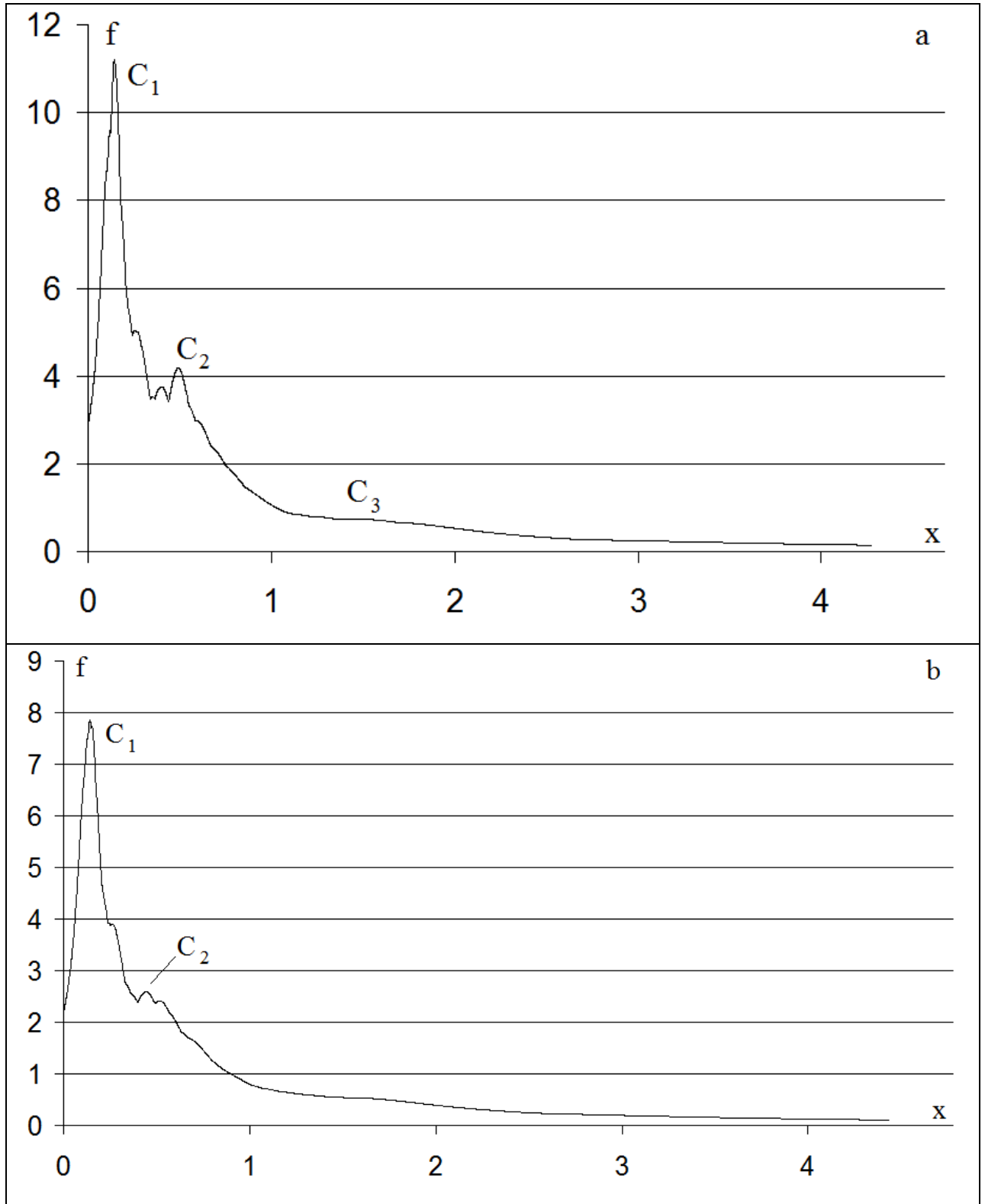


Fig. 5. Estimations of density function  $f$  for  $k = 5$  (a) and  $k = 7$  (b).

One of the main points on phase plane is  $x_e$ . This is unstable stationary state (repeller) and all outbreak trajectories during the peak phase have bigger values of population density than this amount ( $d > x_e$ ; fig. 1). If so, local minimum of density function can give us an estimation of occupation of this repeller. Thus,  $x_e \approx 1.238$ ,  $f(x_e) \approx 1.11328$ .

For two other cases (fig. 5) estimations of density functions have the similar features. In first case (fig. 5a)  $x_1 \approx 0.144$ ,  $f(x_1) \approx 11.2156$ ; in the second case (fig. 5b)  $x_1 \approx 0.142$ ,  $f(x_1) \approx 7.847$ . Note, for all three cases we have close estimations of stable level  $x_1$ . Point of escape  $x_r$ : in first case  $x_r \approx 0.493$ ,  $f(x_r) \approx 4.1825$ ; in the second case  $x_r \approx 0.443$ ,  $f(x_r) \approx 2.5912$ . Estimations of value of  $x_r$  are also close to each other in all three cases.

In both variants presented on figure 5 we have a problem with identification of occupation of points  $x_e$  and  $x_r$ . It can be explained in a result of increasing of “influence” (on estimations of values of density function) of points which are far from the zone of maximum of outbreak (fig. 1).

## 6. Cluster analysis of trajectories

Let's assume that the distance between two points of the sample  $A = (x_k, x_{k+1})$  and  $B = (x_j, x_{j+1})$  is determined by the following formula:

$$\rho(A, B) = \sqrt{(x_k - x_j)^2 + (x_{k+1} - x_{j+1})^2}.$$

Results of clustering are presented in Figure 6. As we can see in this figure first step of process correlates with appearance of two clusters (distance between points are equal to zero): coordinates of point 11 (1891/1892) are equal to coordinates of point 26 (1906/1907), and coordinates of point 44 (1924/1925) are equal to coordinates of point 56 (1936/1937). On two last steps of cluster process (fig.6) two points – 47 (1927/1928) and 48 (1928/1929) – combined together with big cluster (we will write as step  $S_{-1}$  for point 48 and step  $S_{-2}$  for point 47). These points belong to biggest outbreak trajectory: we can observe biggest value of amplitude of insect outbreak (fig. 2 and 7). On previous step  $S_{-3}$  we have combining of small two-point cluster {8,49} with big cluster. It allows concluding that  $x_r \geq 4.4817$  but we cannot say that rather big cluster appeared near this saddle point.

Before combining of big cluster with set {8,49} point 7 (1887/1888) becomes the element of big cluster (step  $S_{-4}$ ; fig. 6). Curve  $L_1$  divides (conditionally) pointed out points from big cluster (fig. 7). After this step more interesting situations can be observed: first of all, three-point cluster {20,37,56} combines with big cluster (step  $S_{-5}$ ).

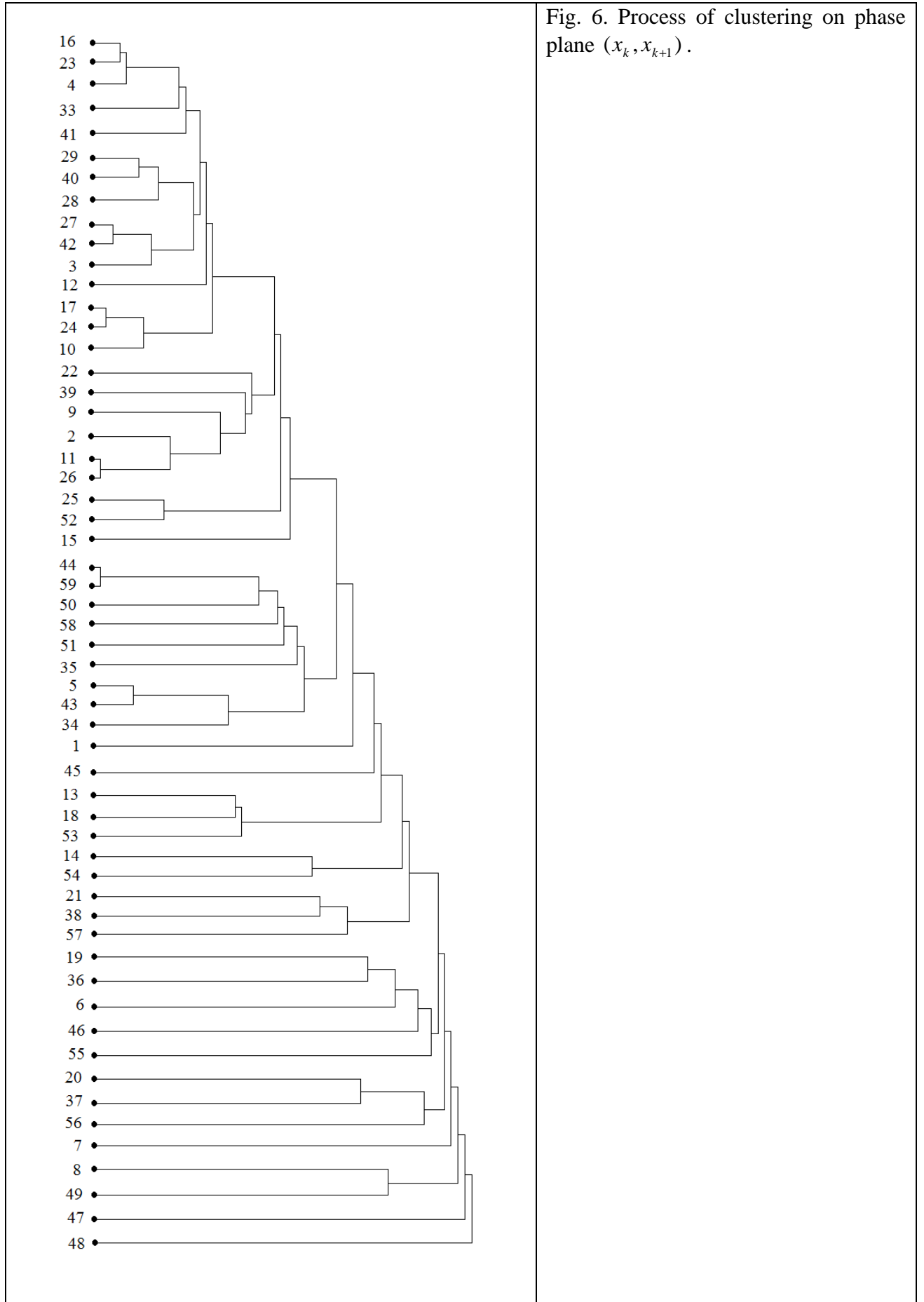


Fig. 6. Process of clustering on phase plane  $(x_k, x_{k+1})$ .

Let  $W_1 = \{20,37,56\}$  (fig. 7). Points of cluster  $W_1$  have following property: birth rate is less than one – population size decreases after respective time moments. Moreover, these points characterize maximums of outbreaks: it allows us assuming that appearance of this cluster on phase plane can be explained as a result of “deceleration” of system moving near saddle point  $x_T$ . Taking into account that points of super-outbreaks 7 and 47-48 are far from all points of sample, it looks rather natural to add these points to cluster  $W_1$ . Thus, points  $\{20,37,56,7,47,48\}$  can be used for determination of boundaries of zone of attraction of saddle point  $x_T$ .

On the step  $S_{-6}$  big cluster combines with five-point cluster  $W_2 = \{6,19,36,46,55\}$  (fig. 6). All points of cluster  $W_2$  have birth rates which are bigger than 1; moreover, next points belong to maximum of outbreak or super-outbreak. It allows concluding that considering points belong to zone of outbreak (phase of outbreak increasing; Isaev et al., 1984, 2001).

Cluster  $W_3 = \{21,38,57\}$  combines with big cluster on the step  $S_{-7}$  (fig. 6, 7). All points of this cluster have birth rates which are less than 1. Next points (22, 39, 58) have birth rates which are bigger than 1. Such kind of behavior of trajectory is typical for zone of stability of system and special zone on phase portrait which is bounded by incoming separatrix  $y_r$  in domain  $\{y < 1\}$  (fig.1). But as it was obtained before points of cluster  $W_1$  belong to outbreak zone – taking it into account we can conclude that points of cluster  $W_3$  belong to phase of depression or to phase of restoration of stable conditions (close to points  $m$  and  $n$  of outbreak phase trajectory; fig. 1).

Cluster  $W_4 = \{14,54\}$  combines with big cluster on the step  $S_{-8}$  (fig. 6, 7). These points have birth rates which are less than 1. It means that these points cannot belong to outbreak zone (fig. 1). On the other hand, point 55 belongs to outbreak zone. After point 14 we have further decreasing of population density. Thus, these points belong to zone of stability, but points have different properties.

We cannot exclude an assumption that after that step we will have process of clustering of points which belong to zone of stability (step  $S_{-9}$ ): next cluster  $W_5 = \{13,18,53\}$  contains points which have birth rates bigger than one. But after points 13 and 53 we have cluster  $W_4$  with points from zone of stability, and it allows us concluding that these points 13 and 53 belong to zone of stability too. We cannot exclude a situation when points 13 and 53 belong to outbreak zone but returning back to zone of stability is possible after extra-unfavorable weather conditions. It requires in combined analysis of population dynamics with dynamics of weather conditions.

After point 18 we can observe outbreak trajectory 19-21. It means that this point can belong to outbreak zone. If so, cluster  $W_5$  isn't homogenous and contains points as from zone of

stability of system as from the outbreak zone. It is possible situation (appearance of cluster  $W_5$ ) because points of these zones can be close to each other (Isaev et al., 1984, 2001), and it was observed for some other species (Nedorezov, 1981, 1989, 1999).

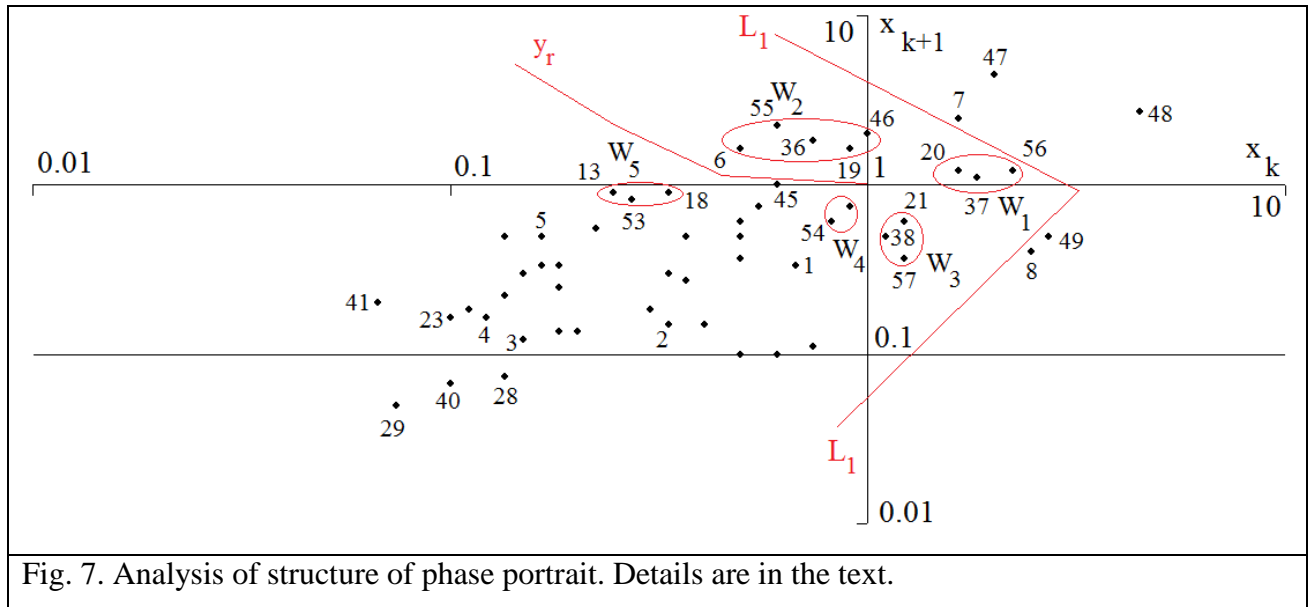


Fig. 7. Analysis of structure of phase portrait. Details are in the text.

The same property (like for point 18) is observed for point 45 which combines with big cluster at the next step  $S_{-10}$  (fig. 6). May be, this point belong to outbreak zone: birth rate is bigger than one, and after this point super-outbreak trajectory is observed. We can't determine truthful position of points 45 and 18; in figure 7 there is behavior of threshold curve  $y_r$  for the case when both points belong to zone of stability of system. But we have to note that presented position of separatrix  $y_r$  isn't real – estimation of real position of this curve must be determined as non-linear curve which separates points of zone of stability and outbreak zone.

At the next step  $S_{-11}$  (fig. 6) point 1 (1881/1882) combines with big cluster. Birth rate for this point is less than one (fig. 2a) and during several time steps population density decreases (1-2-3-4). Thus, we have a background for conclusion that this point belongs to zone of stability. As we can see in figure 6 there are several important steps in forming of big cluster of points within the limits of stable zone – these steps correspond to situations when we observe combination of rather big clusters. It can give a background for conclusion that moving of system in zone of stability may have complicated character. For example, analysis of time series of *Dendrolimus pini* L. allowed concluding that within the limits of zone of stability this pest may have two stable levels (Nedorezov, 1999). But on the other hand model which is on the base of set of phase portraits of insect dynamics (Isaev et al., 1984, 2001), doesn't allow analyzing population dynamics when its

density is small. It means that we haven't good mathematical background for analysis of behavior of time series with rather small values.

Last step in analysis of structure of phase portrait is following: we have to divide of space on zones which belong to every determined cluster. After that we can estimate probabilities of transmission of system from one zone to another: it can be considered as element of forecasting of system behavior.

### **Conclusion**

Provided analysis of time series on pine looper moth population dynamics shows that we cannot reject hypothesis that insect dynamics in Germany corresponds to outbreak proper (fig. 1). Applied methods of analysis allowed estimating positions of basic stationary points on phase portrait (point of stability, point of escape etc.). With the help of cluster method we obtained possibilities in determination of position of threshold curve which divides zone of stability and outbreak zone; additionally we obtained possibility in estimating of probabilities of system transmission from one zone of phase portrait to another – it can be considered as element of pest population forecasting.

### **References**

- Gubarev V.V. 1985. Algorithms of statistical measurements. Moscow: Energoatomizdat, 272 pp.
- Isaev A.S., Khlebopros R.G., Nedorezov L.V., Kondakov Yu.P., Kiselev V.V., 1984. Forest Insect Population Dynamics. Novosibirsk: Nauka, 224 pp.
- Isaev A.S., Khlebopros R.G., Nedorezov L.V., Kondakov Yu.P., Kiselev V.V., Soukhovolsky V.G., 2001. Population Dynamics of Forest Insects. Moscow: Nauka, 347 pp.
- Isaev A.S., Nedorezov L.V., Khlebopros R.G. 1979. Mathematical Model of Escape Effect in Interaction of Predator and Prey. In: Mathematical Modeling of Components of Forest Biogeocenoses (R.G. Khlebopros Ed.). Novosibirsk: Nauka, 74-82.
- Isaev A.S., Nedorezov L.V., Khlebopros R.G. 1980. Qualitative Analysis of the Phenomenological Model of the Forest Insect Number Dynamics// Pest Management Network, V. 9, IIASA, Austria, 1-44.
- Isaev A.S., Ovchinnikova T.M., Palnikova E.N., Soukhovolsky V.G. 1997. Imitation modeling of pine looper moth population dynamics under various climatic conditions// Lesovedenie 4: 40-48.

- Kendall B.E., Ellner S.P., McCauley E., Wood S.N., Briggs C.J., Murdoch W.W., Turchin P., 2005. Population cycles in the pine looper moth: dynamical tests of mechanistic hypotheses// *Ecological Monographs* 75(2): 259-276.
- Khlebopros R.G., Aizenberg L.A., Kitmanov A.M., Nedorezov L.V. 1979. Analysis of Mathematical Models of Phytophagous – Entomophagous System Dynamics. Krasnoyarsk: Institute of Physics SB AS USSR, 43 pp.
- Khlebopros R.G., Aizenberg L.A., Kitmanov A.M., Nedorezov L.V. 1980. Escape – Effect in Predator – Prey System. In: Problems of Ecological Monitoring and Ecosystem Modeling (S.M. Semenov Ed.), V. 3. Leningrad: Gidrometeoizdat, 213-223.
- Klomp H., 1966. The dynamics of a field population of the pine looper, *Bupalus piniarius* L. (Lep., Geom.)// *Advances in Ecological Research* 3: 207-305.
- Lakin G.F. 1990. Biometrics. Moscow: High School, 350 pp.
- Nedorezov L.V. 1981. Model of Siberian Silkworm Population Dynamics. In: Spatial – Time Structure of Forest Ecosystems (Khlebopros R.G. Ed.). Novosibirsk: Nauka, 112-125.
- Nedorezov L.V., 1986. Modeling of Forest Insect Outbreaks. Novosibirsk: Nauka, 125 pp.
- Nedorezov L.V. 1989. The Phase Portrait of *Panolis flammea* Schiff. Dynamics// *Izvestia SB AS USSR*, N 1: 81-86.
- Nedorezov L.V. 1999. Restoration of Phase Portrait Structure for the Dynamics of a Forest Pest, the Pine Moth (*Dendrolimus pini* L.)// *Ecological Modelling* 115: 35-44.
- Nedorezov L.V., 2012. Chaos and Order in Population Dynamics: Modeling, Analysis, Forecast. LAP Lambert Academic Publishing, Saarbrücken, 352 pp.
- Nedorezov L.V. 2013a. About Completeness of Classification of Insects on Their Types of Dynamics: Problems of Application of Cluster Analysis// *Population Dynamics: Analysis, Modelling, Forecast* 2(3): 87-104.
- Nedorezov L.V. 2013b. Dynamics of pine hawkmoth (*Hyloicus pinastri* L.): search for stationary dynamical regime// *Computational Ecology and Software*, 3(4): 81-90.
- Nedorezov L.V., 2013c. Dynamics of Pine Beauty (*Panolis flammea*): search for stationary dynamical regimes// *Population Dynamics: Analysis, Modelling, Forecast* 2(3): 105-116.
- Nedorezov L.V., 2013d. Dynamics of *Bupalus piniarius* in Germany: search for stationary dynamical regimes// *Population Dynamics: Analysis, Modelling, Forecast* 2(2): 61-72.
- Nedorezov L.V., 2015. Application of generalized discrete logistic model for fitting of pine looper moth time series: Feasible sets and estimations of model parameters// *Proceedings of the International Academy of Ecology and Environmental Sciences*, 5(1): 38-48.



- Nedorezov L.V., Nekljudova V.L., 2000. About Some Continuous – Discrete Models of Elementary Ecosystems. Novosibirsk State University, Novosibirsk, 48 pp.
- Nedorezov L.V., Sadykova D.L., 2015. Dynamics of larch bud moth populations: application of Moran - Ricker models with time lag// Ecological Modelling 297: 26-32.
- Nedorezov L.V., Utyupin Yu.V., 2011. Continuous-Discrete Models of Population Dynamics: An Analytical Overview. State Public Scientific-Technical Library, Novosibirsk, 234 pp.
- Palnikova E.N., Sviderskaya I.V., Soukhovolsky V.G., 2002. Pine looper moth in Siberian forests. Novosibirsk: Nauka, 232 pp.
- Schwerdtfeger F., 1941. Über die Ursachen des Massenwechsels der Insecten. Z. Angew. Entomol. 28, 254–303.
- Schwerdtfeger F., 1944. Die Waldkrankheiten. Paul Parey, Berlin, 479 S.
- Schwerdtfeger F., 1957. Forstinsekten im Ur- und Nutzwald. Allgem.: Forstzeitschr. 485 S.
- Schwerdtfeger F., 1968. Ökologie der Tiere. 2. Demökologie. Paul Parey, Berlin, 448 pp.