Article

Dynamics of pine hawkmoth (*Hyloicus pinastri* L.): Search for stationary dynamical regime

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Abstract
In current publication possible population dynamics regimes are analyzed using pre-model statistical method. Method was applied to well-known pine hawkmoth (*Hyloicus pinastri* L.) time series (Schwerdtfeger, 1944, 1968). Provided statistical analysis showed that observed dynamics of pine hawkmoth doesn't correspond to strong 2-, 3-,…, or 9-year cycles which can be generated by one-dimensional discrete models, and doesn't correspond to fluctuations near stable level.

Keywords pine hawkmoth population fluctuations; time series; pre-model statistical analysis; fitting; stationary dynamical regime.

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1 Introduction

Search for suitable mathematical model, estimation of model parameters using empirical datasets, and determination of basic features of population phase portraits are among of the main elements of population dynamics analysis (Isaev et al., 1984, 2001; Bazykin, 1985; McCallum, 2000; Tonnang et al., 2009, 2010, 2012; Turchin, 2003; Wood, 2001; Gao, Chang, Wang, 2012; Nedorezov, 2013 a, b and many others). Without finding of a suitable model (or without constructing of new suitable model) it is impossible to prepare strong scientifically-based forecasts of pest population changing in time and optimal methods of its management. But up to current moment there are no criterions, which can help in finding of a suitable model before comparison of theoretical trajectories and empirical datasets (Isaev et al., 1984, 2001; Nedorezov, Utyupin, 2011; Nedorezov, 2012 a). Even comparison of model trajectories with empirical time series can give us a set of suitable models (for fitting of empirical datasets), and again we may have a situation when it is necessary to find a best one (Nedorezov, 2010, 2011 a, b, 2012 a, b). In such a situation preliminary and pre-model statistical analysis of existing time series can be very useful in a process of searching of suitable model and/or group of suitable models.

Pre-model analysis is a testing of correspondence of observed population fluctuations to any dynamical regimes which can be generated by various mathematical models (first of all, by models with discrete time; Kostitzin, 1937; Varley, 1949; Skellam, 1951; Ricker, 1954; Nedorezov, 1986, 1997; Elsadany, 2012; Elsadany et al., 2012 and many others). For example, it is a testing of correspondence of population dynamics to 1-cycle (fluctuations near stable level), 2-cycle etc. (Nedorezov, 2013 a, b, c). All deviations from coordinates of n-cycle must be explained as results of influence of external stochastic factors, by used methods of data collection etc. In other words, before choosing of model we can try to determine a dynamical regime which is observed in natural conditions. More precisely, we can try to find a dynamical regime with the following property: modern statistical methods don't allow us concluding that considering regime doesn't correspond to observed fluctuations (Nedorezov, 2011a, 2013 a, b, c).

It is known, that for estimation of model parameters under the use of *global fitting* for empirical time series, researches use *initial parts* of model trajectories, and don't use parts of trajectories which correspond to *stabilized regime* of population fluctuations (McCallum, 2000; Nedorezov, 2010, 2012; Turchin, 2003; Wood, 2001 and others). Approximation of empirical time series by initial parts of model trajectories is correct if we analyze a process of population size changing in time which corresponds to *non-stabilized dynamic regime* (Gause, 1934; Nedorezov, 2011 b, 2012 a, b). But if we analyze dynamics of species which exist in local habitat (and where datasets were collected) during long time period the use of initial parts of model trajectories for fitting of empirical time series needs in additional explanation.

2 Algorithm

Let x_1, $x_2, \ldots, x_N$ be a time series of considering hypothetical population. Time step is equal to one year, thus x_k is a population size (or density) at k th year. First of all, we have to solve the following question: what kind of datasets we have now? If, for example, we analyze time series presented in book by G.F. Gause (1934), it is obvious, that for every trajectory we can point out initial part (it can be exponential phase of population growth), mid part of trajectory (where we can observe growth of influence of intra-population self-regulative mechanisms on process of population size changing), and stabilized behavior (fluctuations near stable level). In such a situation we have a good background for application of initial parts of theoretical (model) trajectories for fitting of experimental datasets (Nedorezov, 2011 b, 2012 a, b).

But in the case when we analyze insect population dynamics in locations where insects live thousands and thousands years, we haven't a background with the same properties. In these situations we observe *stabilized dynamical regime*. Thus, for the estimation of model parameters we have to minimize, for example, the sum of squared deviations of real datasets from coordinates of *asymptotically stable attractors*.

First of all, we must determine a dynamical regime which is realized for population: it is a hypothesis we have to check. For example, we can start with assumption that observed fluctuations of population size correspond to cycle of the length two: $ababab...$ Let's assume that minimizing functional form is equal to sum of deviations squared. In this case we have:

$$Q(a,b) = \sum_k (x_k - a)^2 + \sum_k (x_k - b)^2 \to \min_{a,b} . \tag{1}$$

From (1) we get the following estimations for coordinates of 2-cycle:

$$a = \frac{1}{N^*} \sum_k x_k \ , \ \ b = \frac{1}{N^{**}} \sum_k x_k \ , \tag{2}$$

where $N^* + N^{**} = N$, and $N^* = N^{**}$ or $N^* = N^{**} + 1$. After estimation of coordinates of 2-cycle (2) we have to check hypothesis that observed regime is 2-cycle: more precisely, we have to analyze two sequences $x_1 - a$, $x_3 - a, \ldots$ and $x_2 - b$, $x_4 - b, \ldots$ and to show that arithmetic averages are equal to zeros, distribution functions for both sets are symmetric functions, and there are no serial correlation in sequence $x_1 - a$, $x_2 - b$, $x_3 - a$,... (Bolshev, Smirnov, 1983; Draper, Smith, 1986, 1987). In the end we have to reject Null hypothesis about equivalence of coordinates of cycle: Null hypothesis is $a = b$.

If all used tests show that there are no reasons for rejecting of the respective Null hypotheses and Null hypothesis $a = b$ must be rejected for selected significance level, we have to start the process of selection of mathematical model. It is obvious, if observed changing of population size corresponds to 2-cycle there are no reasons for consideration of the Skellam model or Kostitzin model – in both models there are the regimes of asymptotic stabilizations of population size at any levels only for all values of model parameters (Skellam, 1951; Kostitzin, 1937). In this situation it is better to use Moran – Ricker model or discrete logistic model: both models contain a lot of various dynamical regimes (Moran, 1950; Ricker, 1954; Isaev et al., 1984, 2001; Bazykin, 1985; Nedorezov, 1986, 1997 and others).

3 Datasets

In current publication algorithm described above was applied to time series of pine hawkmoth (*Hyloicus pinastri* L.) (Schwerdtfeger, 1944, 1968; Varley, 1949; NERC Centre for Population Biology, Imperial College (1999) The Global Population Dynamics Database, N 3757). Population densities are presented in units "logarithm of individuals (larvae) per squared meter" from 1881 to 1930. Total sample size is equal to 49 (information on population density for 1912 is absent).

On figure 1 there are graphics of changing of density of larvae of pine hawkmoth (curve 2) and logarithm of density (curve 1) in time. These fluctuations look like as periodic process under (very) strong influence of external stochastic factors: hypothesis about periodicity of observed fluctuations cannot be rejected a'priori.

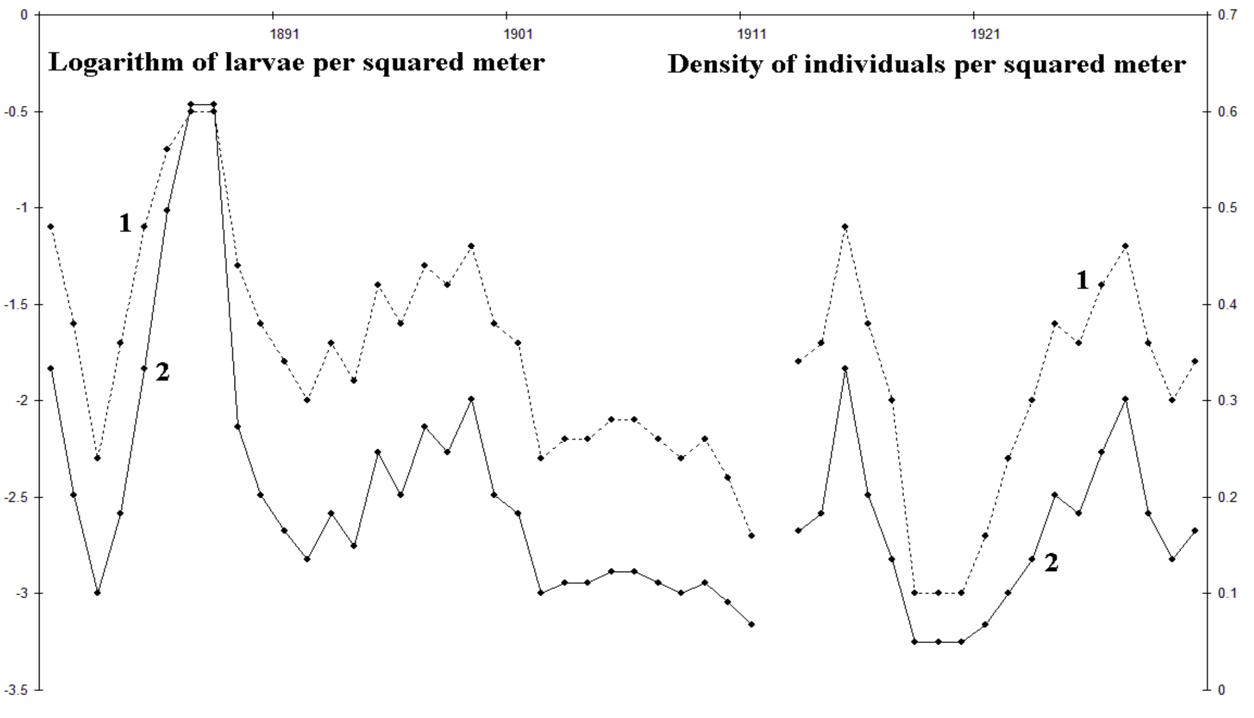

Fig. 1 Changing in time of logarithm of individuals (larvae) per squared meter (curve 1, left ordinate line) and density of individuals per squared meter (curve 2, right ordinate line).

4 Results

In table 1 there are the estimations of cycle's coordinates (under the assumptions that one or other attractor is realized for pine hawkmoth fluctuations), and respective values of minimizing functional form Q (it is a sum of squared deviations of real values from the estimated coordinates of cycle; in particular case Q is presented for 2-cycle with formula (1)). It was assumed that maximum length of cycle is 9.

It is obvious that increasing of the length of cycle must lead to decreasing of the value of minimizing functional form Q (as we can see from the table 1, it can be non-monotonic process). It is obvious, if length of cycle is equal to 50 or more then $Q = 0$. But in table 1 there is no strong decreasing of Q: local minima are observed for 3-cycle, 7-cycle, and 9-cycle. At the same time, differences between values of functional Q are rather small.

Table 1 Estimations of coordinates of cycles and respective values of sums of squared deviations between theoretical and empirical trajectories.

	1^*	2	3	4	5	6	7	8	9
1	0.195	0.201	0.193	0.192	0.208	0.224	0.237	0.195	0.22
2		0.189	0.212	0.181	0.218	0.212	0.174	0.174	0.172
3			0.18	0.211	0.188	0.164	0.141	0.191	0.124
4				0.198	0.17	0.158	0.169	0.171	0.12
5					0.193	0.212	0.201	0.188	0.165
6						0.196	0.204	0.189	0.224
7							0.23	0.23	0.25
8								0.23	0.307
9									0.203
Q	0.731	0.729	0.723	0.725	0.717	0.7	0.679	0.71	0.572

[*] 1-cycle is stationary level

Below we'll consider the following way for analysis of correspondence between empirical values and theoretical assumptions that observed fluctuations correspond to cyclic dynamics with cycle of the certain length. Traditional way is based on the next assumptions: average of sample of deviations between theoretical and empirical is equal to zero (there are no reasons for rejecting of the respective hypothesis), distribution must correspond to Normal, and serial correlation cannot be observed in sequences of residuals. Absence of serial correlation can be checked with Durbin – Watson criteria, with analysis of behavior of auto-correlation function etc. (Draper, Smith, 1986, 1987; Nedorezov, 2013 a, b, c).

Let's note that assumption about Normality of deviations is rather strong, and it is never realized for biological datasets (Orlov, 2004). More realistic assumptions are following: deviations must have symmetric density function with respect to the origin, both tails of density must be monotonic functions, and second derivative of density function can change its sign two times of less. It is obvious density function for Normal distribution satisfies these requirements.

For testing symmetry of density function we used the well-known Kolmogorov – Smirnov test. It is obvious, if distribution of deviations is symmetric with respect to origin distribution function $F(x)$ for $\{e_i^+\}$ must be equal to distribution function $G(x)$ for $\{-e_i^-\}$. Thus, Null hypothesis for Kolmogorov – Smirnov test is $F(x) = G(x)$.

If we assume that considering time series correspondents to stochastic fluctuations near one stable level, Kolmogorov – Smirnov test shows that with 1% significance level hypotheses about Normality of residuals must be rejected. Testing of symmetry gives the following results: $d = 0.3158$ with corresponding probability $p = 0.159$. Thus, even with 10% significance level we cannot reject Null hypothesis about symmetry of density function. With rather big probability $p = 0.32$ dataset $\{e_i^+\}$ has log normal distribution; dataset $\{-e_i^-\}$ has Normal distribution with $p = 0.54$. It means that with big probability $G(x)$ isn't monotonic function.

For testing the property of monotonous behaviour of branches of density function we used the following criterion. Let's assume that $\{e_i^+\}$ is ordered set, $e_1^+ < e_2^+ < ... < e_m^+$, and let $\delta_0 = e_1^+$, $\delta_1 = e_2^+ - e_1^+, \ldots, \delta_{m-1} = e_m^+ - e_{m-1}^+$ be intervals between deviations. Thus, we get the following set of points on the plane: $(0, \delta_0)$, $(e_1^+, \delta_1), \ldots, (e_{m-1}^+, \delta_{m-1})$. It is obvious, that with ideal variant we have to have the following inequalities for set $\{\delta_k\}$: $\delta_0 < \delta_1 < ... < \delta_{m-1}$. In such a situation non-parametric Theil criterion (Hollander, Wolfe, 1973; Theil, 1950) will show that we have confident tendency in increasing of respective values: coefficient of linear regression line doesn't equal to zero confidently. Let

$$y = ax + b,$$

be the linear regression line for points on plane. Thus, Null hypothesis for Theil criterion is following H_0 : $a = 0$; alternative hypothesis is $H_1: \ a > 0$.

We can also use the same criterion in the following manner: we can analyze behavior of the intervals - $\delta_0^1 = e_2^+$, $\delta_1^1 = e_3^+ - e_1^+$, …, $\delta_{m-2}^1 = e_m^+ - e_{m-2}^+$. Ideal variant for these intervals is the same: $\delta_0^1 < \delta_1^1 < ... < \delta_{m-2}^1$. After calculation of all elements of set $\{\delta_k^1\}$ we can use Theil criterion for checking of the same Null hypothesis. The similar procedure can be provided for other intervals $\{\delta_k^j\}$, $j > 1$, which are determined by the initial sample $\{e_i^+\}$. It is obvious that $\{-e_i^-\}$ must be initial sample too.

Other possible way for testing of the same property is following. In the case when we have ideal variant for set $\{\delta_k\}$ we have to provide 0 permutations for ordering of the set. When we have the situation δ_{m-1}, $\delta_{m-2}, \ldots, \delta_0$, number of permutations has its maximum value:

$$S_{\max} = \frac{m(m-1)}{2}.$$

In this situation Null hypothesis must be rejected, and alternative hypothesis $H_1: \ a < 0$ - must be accepted. If for any concrete situation number of permutations is rather small (for example, it is less than $S_{\max}/20$) then we can assume (we have a good background for this conclusion) that sequence of intervals was produced with the help of monotonic decreasing density function.

For the first assumption that considering time series correspondents to stochastic fluctuations near one stable level, for right tale of initial sample $\{e_i^+\}$ Theil criterion for $\{\delta_k\}$ shows the following result: $C = 31$. Critical value (for $p = 0.054$ and $m = 19$ where m is number of positive deviations $\{e_i^+\}$; Hollander, Wolfe, 1973; Theil, 1950) is equal to 47. Thus, we cannot reject Null hypothesis $H_0: \ a = 0$ and, respectively, we haven't a background for conclusion that right tale of density function is monotonic decreasing function.

For left tale we have $C = 7$. It means that for $m = 30$ probability that value of criterion is bigger than 7 is about 0.45. Thus, for left tale we cannot reject Null hypothesis too, and we haven't a background for conclusion that left tale of density function is monotonic increasing function. Finally, it gives us a background for conclusion that branches of density function are non-monotonic functions, and assumption that observed dynamics corresponds to fluctuations near stable level isn't correct.

Let's assume that observed fluctuations correspond to 2-cycle. As it was showed before in our publications (Nedorezov, 2012 a, 2013 b) variance of measurements of population size (or density) has strong dependence on real value, and it may have non-linear character. It means that we have to analyze all sub-sets separately: we have to be sure deviations from cycle's coordinates correspond to one and the same distribution. Deviations from various coordinates of cycle will have different variances.

On the other hand, for 2-cycle we have 4 branches for two density functions – respectively, we have about $m/4$ deviations per branch. For 3-cycle we have 6 branches for three density functions – it is obvious, that number of deviations per branch decreases very fast, and very fast we can get situations when we cannot apply Kolmogorov – Smirnov test for comparison of two independent samples.

Taking into account that combination of several samples which were generated by independent stochastic variables with symmetric (with respect to origin) density functions, gives new sample which is generated by stochastic variable with symmetric density function. Moreover, if every density function has monotonic left and right branches, new stochastic variable has density function with the same property. Combined sample can be generated by the following stochastic variable:

$$\xi = \begin{cases} \xi_1, p_1 \\ \xi_2, p_2 \\ \ldots \\ \xi_k, p_k \end{cases}$$

where p_j is equal to relation of number of deviations of empirical numbers from the j-coordinate of k-cycle. Thus, $\forall j \quad p_j > 0$, and $p_1 + p_2 + \ldots + p_k = 1$. Let $F_j(x)$ be a distribution function for ξ_j: $F_j(x) = P\{\xi_j < x\}$. Let also H_j be the event that $\xi = \xi_j$. Taking into account that $\forall j \quad p_j > 0$, $P\{H_j\} = p_j > 0$, $H_i \cap H_j = \varnothing$ if $i \neq j$, and

$$\bigcup_{j=1}^{k} H_j = \Omega,$$

$\{H_j\}$ is a full set of events. Thus, distribution function $F_\xi(x)$ for ξ is determined by the following expression:

$$F_\xi(x) = P(\xi < x) = \sum_{j=1}^{k} P\{\xi < x / H_j\} P(H_j) = \sum_{j=1}^{k} p_j F_j(x).$$

If for all j distribution functions $F_j(x)$ have derivatives $f_j(x)$ which are symmetric with respect to origin and monotonic functions, we have

$$f_\xi(x) = \frac{dF_\xi(x)}{dx} = \sum_{j=1}^{k} f_j(x).$$

Thus, density $f_\xi(x)$ is symmetric function with monotonic branches.

For first (bigger) value of 2-cycle (Table 1) we have the following results. Kolmogorov – Smirnov test shows that with 5% significance level hypotheses about Normality of residuals must be rejected. For right branch (for $\{e_i^+\}$) Theil criterion for $\{\delta_k\}$ is equal to -2. Thus, we cannot reject Null hypothesis H_0: $a = 0$. For the left branch of sample we have that with very big probability $p = 0.9$ set of deviations correspond to Normal distribution (with average ≈ -0.077 and standard deviation ≈ 0.047), and with

$p = 0.27$ it may have log-normal distribution.

For the second (smaller) value of 2-cycle (table 1) we have the following results. Kolmogorov – Smirnov test shows that with 1% significance level hypotheses about Normality of residuals must be rejected. Kolmogorov – Smirnov test shows also that with rather big significance level we cannot reject Null hypothesis $H_0: \; F(x) = G(x): \; d = 0.3857$ with respective probability $p = 0.275$. For left tale of the sample with very big probability $p = 0.96$ it corresponds to Normal distribution with small average (≈ -0.067) and standard deviation (≈ 0.051), and with $p = 0.43$ it may have log-normal distribution.

For combined sample we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2211$ with respective probability $p = 0.564$. It means that with very big significance level we cannot reject Null hypothesis $H_0: \; F(x) = G(x)$. For right (positive) tale of sample with 1% significance level we have to reject Null hypothesis about Normality; for left tale of the sample with very big probability $p = 0.84$ it corresponds to Normal distribution with small average (≈ -0.072) and standard deviation (≈ 0.044). It means, that with rather big probability we can observe a local minimum which is closed to origin.

The next important test is a test for behavior of increments of population size. If there is a big number of cases when theoretical time series demonstrates population size increasing and at the same time moments empirical time series shows decreasing of population size (or vice versa) we have a background for conclusion about impossibility to use considering model for fitting of dataset. If there is a small number of cases when theoretical and empirical time series demonstrate population size increasing or decreasing at one and the same time moments we have a good background for conclusion that there is a good correspondence in behavior of theoretical and empirical trajectories.

We will assume that stochastic variable η which is equal to 1, $\eta = 1$, when we observe the equivalence between signs of increments and equal to 0, $\eta = 0$, when we have different signs, corresponds to independent Bernoulli trials. In such a situation, we have to check the Null hypothesis $H_0: \; P = 0.5$ with alternative hypothesis $H_1: \; P < 0.5$ where P is a frequency of cases when $\eta = 0$. But it is possible to use more primitive test: if number of cases when $\eta = 0$ is bigger than 5% of all cases it doesn't give us a reason for rejecting Null hypothesis.

If we reject Null hypothesis on previous stage of analysis, we have to continue analysis of correspondence between theoretical and empirical time series. Next step must contain analysis of correspondence between second derivatives of trajectories which can be estimated with the following formula:

$$x_k^{''} \approx x_{k+1} - 2x_k + x_{k-1}$$

(it is assumed that time step is equal to one). This process can be continued: model gives very good approximation of real time series if we have good correspondence for time series, first derivatives, second derivatives, and so on.

For 2-cycle we have $\eta = 0$ in 15 times, and $\eta = 1$ in 27 times; in 5 cases we have undetermined situations. Thus, $P \approx 0.372$. Taking into account results presented above, we can conclude that dynamics of pine hawkmoth doesn't correspond to 2-cycle.

For 3-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2632$ with respective probability $p = 0.343$. It means that with big significance level we cannot reject Null hypothesis $H_0: \; F(x) = G(x)$. For right branch (for $\{e_i^+\}$) of considering sample Theil criterion for $\{\delta_k\}$ is equal to 70. Thus, we have to reject (even with 1% significance level) Null hypothesis $H_0: \; a = 0$ (for sample size 19 we have $P\{C \geq 69\} = 0.008$; Hollander, Wolfe, 1973; Theil, 1950). It means that with very big probability alternative hypothesis is truthful ($a > 0$), and right branch of density function is monotonic decreasing function. For left branch of considering sample Theil criterion

$C = 90$. Thus, we cannot reject (with 5% significance level) Null hypothesis $H_0: \ a = 0$ (for sample size 30 we have $P\{C \geq 91\} = 0.054$). But it is important to note, that it is rather close to critical situation, and it gives a background to continue analysis of correspondence of real datasets to 3-cycle. Analysis of changing of increments gave the same results we obtained for 2-cycle: number of situations when $\eta = 0$ is rather big, and it means that we cannot conclude that dynamics of pine hawkmoth corresponds to 3-cycle.

For 4-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.25$ with respective probability $p = 0.395$. It means that with very big significance level we cannot reject Null hypothesis $H_0: \ F(x) = G(x)$. For right branch (for $\{e_i^+\}$) of considering sample Theil criterion for $\{\delta_k\}$ is equal to 52. For sample size 20 we have $P\{C \geq 52\} = 0.049$. Thus, we have to reject with 5% significance level Null hypothesis. For left branch of considering sample Theil criterion $C = 88$. Thus, we cannot reject (with 5% significance level) the Null hypothesis $H_0: \ a = 0$ (for sample size 29 we have $P\{C \geq 88\} = 0.052$). But like in previous situation with 3-cycle it is rather close to critical situation, and it gives a background to continue analysis of correspondence of real datasets to 4-cycle. Analysis of changing of increments gave the following results: η is equal to 1 in 25 times. Thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 4-cycle.

For 5-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2599$ with respective probability $p = 0.37$. It means that with very big significance level we cannot reject Null hypothesis $H_0: \ F(x) = G(x)$. For right branch (for $\{e_i^+\}$) of considering sample Theil criterion for $\{\delta_k\}$ is equal to 60. For sample size 18 we have $P\{C \geq 59\} = 0.013$. Thus, we have to reject Null hypothesis with 5% significance level. For left branch of considering sample Theil criterion $C = 16$. Thus, we cannot reject the Null hypothesis $H_0: \ a = 0$ (for sample size 31 we have $P\{C \geq 17\} = 0.394$). Analysis of changing of increments gave the following results: η is equal to one in 20 times and in 22 times $\eta = 0$: thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 5-cycle.

For 6-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2024$ with respective probability $p = 0.658$. It means that with very big significance level we cannot reject Null hypothesis $H_0: \ F(x) = G(x)$. For right branch (for $\{e_i^+\}$) Theil criterion for $\{\delta_k\}$ is equal to 47. For sample size 21 we have $P\{C \geq 48\} = 0.079$. Thus, we cannot reject Null hypothesis with 5% significance level. For left branch of considering sample Theil criterion $C = 65$. Thus, we cannot reject the Null hypothesis $H_0: \ a = 0$ even with 10% significance level (for sample size 28 we have $P\{C \geq 66\} = 0.101$). Analysis of changing of increments gave the following results: η is equal to one in 30 times and in 12 times $\eta = 0$: thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 6-cycle.

For 7-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2596$ with respective probability $p = 0.359$. It means that with very big significance level we cannot reject Null hypothesis $H_0: \ F(x) = G(x)$. For right branch (for $\{e_i^+\}$) Theil criterion for $\{\delta_k\}$ is equal to 27. For sample size 19 we have $P\{C \geq 27\} = 0.184$. Thus, we cannot reject Null hypothesis even with 10% significance level. For left branch of considering sample Theil criterion $C = 52$. Thus, we cannot reject the Null hypothesis $H_0: \ a = 0$ with 10% significance level (for sample size 30 we have $P\{C \geq 53\} = 0.178$). Analysis of changing of increments gave the following results: η is equal to one in 27 times and in 15 times $\eta = 0$: thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 7-cycle.

For 8-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.1621$ with respective probability $p = 0.887$. It means that with very big significance level we cannot reject Null hypothesis H_0 : $F(x) = G(x)$. For right branch (for $\{e_i^+\}$) Theil criterion for $\{\delta_k\}$ is equal to 33. For sample size 20 we have $P\{C \geq 34\} = 0.144$. Thus, we cannot reject Null hypothesis even with 10% significance level. For left branch of considering sample Theil criterion $C = 89$: it corresponds to critical situation. For sample size 29 we have $P\{C \geq 88\} = 0.052$ and $P\{C \geq 90\} = 0.048$. Analysis of changing of increments gave the following results: η is equal to one in 23 times and in 19 times $\eta = 0$: thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 8-cycle.

For 9-cycle for combined sample of deviations we have the following results. Kolmogorov – Smirnov test shows that $d = 0.2014$ with respective probability $p = 0.658$. It means that with very big significance level we cannot reject Null hypothesis H_0 : $F(x) = G(x)$. For right branch (for $\{e_i^+\}$) Theil criterion for $\{\delta_k\}$ is equal to 100. For sample size 21 we have $P\{C \geq 100\} = 0.001$. Thus, we have to reject Null hypothesis with 1% significance level. For left branch of considering sample Theil criterion $C = 60$. For sample size 28 we have $P\{C \geq 60\} = 0.123$. Thus, we cannot reject the Null hypothesis H_0 : $a = 0$ with 10% significance level. Analysis of changing of increments gave the following results: η is equal to one in 33 times and in 9 times $\eta = 0$. Thus, we cannot conclude that dynamics of pine hawkmoth corresponds to 9-cycle.

5 Discussion

Finally, in all considering cases we cannot reject the hypothesis that deviations have symmetric distribution. The best situation is observed for 8-cycle when $p = 0.887$. At the same time for all considering situations we cannot conclude that branches of density functions are monotonic decreasing functions. Moreover, in all situations we have strong differences in behavior of increments of theoretical trajectories and empirical time series: the best result was obtained for 9-cycle but even for this cycle in 21.4% of all cases we can observe different signs of increments. It is rather big number, and it allows us concluding that we haven't a good correspondence between empirical time series and theoretical cyclic fluctuations.

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