High Probability Cycles of the Sugar Subcomplex Activities in the Agro-Industrial Complex

D Yu Zhmurko

1Krasnodar University of the Ministry of Internal Affairs of the Russian Federation
2Kuban State Agrarian University, Krasnodar, Russia

E-mail: danis1982@list.ru

Abstract. The article aims at defining the sets of high probability cycles and at revealing the common cyclic genome for sugar industry which, taken as a whole, affect the production of sugar, sugar beet, and sugarcane. The author also studies the principles of big regional structures in the sugar subcomplex. For the first time, the concept of revealing a cyclic genome by means of the forward analysis (instead of the spectral analysis) is realised in practice, i.e. periodograms are built on the basis of a forward analysis and not of a spectral analysis. It has been confirmed in practice that the forward analysis shows substantially better results in building periodograms than the traditional spectral analysis. The author has revealed new principles in shift (mutation) of the cyclic genome of the world sugar production and has defined the sociogenetic principles (cycles of various nature), such as following: the cycle of the developed countries group is 8.23 years, the cycles of the developing countries is 8.39, the cycle of the Third World countries in 7.6. The article has also revealed a cyclic “drift” in the world sugar production. So, after World War II it has shifted from 9.49 years (typical for the period from the 19th century until the middle of the 20th century) to the current value of 7.12 years.

1. Relevance of the Topic
Socioeconomical genetics deals with the principles and mechanisms of development of social and economic relations, market mechanisms, dynamics of industrial structure, and interactions between the factors affecting the changes in life level of the population and the causes and consequences of recurring economics crises of various depth. This field of science was of great interest for A. Smith and D. Ricardo, for K. Marx and V. Lenin, for N. Kondratyev and A. Bogdanov, as well as for numerous modern researchers. There is voluminous literature concerning these issues, however, the principles of socioeconomic genetics remain mostly unstudied which leads to a plenty of contradictory recommendations [3].

When realising one’s objects it is important to define the principles and mechanisms correctly, to measure the tempo of changes in production technologies, in technological structure, to show the cumulativeness and changeability in the dynamics of technical systems, energy sources, base materials, informational systems, to assess the causes, mechanisms and consequences of technical innovations series in any production.

About 110 countries in the world are engaged in sugar production. Most of them, 75, make sugar from sugarcane, 35 of them – from sugar beet, and 11 countries cultivate both of these cultures.
The main purpose of the study is to reveal new principles in the form of cyclic trajectories common for the sugar manufacturers which will let us predict the activities both of certain units of output, regional segment participants and all the sugar subcomplex more accurately [1].

The subject of the study is high probability cycles and periodograms of high probability cycles (cyclic genomes).

The article presents the concept of high probability cycles. The key moment here is revealing high probability cycles which will be received along with permanent cycles (i. e. cycles that work identically all the time). For example, one cannot suppose that a 18-year cycle will always work identically for all the values. Studies show that the cyclic profile is constantly changing. For instance, a 15-year cycle is relevant nowadays, but it can disappear in 40 years and, possibly, be replaced by a new 13.5-year one. Such changeability of cycles is a subject of research for spectral transformation (wavelet analysis, forward analysis etc.).

Any cycles show themselves as a reaction to certain fundamental events. In our case, it is relations of the sugar subcomplex economy with the “outer world.”

Since world events are reflected in this segment as a set of cycles, it is necessary to supplement, to correct the given task with the following subtask: to reveal the cycles of the sugar subcomplex that represent a reaction to certain fundamental world events, on the assumption of that various cycles work in various periods of time. One should remember that there are a plenty of events in the world, and the sugar subcomplex reacts to them by various cycles (or set of cycles).

Let us explain the concept of realisation of high probability cycles on the following example: suppose that the sugar subcomplex shows cycles of 7, 9, 11.5, 14 years etc. All these cycles show themselves from time to time. But the 7-year cycle, for an unknown reason, appears more often than the others [6, 9]. It is not a permanent cycle (which works identically all the time). It may appear several times in the history of socioeconomic time series and it is not always seen in a periodogram. However, for some reason, it has a greater probability of being observed in the time series under study than the cycles of 9, 11.5, 14 years etc.

High probability cycles will be used as a kind of behavioural model which is common for a certain set of homogeneous values (i. e. for one segment in the agro-industrial complex economics, in our case, it is production of sugar beet, sugar cane, and sugar).

Fig. 1 shows a generic form as a single periodogram (cyclic genomes).

![Figure 1. Cyclic genomes of sugar beet (C and D) and sugarcane (E and F) crop capacity: A, C, and E are the spectral profile, B, D, and F are the forward profile.](image)

1 The spectral profile (and all the other charts hereinafter) is made in Spectrum Viewer software by S. Tarassov.
Note: $A = C + E$, $B = D + F$.

Forward and spectral analysis usually show the same cycles, the only difference is that the classic approach marks out the other less important ones.

The results of the periodograms show that it is more preferable to use the forward analysis (as it is based on the criteria of the forward analysis), for it is closer to the real pattern of the study. At the same time, the classic spectre is more closely related to curve fitting (a standard mathematical procedure for defining active cycles). So, the obtained results let us to go over to work with the cyclic genome.

2. Cyclic genome

This study shows that nowadays there are 5–6 such high probability cycles in the sugar subcomplex. This set is called a high probability periodogram, or a cyclic genome (CG). So, its definition, from the mathematical point of view, is as follows: it is a minimal set of cycles which describes the movement of all the values under study towards the standard as close as possible. In other words, it is a minimal set of cycles which gives the maximum of information about the movement of the object under study [16].

In order to calculate the cyclic genome, this work uses specific mathematical algorithms: we have conducted a cyclic analysis of the values (398 time series) related to the sugar subcomplex, has retrieved the most important cycles, and has performed their clusterisation. To reveal these clusters, the data related to them has been combined in a common histogram which let us to define the areas of high probability cycles. Such spectrogram is called a high-frequency periodogram. It may be used in the same way as in the classic cyclic analysis for revealing the most substantial cycles. There is only one difference: a high-frequency periodogram allows for simultaneous conducting of a cyclic analysis for many time series (see Fig. 2).

![Figure 2](image-url)

Figure 2. A forward periodogram of high probability cycles of the world crop capacity of sugar beet and sugarcane (1961–2017), A; a cyclic genome and cyclo-clusters, B.

Fig. 2 shows high-frequency periodograms and a cyclic genome calculated for the time series under study. The vertical lines represent the five most important cycles (cyclo-clusters) found for these curves, i. e. it is the current cyclic genome for most of the time series of the sugar subcomplex.

The peaks noted in the lower part of the chart are very sharp. It means that these cycles have convincingly showed themselves (and are still doing it) in the sugar subcomplex. The green area represents whole clusters of cycles which the most statistically important of them are divided to. One can see that these five cyclo-clusters comprise about 80% of all the revealed cycles.

The clusters, accordingly, refer to the cycles that show themselves most often.
The red histogram (see Fig. 2, B, the line in the bottom) shows the difference in the activity of these clusters in another way: the higher the histogram, the more often this cycle appears in the chart of the time series under study.

In all, 180 most important cycles (from 110 producing countries) have been revealed. The high-frequency periodogram shows how these cycles are allocated and which of them are more or less homogeneous. For instance, it can be seen the most high peaks (cycles) correspond to the values of 7.003, 7.497, 8.488, 9.364, 9.865, and 11.113 years. It tell us that these cycles show themselves in the field of sugar beet and sugarcane production more often than the others.

3. Mutations in the cyclic genome
When studying all the world sugar subcomplex (WSS) we have revealed 646 various cycles, but the problem with their assessment makes a visual cluster analysis impossible. At this stage, a histogram should be used in order to see how these cycles are allocated. By mutation in CG we understand a shift in the general aggregate of a pre-defined selection. Such histogram is called a high-parametric periodical [18, 19].

As the cyclic genome of the world is changing in the course of time, some cycles disappear and new ones appear. A very important fact is that the cyclic genome is quite stable (in a certain period of time) and exists almost without changes. So, if we examine three time spans in the world sugar production from 1864 to 2016 (i.e. an averaged pattern for the last 150 years), we will see the following “mutations”: 1) 1864–1915 – 9.4934 years; 2) 1916–1966 – 9.3712 years and 3) 1967–2016 – 7.12 years, i.e. all this time, WSS reacted to the external events by the same set of cycles (showed itself through the given cyclic genome). It is seen that this cyclic genome is stable for the last 50 years.

So, with the help of calculations one can see the most important cycles for the production index under study combined on a single chart, as well as the cyclic genome which shows the most probable cycles.

Genetic shifts in cycles on a larger or lesser scale change the existing picture of the world and become a hereditary kernel, a reference base for appearance of a new cluster in a more and more differentiating system in the structure of the sugar subcomplex [20].

It is important to note that this work says about the possibilities and not about power or significance of the cycles under analysis.

4. Conclusions
In conclusion, we are sure to say that only with the help of sociogenetics (of the cyclic genome) one can investigate the inner mechanism, the principles of development, define the invariant kernel representing the essence of the field under study, measure the content and prospects of mutation clusters which appear from time to time, selecting those which will become a part of the enriched genotype of the society system (WSS, in our case), which, after all, makes it a useful instrument for making reliable predictions [20].

1. In our study (and for the first time in practice), the cycles were calculated using a forward analysis.
2. These cycles can be displayed (presented) as high-stable in practice, when working with the spectral or forward analysis.
3. All the cycles revealed in the work are quite stable. The work almost identically for the last 50 years.
4. The underlying principles of the heredity and changeability in the dynamics of the agro-industrial complex remain mostly unstudied due to the absence of researches in its other segments in the field of sociogenetics (cyclic genome).

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