Application of the Principle of Symmetry for Synchronization of Biosignals in their Sample

Bohdan Yavorskyy

Abstract - **In this paper results of computing simulation of symmetry principle application for developing automation synchronization of stochastic homogeneous biosignals in their sample at estimation of their probabilistic statistic are discussed. The biosignals are responses of bioobject after excitations as test of this bioobject. Results are used for processing of evoked biosignals at active researching of different bioobjects.**

Keywords - **Biosignal, Sample, Symmetry, Statistic.**

I. INTRODUCTION

When monitoring the functional state of biobjects, it is necessary to test influence on it. Reviewed of bioobject evoked responses (biosignals) $x_k(j)$, where $j=\overline{1,J}$ - a number of a readout of the biosignal, $k=\overline{1,K}$ – a number of a biosignal in the sample, contain the stochastic initial (latent) parts $x_k(j)$, $j=\overline{1,J_k}$, Fig. 1 (c.u. – conditional units; x – damped sine function with latent parts are Gaussian and plus additive Gaussian noise).

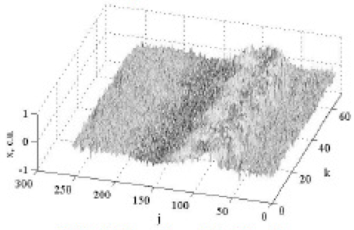

Fig.1. Sample of biosignals

In clinical practice, morphological parameters of biosignal are used. So, requirement the visibility of evoked biosignal in domain space. Typical estimation procedure is to average. It is regulated and medical statistics. However, the natural unsteadiness biosignals require special measures to ensure coherence in the ensemble of biosignals [1]. In practice, the synchronization procedure is interactive (hand- shifts of samples), or automated (to phases of vascular perfusion, heart rhythm etc.). These greatly complicate both the hardware and software implementation of diagnostic systems. Therefore, improving the automation of synchronization for ensure coherence in the formation of an ensemble of samples is relevant.

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II. THE CONSTRUCT OF SYMMETRY SAMPLE

On the synchronized sample definition of biosignals (Fig. 1) must be symmetry with the plane of symmetry (K/2, j, x) in (k, j, x) coordinate system (Fig. 2). To perform this cyclic, left shift of every k-th biosignal to J_k is needed. For estimation of J_k is applied an optimization procedure

$$\underset{\substack{\forall k,i\to|x_k(j_{min})|<h_i,\\ J_{ki}=j_{min}}}{\arg\min} F(\hat{m}_x,\hat{\sigma}_x), \qquad (1)$$

where $F(\hat{m}_x,\hat{\sigma}_x)$ - functional, constructed with estimations of mathematical expectation and dispersion of coherent estimation $\hat{x}(j)$, $h_i \in \{ih_0, i=\overline{1,I}\}$ - test thresholds.

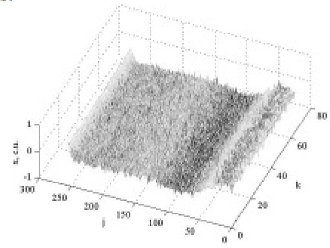

Fig.2. Synchronized sample

On Fig. 2 result of synchronization is shown. Additive noise was with zero mathematical expectation and 0.1 c.u. dispersion and mathematical expectation of latent parts $J_k = 50$, and its dispersion equal 10 points. Were used the mean of mean square deviation (MSD) of $\hat{x}(j)$ as functional $F(\bullet)$, and maximal MSD of estimation of biosignal from non synchronized sample - as threshold h_0.

III. CONCLUSION

For given above conditions were obtained means of MSD for a priory known, not known, and estimated J_k (when synchronize) as 0.0124, 0.0166, and 0.0123 c.u. subsequently.

REFERENCES

[1] B. Yavorskyy, "A new Approach to Preliminary Processing of Random Signals", *Analysis of Biomedical Signals and Images*, Brno Press. Technical University, Prague, 1996, pp. 134-136.

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Abstract - **The paper gives the rationale for the mathematical model of the response of bioobjects when that is stimulated with very low-intensity. It has been established that the noise of the response can be considered to be independent from the stimulation intensity. Moreover, it influence on response additively. The resolution of the measurement increase significantly when intensity of stimulation is decrease. Since this significantly reduces signal to noise ratio, an optimal filtering of responses requires. Reasons for the optimal filter structure realization include assumptions for a sequence of responses to be stationary. In this paper discussed results of computing simulation of application of the principle of symmetry for developing automation synchronization of stochastic homogeneous biosignals in their sample at estimation of their probabilistic statistic. The biosignals are responses of bioobject after excitations of as a test of this bioobject. Results are used for processing of evoked biosignals at active researching of different bioobjects.**

Keywords - **Biosignal, Sample, Symmetry, Statistic.**

I. Introduction

When monitoring the functional state of biobjects do test influences on it. Very low intensity of the test lead to that that in reviewed of bioobject evoked responses (biosignals) arise the stochastic initial (latent) parts $x_k(j)$, $j=\overline{1,J_k}$ (Fig. 1, where c.u. – conditional units; x – α-damped sine function with stochastic latent parts of J_k length are Gaussian, and plus additive Gaussian noise n). The typical expression of the ensemble of responses is

$$x_k(jT_d) \equiv \begin{cases} n(j), & j=\overline{1,J_k}, \\ \exp(-\alpha j)\sin(2\pi j/\mu)+n(j), & j=\overline{J_k,J}, \end{cases} \qquad (1)$$

where $j=\overline{1,J}$ - a number of a readout of the biosignal, $j \equiv jT_d$, T_d – readout period, μ – a quantity of readouts in the period of sine, $k=\overline{1,K}$ a number of a biosignal in the sample.

In clinical practice, morphological parameters of biosignal are used. So, requirement the visibility of evoked biosignal in domain space. Typical estimation procedure is to average. It is regulated and medical statistics. However, the natural unsteadiness biosignals requires special measures to ensure coherence in the ensemble of homogeneous but complex biosignals [1].

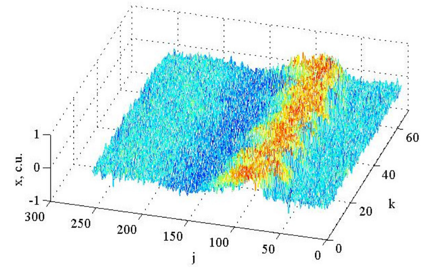

Fig.1. Sample of biosignals

In practice, the synchronization procedure is interactive (hand-shifts of samples), or automated- (to phases of vascular perfusion, heart rhythm etc.). These greatly complicate both the hardware and software implementation of diagnostic systems. Therefore, improving the automation of synchronization for ensure coherence in the formation of an ensemble of samples is relevant.

II. The Construct of Symmetry Sample

For interactive processing of biosignals on the first step needs determine values $J_k, k=\overline{1,K}$. Mathematical expectation of the oscillatory part of biosignal then is determined with taking into account these known values as synchronization values.

For automatic processing of biosignals one can build a number of heuristic algorithms to synchronize with different efficiency. For example, when a priori known values $\{J_k|_{min}, J_k|_{max}\}$, direct selection for each of the ensemble biosignals such values $J_k \in \{J_k|_{min}, J_k|_{max}\}$ at which the average of the standard deviation of an estimate of the expectation will be minimal. The complexity of this type of synchronization is $O(2^{\mathrm{int}(\log_2 J)+\log_2 \mathrm{int}(J_k|_{max}-J_k|_{min})})$. This algorithm may be extending to each of $\{J_k|_{min}, J_k|_{max}\}_\kappa$, $\kappa \in 1,2,3,\ldots$ biosignals fluctuations (in particular, on the basis of their entire genesis) and improved by the method of study selection of intervals $\{J_k|_{min}, J_k|_{max}\}_\kappa$, $\kappa \in 1,2,3,\ldots$ and criteria its completion.

By definition, is synchronized sample of biosignals must to be symmetry with the plane of symmetry (K/2, j, x) in (k, j, x) coordinate system (k-symmetry). For deterministic responses $x_k(j)$ to be k-symmetry means, that for all j-th

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$$x_k(j) = x_{K-k+1}(j) \qquad (2)$$

where $\begin{cases} k = \overline{1, K/2}, & K \text{ is an even number,} \\ k = \overline{1, (K-1)/2}, & K \text{ is an odd number} \end{cases}$.

For k-symmetric sample of the stationary stochastic responses are two common ways for like as relation (2) presentation – in probabilistic or correlation-spectral frames. E.g., for the first ones may be used estimations of parameters of the probability density function of $p(x_k(j))$ and $p(x_{K-k+1}(j))$ for all j-th (then equality sign is in an appropriate probabilistic sense).

For perform relation (2) with a data (1) need the cyclic left shift on to J_k of every k-th biosignal.

For estimation of J_k would be good an automation optimization procedure

$$\underset{\substack{\forall k, i \to |x_k(j_{min})| < h_i, \\ J_{ki} = j_{min}}}{\arg\min} F(\hat{m}_x, \hat{\sigma}_x), \qquad (3)$$

where $F(\hat{m}_x, \hat{\sigma}_x)$ - functional, constructed with estimations of mathematical expectation and dispersion of an estimate $\hat{x}(j)$ at test thresholds $h_i \in \{ih_0,\ i = \overline{1, I}\}$, h_0 – a beginning threshold. For the threshold h had been choose a phase of beginning oscillatory part of biosignal, that explain using of j_{min} in expression (3).

III. Results of Application of Symmetry

Algorithm for automatic determine of left cycle shift parameter J_k for the biosignals with ensemble of normal probability distribution of its values is shown in Fig. 2.

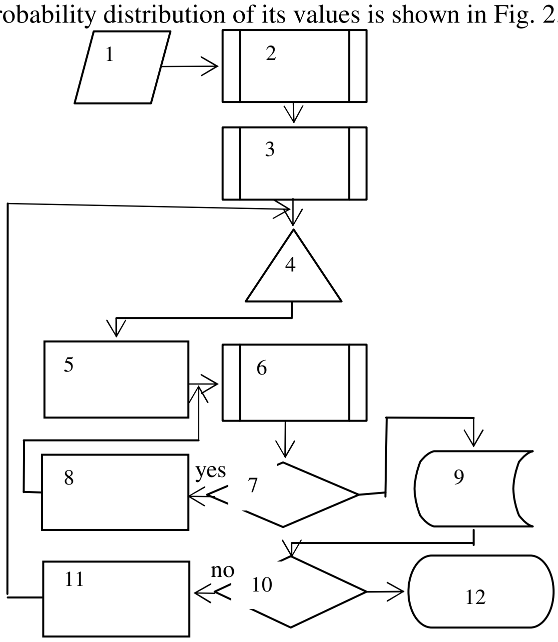

Fig.2. Algorithm for determine parameters of left cycle shifts

On Fig.2. are indicated: 1 – data, ensemble $\{x_{kj},\ k = \overline{1, K},\ j = \overline{1, J}\}$, k = 1; 2 - a first approximation to estimate the expectation m_x and variance σ_x; 3 - to define a threshold h value (the value of the functional $F(\hat{m}_x, \hat{\sigma}_x)$; 4 - choose the implementation of biosignals of k-th experiment; 5 - j = 1; 6 - to determine the metric $\rho = \|x_{kj} - h\|$ are based on a norm of the space of functions that are modeled biosignals x_{kj}; 7 - to compare the value of the metric with threshold $\rho < h$, ; 8 - j = j +1; 9 – to remember the value J_k; 10 – check $k > K$; 11 - k=k+1; 12 - to complete the analysis.

Synchronization by left cycle shifts of $k = \overline{1, K}$ biosignals are presented by the expressions

$$\begin{aligned} \hat{x}_k(j) &= x_k(j + J_k - 1),\ j = \overline{1, J - J_k}, \\ \hat{x}_k(j) &= x_k(j - J + J_k),\ j = \overline{J - J_k + 1, J}, \end{aligned} \qquad (4)$$

On Fig. 3 is shown a result of synchronization. Additive noise n(j) was with equal zero mathematical expectation and 0.1 c.u. dispersion. The mathematical expectation of latent parts $J_k = 50$, and its dispersion equal 10 c.u. Were used the mean of mean square deviation $\sigma_x(j)$ (MSD) of $\hat{x}(j)$

$$m_\sigma = \frac{1}{J} \sum_j \sqrt{\sigma_x(j)} \qquad (5)$$

as functional F(•). The maximal MSD of estimation of biosignal from non synchronized sample was chose as threshold h_0.

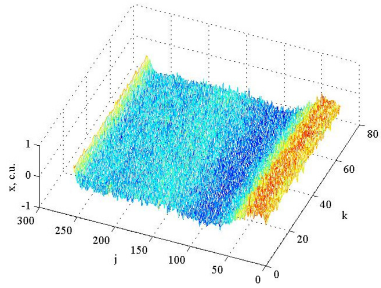

Fig.3. Synchronized sample

For given above conditions were obtained means of MSD (5) for synchronization values J_k that are - a priory known (a), not known (b), and estimated by given on Fig.2. algorithm (c), and next synchronization (4):
(a) - 0.0122, (b) - 0.0166, and (c) - 0.0123 c.u.

IV. Conclusion

The principle symmetry is a background for construct synchronization of complex homogeneous biosignals in their ensemble and does better results of a coherent filtration.

References

[1] B. Yavorskyy, "A new Approach to Preliminary Processing of Random Signals", *Analysis of Biomedical Signals and Images*, Brno Press. Technical University, Prague, 1996, pp. 134-136.

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