Immune network based method for identification of turbine engine surging

P.I. Bidyuk, V.I. Litvinenko, A.S. Gasanov

Abstract. *An application of the new method and combined algorithm on the basis of immune network and negative selection for identification of aviation engine surging is considered. The problem of identification of the engine surging is examined as a problem of anomaly detection. The basic drawbacks of the negative selection algorithm are examined. It is offered to use the method based on artificial immune network for data processing of detectors set, and for a monitoring phase the scheme of classical negative selection algorithm is used. The results achieved have shown high efficiency of the offered method and algorithm.*

Keywords

Surging (pompage), engine surging, gas turbine engine (GTE), negative selection algorithms, artificial immune network learning algorithm, combined algorithm

1 .1 Introduction and Motivation

The modern methods of gas turbine engine (GTE) diagnostics allow to determine malfunctions of an engine, identification of the malfunctioning reasons and their possible subsequent elimination [1]. One of the problems of technical diagnostics of GTE is timely identifying of the surging (pompage). Surging is a stalled operating mode of an avionic GTE, accompanied by infringement of its gas-dynamic stability of functioning, sharp decrease of thrust and powerful vibrations that may destroy the engine [2]. The air stream, flowing around the turbine blades, sharply changes its direction. Subsequently substantial turbulences are observed inside the turbine, and the pressure at the compressor input becomes equal or larger than that at its exit. Instabilities of functioning of a GTE are characterized by the oscillatory processes producing vibration of an engine body and substantial growth of dynamic load on elements of a system at specific points that creates conditions for their destruction. In the pompage mode self-inflammation and self-destruction of a GTE [3, 4] is possible with high probability. Prevention of the surging demands forecasting and preventing of approaching the system to this mode. Modern methods of GTE surging identification are mainly based on diagnostics of any signal or the groups of signals generated by control devices and gauges. Existing spectral methods of signal diagnostics are fit well for revealing of the features. However, they become useless when the signal under study has components that quickly vary at several important measuring points. Usually the Fourier transform is used for spectral analysis of measurements [5]. More universal method of time-varying signal analysis is based on the wavelet-analysis. Wavelet transform allows perform the following: (1) to locate

special points where a fault may occur; (2) to reveal irregular changes of a function and its derivatives; (3) to calculate fractal signal characteristics.

In this paper an alternative method of GTE surging identification is offered that is based on vibration measurements. We consider identification of an engine surging as a problem of anomalies detection. In general, the problem of anomaly detection can be seen as a two class classification problem. Given an element from a given problem space, the system should classify it as normal or abnormal. However, this is a very general characterization since it can correspond to very different problems depending on the specific context where it is interpreted. From a statistical point of view the problem can be seen as that of outlier detection [6]. According to Hawkins, an outlier is *"... an observation that deviates so much from other observations as to arouse suspicion that it was generated from a different mechanism"* [7]. A common statistical approach to solve this problem [8] is to build a statistical model of the normal mode and use it to determine if a given observation is an outlier or not; basically, if the probability of the observation being generated by the normal distribution is low, then the observation is an outlier. A more complex approach can also model the outlier generation mechanism. In the previous approach, the idea is to remove any observation that can be classified as an outlier. Another possibility is to use the methods that accommodate the outliers, i.e. methods that can produce good estimates or inferences even in the presence of outliers. This kind of methods belongs to a more general area of statistics called robust statistics [9, 10]. The outlier detection point of view implicitly assumes that the data belongs to both normal data and outliers (which are possibly caused by errors occurred during the data collection or by noise). The interpretation of anomaly detection that we are interested in relates to dynamic context. In this case an anomaly is considered as a state of a given system that is not consistent with the normal behavior of this system. According to this, an anomaly detection algorithm will perform a continuous monitoring of the system and explicit classification of each state as normal or abnormal. Let's keep in mind that statistical modeling of the normal can be applied to this definition of anomaly detection, but the robust statistics approach cannot. The main problem regarding statistical model constructing is that it needs to make assumptions of distribution properties of the monitored variables, which in general are unknown. In this work we propose alternative approach to solution of the problem in view that is based on the combined use of artificial immune network (AIN) and algorithm of negative selection [6, 16, 17, 19].

2 .2 Definition and methods
2.1 Negative Selection Algorithm
The process of negative selection of T-cells is responsible for eliminating the T-cells whose receptors are capable of binding with self-peptides. This process guarantees that T-cells that leave the thymus do not recognize any self-cell or molecule. Forrest et al. [12] proposed a change detection algorithm inspired by the negative selection of T-cells within the thymus. This procedure was named *negative*

selection algorithm, and its original application is related to computer net security. A single type of immune cell was modeled: T-cells were represented as *L*-length strings of bits. The Forrest and his collaborators negative selection algorithm is rather simple [12]. Given a set of self-peptides, named self-set S, the T-cell receptors will have to be tested for their capability of binding the self-peptides. If a T-cell recognizes a self-peptide, it is discarded, otherwise it is selected as an immuno-competent cell and enters the available repertoire **A**. The chart of negative selection algorithm is illustrated in Fig. 1.
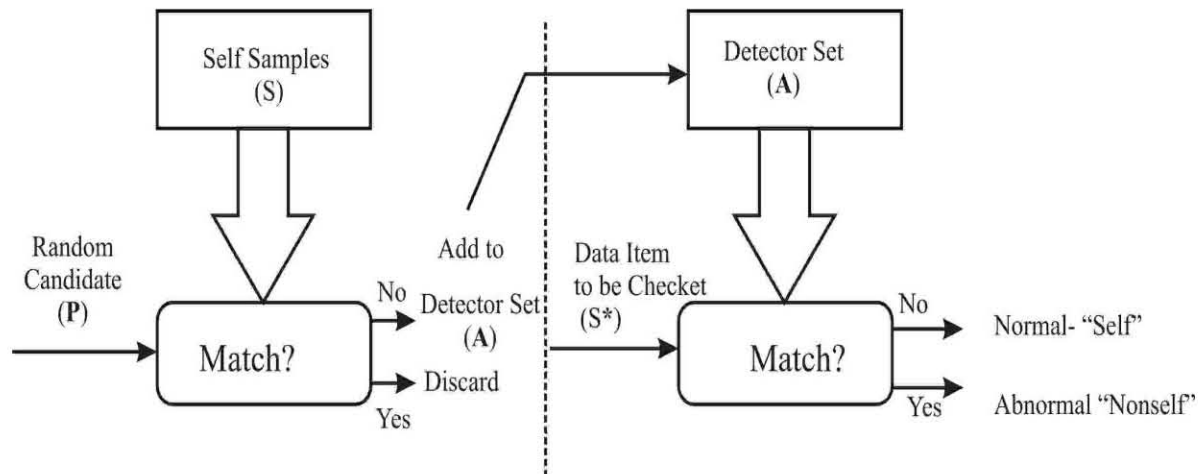
Fig.1. The negative selection algorithm [15]

The negative selection algorithm can be summarized as follows [11]:

- *Initialization:* generate random strings and place them in the set **P** of immature T-cells, assuming all the molecules (receptors and self-peptides) are represented as binary strings of the same length *L*.

- *Affinity evaluation:* determine the affinity of all T-cells in V with all elements of the self-set **S**.

- *Generation of the available repertoire:* if the affinity of an immature T –cell (element of **P**) with at least one self-peptide is greater than or equal to a give cross reactive threshold, then the T-cell recognizes this self-peptide and has to be eliminated (negative selection); else the T-cell is introduced into the available repertoire **A**.

The process of generating the available repertoire in the negative selection algorithm was termed by the authors as *censoring phase*. The algorithm also includes a *monitoring phase*. In the monitoring phase, a set S^* of protected strings is matched to the elements of the available repertoire A. The set **S*** might be the own set **S**, a completely new set or composed of elements of the set **S**. If recognition occurs, then a non-self pattern (string) is detected.

The negative selection algorithm suggests generation of random strings until repertoire **A** of appropriate size is generated. This approach could be adopted in both algorithms.

Even random generation of the **P** repertoire results in algorithms with some drawbacks. First, this approach results in an exponential cost to generate the available repertoire A in relation to the number of self strings in **S**. Second, random generation of **P** does not account for any adaptability in the algorithm and neither any information contained in the set **S**.

The algorithm of negative selection has also other restrictions and limitations [11]. When it is not appropriate, for example, the number of self samples is small and sparse.

Some limitations of the (binary) string representation in NS algorithms are as follows:

- The binary matching rules are not able to capture the semantics of some complex self/non-self spaces.

- Some difficulties with extracting meaningful domain knowledge.

- In some cases a large number of detectors are needed to guarantee better coverage (detection rate).

- Difficulties with integrating the NS algorithm with other immune algorithms.

- The crisp boundary of self and non-self may be hard to define.

In real-valued representation the detectors are represented by hyper-shapes in n-dimensional space. The algorithms use geometrical spaces and use heuristics to distribute detectors in the non-self space.

Some limitations of the real-valued representation in NS algorithms are:

- The issue of holes in some geometrical shapes, and may need multi-shaped detectors.

- Curse of dimensionality.

- The estimation of coverage.

- The selection of distance measure.

During our experimental study it has been established that generation of a set of detectors at training phase occurs casually owing to what it is in advance impossible to define is minimum necessary quantity of detectors which will provide the maximum quality of recognition. The increase in quantity of detectors conducts to delay of a phase of recognition, and its reduction – to deterioration of work of algorithm. It occurs because the probability of formation of the "cavities" (areas in the space of "non-self") that are not sensed by detectors increases. Thus, a problem of the given research is development of advanced method of the detectors generation

that are adaptive regarding their functionality. The method proposed in the paper is based on artificial immune network.

2.2 The Algorithm of artificial immune network

According to the network theory the immune system is composed of a network whose dynamics is disturbed by foreign antigens [20]. This interaction with foreign antigens results in the network that corresponds to *internal image* of the universe of antigens. Groups of cells and molecules within the immune networks correspond to antigenic groups. There are basically two levels of interactions in the network: 1) the interaction with the environment (foreign antigens), and 2) the interaction with other network elements. The theory of immune network confirms, that even in absence of external stimulus (pathogenic microorganisms), the immune system is in constant movement. Its cells are capable to co-operate not only with antigens, but also with themselves, i.e. to distinguish similar antibodies. As a result of this mutual recognition of molecules of antibodies the connected network arises within immune system. The artificial immune network [5, 8] can be presented as a graph which consists of a set of nodes – cells of the network (antibodies), and a set of weighed edges meaning communications between the cells. A value of weight of an edge corresponds to affinity of communication of cells with each other.

The immune networks have two kinds of affinity:

– Affinity of communication "antigen-antibody" (*Ag-Ab*) – distinction level.

– Affinity of communication "antibody-antibody" (*Ab-Ab*) – similarity level.

Formally it is possible to represent the artificial immune network as follows:

$$immNET = (P^l, G^k, l, k, m_{Ab}, \delta, f, I, \tau, AG, AB, S, C, M, n, d, H, R) \qquad (1)$$

,

where P^l is the search space (shape-space); G^k is the space representation; l is a length of vector of attribute vector; k is a length of a cell receptor; m_{Ab} is size of cell population; δ is expression function; f is affinity function; I is the function of initialization of initial population of cages of a network; τ is a stop condition for the algorithm; AG is a subset of antigens; AB is a population of cells of a network (antibodies); S is selection operator; C is cloning operator; M is the operator of a mutation; n is a quantity of the best cells selected for cloning; d is quantity of the worst cells that are subject to replacement by new ones; H is the operator of clonal deleting; R is the network compression operator.

In the given work we have used the model of artificial immune network learning offered by L. N. de Castro and F. J. Von Zuben [15], named aiNet (*Artificial Immune NETwork*). The network is initialized with a small number of randomly generated

elements. Each network element corresponds to an antibody molecule, i.e. an attribute string is represented in Euclidean shape-space.

The next stage is representation of antigenic patterns. Each pattern is presented to each network cell, and their affinity is determined according to (1):

$$D = \sqrt{\sum_{i=1}^{L} (Ab_i - Ag_i)^2} \; . \tag{2}$$

A number of high affinity antibodies is selected and reproduced (*clonal expansion*) according to their affinity: the higher is the affinity, the higher is the number of clones to be produced. The clones generated undergo somatic mutation inversely proportional to their antigenic affinity: the higher is the affinity, the lower will be mutation rate. A number of high affinity clones is selected to be maintained in the network, constituting what is defined as a clonal memory.

Then the affinity between all remaining antibodies is determined. Those antibodies whose affinity is less than given threshold are eliminated from the network (*clonal suppression*). All antibodies whose affinity with the antigen is less than given threshold are also eliminated from the network. Additionally a number of new randomly generated antibodies are incorporated into the network (*metadynamics*).The remaining antibodies are incorporated into the network, and their affinity with the existing antibodies is determined. All but one antibody whose affinity is less than a given threshold are eliminated.

The aiNet learning algorithm can be summarized as follows[15]:

1. *Initialization:* create initial random population of network antibodies.

2. *Antigenic presentation:* for each antigenic pattern, do:

   2.1. *Clonal selection and expansion:* for each network element, determine its affinity with the antigen presented. Select a number of high affinity elements and reproduce (clone) them proportionally to their affinity.

   2.2. *Affinity maturation:* mutate each clone inversely proportional to affinity. Re-select a number of highest affinity clones and place them into a clonal memory set.

   2.3. *Metadynamics:* eliminate all memory clones whose affinity with the antigen is less than a pre-defined threshold.

   2.4. *Clonal interactions:* determine the network interactions (affinity) among all the elements of the clonal memory set.

   2.5. *Clonal suppression:* eliminate those memory clones whose affinity with each other is less than a pre-specified threshold.

   2.6. *Network construction:* incorporate the remaining clones of the clonal memory with all network antibodies.

3. *Network interactions:* determine the similarity between each pair of network antibodies.

4. *Network suppression:* eliminate all network antibodies whose affinity is less than a pre-specified threshold.

5. *Diversity:* introduce a number of new randomly generated antibodies into the network.

6. *Cycle:* repeat Steps 2 to 5 until a pre-specified number of iterations is reached.

2.3 The offered combined algorithm of negative selection and AIN

Solution of the surging identification problem by means of the developed algorithm demands the description of specific implementation of some operators and functions. In this case the immune network uses antibodies coded with real numbers (fig. 2) to which the metrics is applied so that to calculate Euclidian distance. Thus, antibodies form around themselves l-dimensional radial area of recognition with radius which r called cross-reactive threshold. As it is shown in Fig. 2, cross-reactive threshold is included in the structure of an antibody that gives a chance for adaptive adjustment of its value. Thus, the immune network fills space of "non-self" with distinguishing hyperspheres of different radius that gives the chance for its fuller covering [19].

r	Ab_{i1}	Ab_{i2}	...	Ab_{il}

Fig. 2. Representation of antibody of AIN

To calculate the affinity values of communication "antigene-antibody" the following expression is used:

$$f_{Ab-Ag} = \frac{k_r}{r} + D_{E(Ab-Ag)}, \tag{3}$$

where r s the cross-reactive threshold of an antibody (detector); k_r is the coefficient of importance of the cross-reactive threshold (parameter of algorithm adjustment). The parameter k_r is a very important parameter of training. It operates robustness the received decision.

The increase in this parameter forces an immune network to support detectors of larger radius that gives rougher but more stable solution. However, the excessive

increase of k_r negatively affects accuracy of a solution found. Fig. 3 illustrates the influence of parameter k_r on the way of detectors generating.
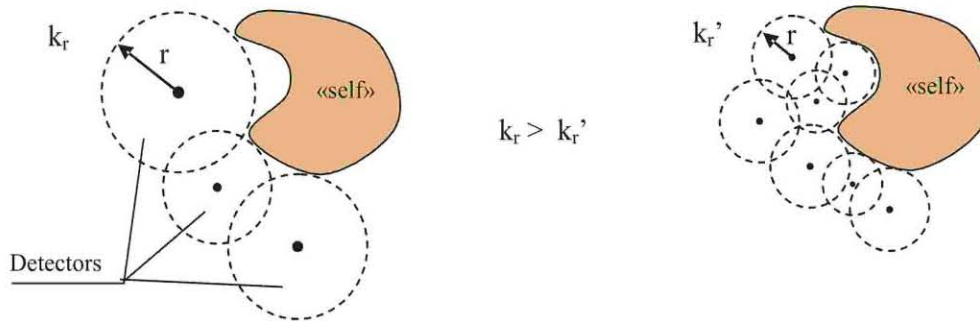
Fig. 3. Influence of value of parameter k_r on a way of generation of detectors

The compression of immune network is carried out on the basis of self-recognition of cells which is numerically expressed via affinity communications of antibodies with each other. For calculation of the affinity value of communication the following expression is offered:

$$f_{Ab-Ab} = -\frac{D_{E(Ab_1-Ab_2)} - (r_{Ab_1} + r_{Ab_2})}{2 \cdot \min(r_{Ab_1}, r_{Ab_2})}. \tag{4}$$

The following interpretation of values is thus possible: $f_{Ab-Ab} \leq 0$ means distinguishing hyperspheres of detectors that are not blocked. This cnoice does not demand compression since antibodies do not distinguish each other (Fig. 4); if f_{Ab-Ab} is in a range of $(0, 1)$, then hyperspheres are blocked by covers, and the value represents overlapping degree (Fig. 4).

Thus, the compression is carried out depending on the size of a parameter of compression threshold where σ_s is a parameter of training algorithm; if $f_{Ab-Ab} \geq 1$, hyper-sphere of smaller radius (r) is completely in the hyper-sphere of larger radius (Fig. 4). In this case the compression is necessary as the redundancy of distinguishing elements is observed.
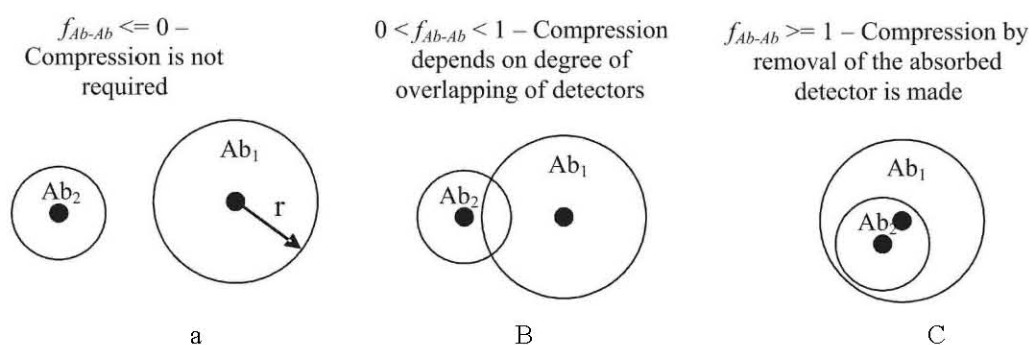
Fig. 4. The various relative positioning of distinguishing hyperspheres of detectors

In this specific implementation the operator of clonal deleting H operates only on those antibodies which distinguish at least one antigen. Thus, it is guaranteed that a resultant AIN at the end of each generation does not contain the detectors distinguishing the "self" antigens. The generalized chart of the algorithm offered is shown in Fig. 5.
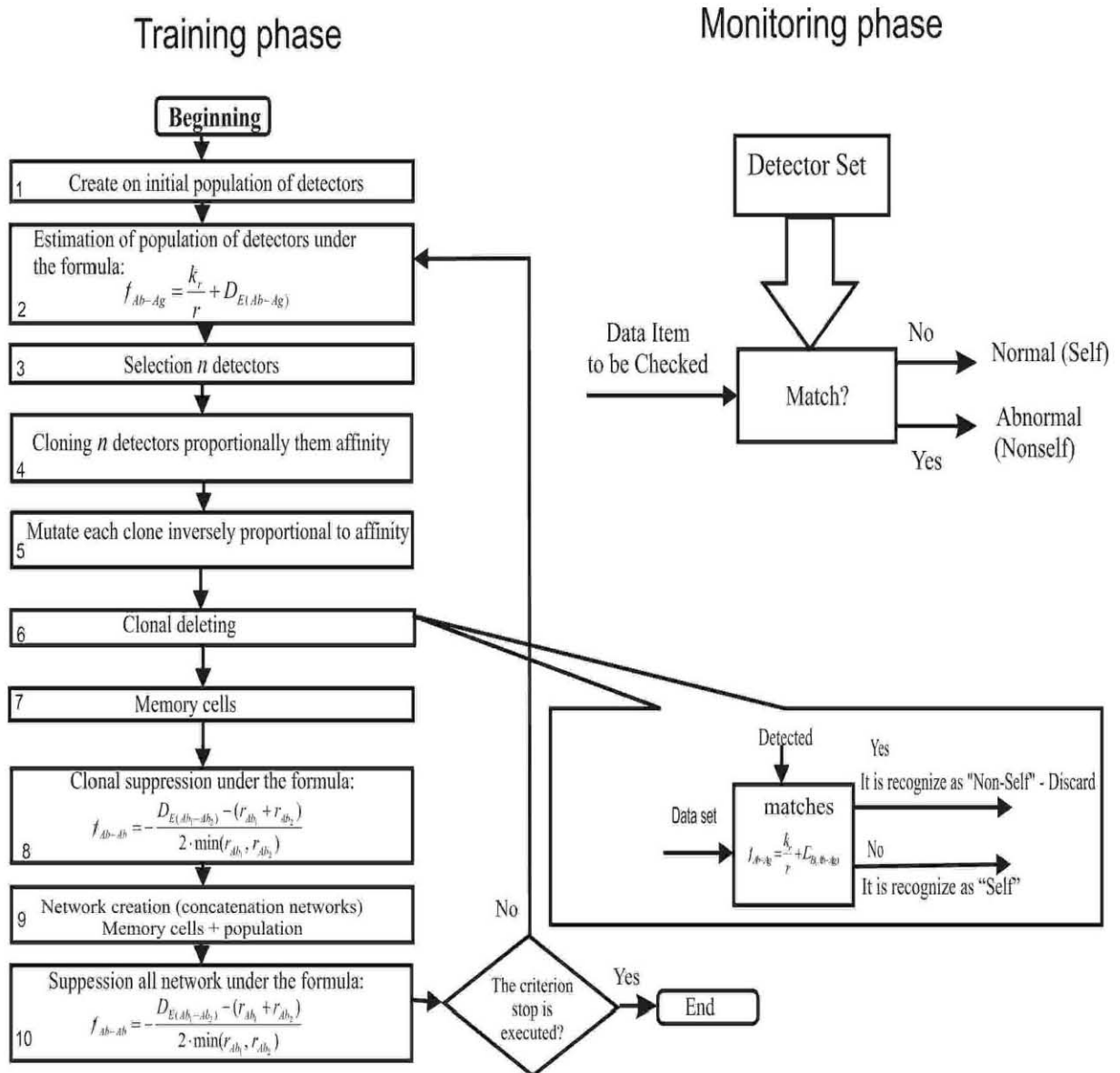
Fig. 5. The generalized scheme of the combined negative selection algorithm and an immune network

3 Results of computer experiment
3.1 Solution of the anomalies detection problem

Generally it is possible to present the problem of anomalies detection as follows [6, 7]. Let a discrete number of values of a process variable is given by: $y_1, y_2, ..., y_n$. It is also supposed that discrete values of the variable $y(t)$ belong to the time interval $[t_1, t_n]$. A given number of measurements time window of width k is $k < n$. The values in the time window form the vector of patterns $Y_t(y_t, y_{t-1}, ..., y_{t-k+1})$. The vector of patterns corresponds to one of the two classes: *normal* (1), if the fragment

of the time series, corresponding to a given vector, does not contain anomalies (i.e. belongs to the class of "self"), otherwise it corresponds to *abnormal* (0). The time window is moving along time axes with step size, Δl, forming a set of vectors which divide the attribute space into two parts: with anomalies and without them. The problem is in referencing of any vector, Y_j, formed by the selected sliding window, to one of the two allocated classes. On the other hand, if we consider the process under study as a dynamic system, the set of vectors received by means of a sliding window represents restored phase portrait of dynamic system, and the vectors formed are the points, belonging to a phase trajectory of the system. In a case of normal behaviour the given trajectory can be perceived as a reference image, any deviation from which creates anomalous pattern (Fig. 5). It is necessary to stress, that the use of negative selection allows avoiding the necessity of including into training sample the vectors, corresponding to abnormal behaviour that gives the chance to recognize any, even not known in advance anomalies.

3.2 The First experiment

For the first experiment the periodic signal, which graph is presented in Fig. 6a, was chosen [9]. The training sample totals 200 values. This training signal does not contain anomalies. For creating the training sample the sliding window of two values width was used. In this case the space of patterns is two-dimensional: (y_t, y_{t+1}). The appearance of the phase portrait restored is shown in Fig. 6b.

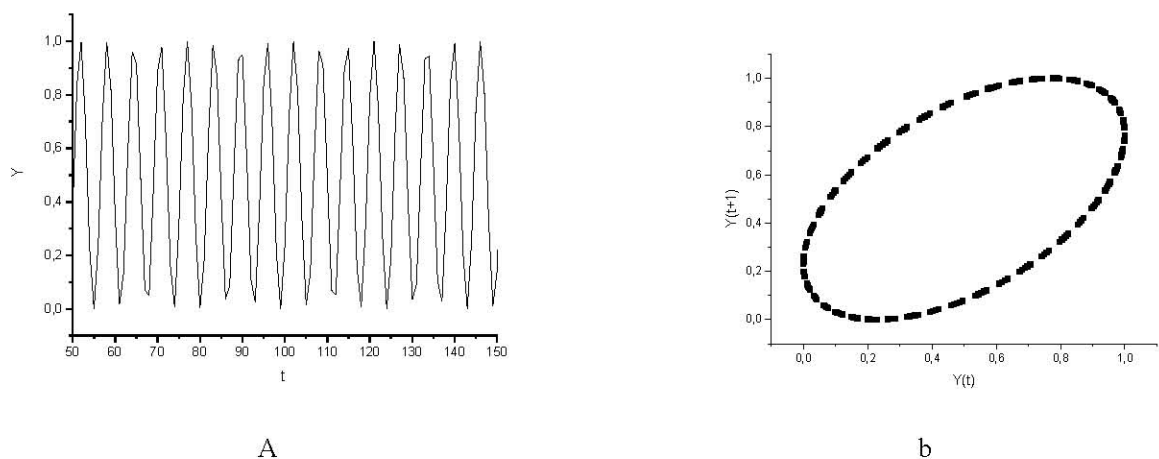A   b

Fig. 6. An experimental signal; a– the graph of the signal which does not contain anomalies; b – the restored phase portrait of the signal which does not contain anomalies

Shown in drawing 6b geometric figure is a display of data of the class «Self» that can be used as a training image for artificial immune network. The results of AIN training for two optional values of the importance cross reactive threshold, k_r, are presented in Fig. 7. The Fig. 7a shows less steady solution since a part of the plane, corresponding to skipped elements of a phase trajectory, is blocked by detectors. It

will lead to their false operation. The solution, shown in Fig. 7b, is steadier, and is taken for further testing.
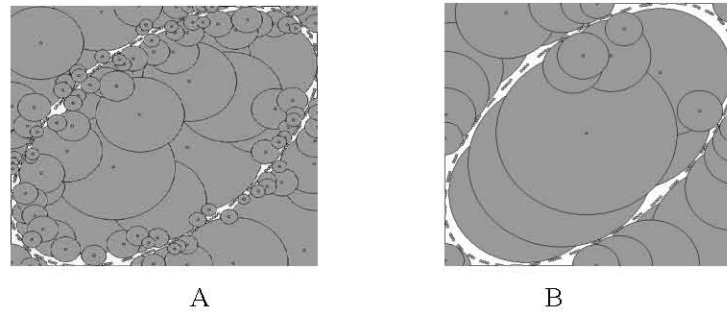

A   B

Fig. 7. A configuration of the trained immune network for two optional values k_r : (a) – at $k_r = 0.01$; b) – at $k_r = 0.1$)

Further on a local anomaly has been added to the signal (Fig. 8a), that has found its reflexion on a phase portrait, as is shown in Figure 8b. In this case two points are deviated from the phase trajectory and have been recognized by corresponding detectors.

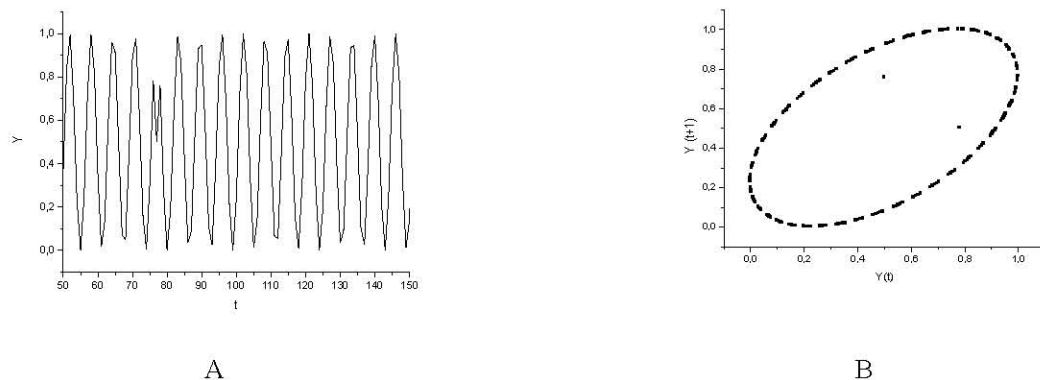A   B

Fig. 8. The test signal with local anomaly and its phase portrait

During detection phase a repeated recognition of the abnormal phenomenon by several detectors simultaneously (Fig. 9a) is quite probable. The histogram in drawing 9b shows the number of detectors, which are activated during detection of anomaly at movement of scanning windows over a signal sequence.
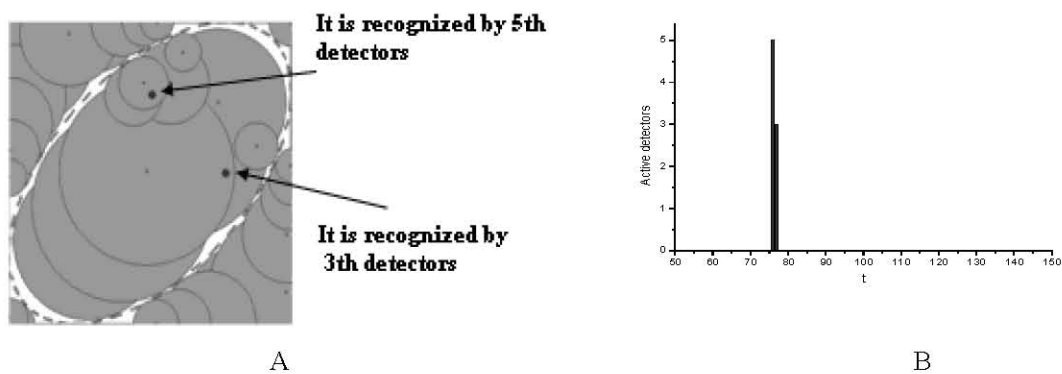
Fig. 9. Illustration of the detection phase: a) – recognition of abnormal vectors
by an immune network; b) – the histogram of detectors activation

3.3 The second experiment

For the second experiment the data have been used received on the test bed for aviation *gas turbine engine*. The data is represented four time series (Vk_3, Vk_P, Vv_3, Vv_P). The signals received from gauges of vibration of the support on which the engine has been fixed. The time series graphs are shown in Fig. 10.
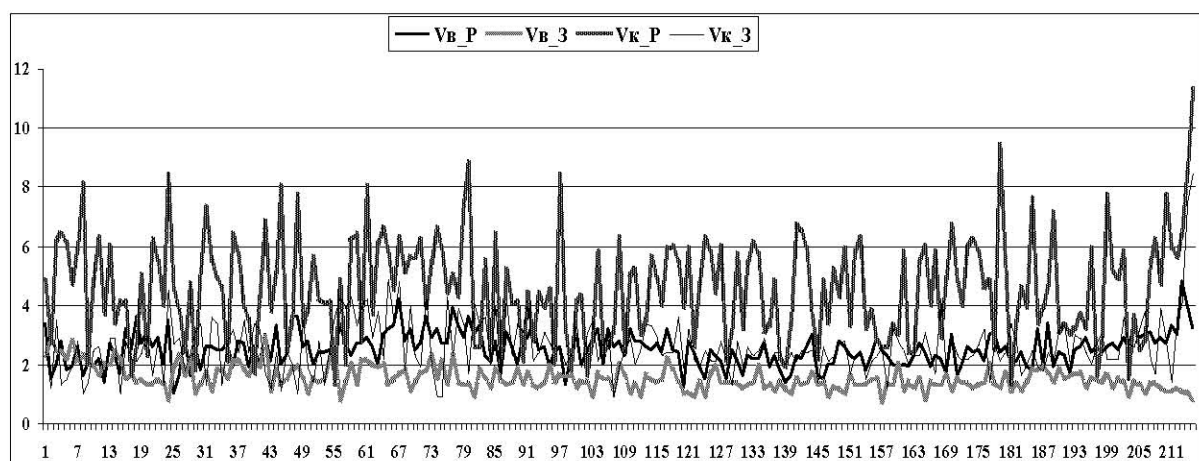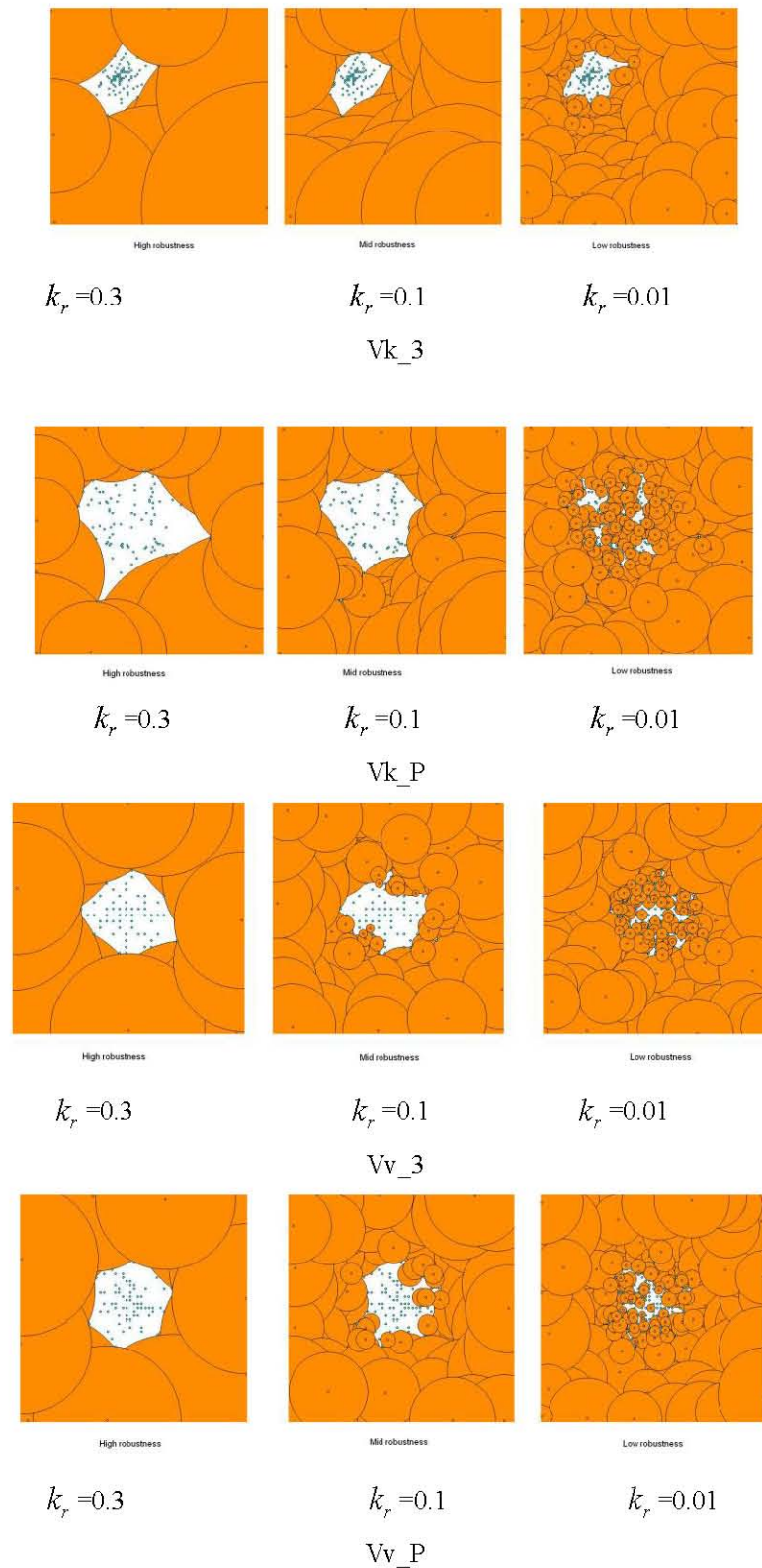

Fig. 10. The graphs of time series, representing the
vibration

The data contain 216 values of each signal sampled with 5 *ms*. The engine functioning ended with surging. By means of the algorithm developed it is necessary to define an anomaly present in data that could be a surging indicator. For training the algorithm the interval from 124 to 179 points has been chosen. The training was performed with various values of sensitivity of the algorithm (k_r). The structure of the trained immune network for various values of sensitivity is presented in Fig. 11.

High robustness   Mid robustness   Low robustness

$k_r = 0.3$ $k_r = 0.1$ $k_r = 0.01$

Vk_3

High robustness   Mid robustness   Low robustness

$k_r = 0.3$ $k_r = 0.1$ $k_r = 0.01$

Vk_P

High robustness   Mid robustness   Low robustness

$k_r = 0.3$ $k_r = 0.1$ $k_r = 0.01$

Vv_3

High robustness   Mid robustness   Low robustness

$k_r = 0.3$ $k_r = 0.1$ $k_r = 0.01$

Vv_P

Fig. 11. The structure of trained immune network for
various values of k_r

Histograms of detectors activation, averaged on several experiments (Fig. 12).
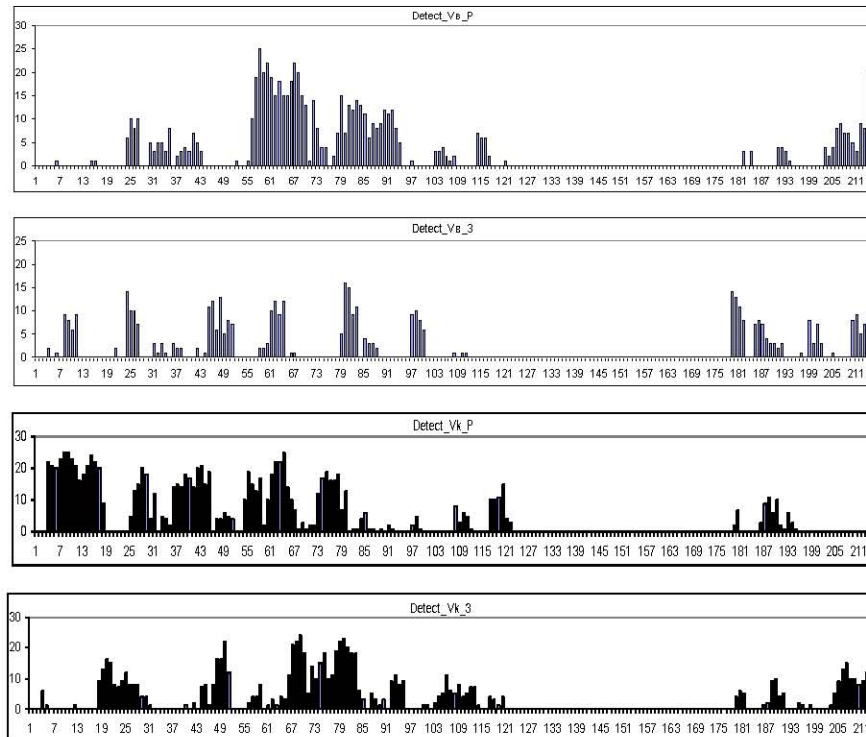
Fig. 12. The histograms of detectors activation

In real world conditions it is difficult enough to select acceptable sensitivity of algorithm (k_r). Therefore the results were averaged for several various values k_r. On the histograms it is visible the approach of the surging moment (points 208–216). An essential anomaly of engine functioning is visible in the interval 55–90, that most likely became the reason of the engine shutdown.

4 Conclusion

The modified method and algorithm of negative selection has been developed to solve the problem of anomalies detection in functioning of complex engineering systems. This method and algorithm for training and anomalies identification uses the mechanisms of artificial immune networks. The distinctive feature of the algorithm is in updating of training process thanks to which the possibility of adaptive selection of options is implemented as well as the quantities and location of detectors is determined. The experimental study has shown a high efficiency of the offered algorithm which is explained by its computing stability thanks to adaptive selection of the cross-reactive threshold. Also optimality is achieved owing to adaptive adjustment of a size of the immune network, i.e. quantity of necessary detectors. A high accuracy of detecting is shown, owing to reduction of quantity and the sizes of "cavities" created. To compare the results of application of the algorithm an exact benchmark diagnostics was used supported by experts. Results of diagnostics testify the affinity of experts estimates and the estimates generated by means of the method and algorithm developed.

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Bidyuk P.I., Litvinenko V.I., Gasanov A.S. Immune network based method for identification of turbine engine surging // A modified method and algorithm of negative selection has been developed to solve the problem of anomalies detection in functioning of complex engineering systems. The method and algorithm for anomalies identification uses the mechanisms of artificial immune networks. The distinctive feature of the algorithm is in updating of training process thanks to which the possibility of adaptive selection is implemented. The experimental study has shown high efficiency of the offered algorithm.

Бидюк П.И., Литвиненко В.И., Гасанов А.С. Метод идентификации помпажа турбинного двигателя с помощью иммунной сети // Для решения задачи обнаружения аномалий функционирования сложной технической системы предлагается модифицированный метод и алгоритм отрицательного отбора. Принцип обнаружения основывается на механизме функционирования искусственной иммунной сети. Отличительным свойством предложенного алгоритма есть возможность обновления процесса обучения, благодаря чему реализуется возможность адаптивной селекции. Эффективность применения алгоритма подтверждена экспериментальными исследованиями.