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Computer Synthesis of Neurotransmitter Images

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Abstract: *He semantic sign system is considered, represented by two different sets of elements, through which creative objects are created, correlated with the natural activity of man and Nature, reproducing numerous species of living organisms. Using the concepts and definitions of work processes in neural networks, the principles of creating neural transmitter images are considered. Formalizing the processes of creation of creative objects, a topological computational model of computer synthesis of neurotransmitter images with a variety of forms is presented.*

Keywords: *neural network, computer model, computational topology of neurotransmitter image*

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Компьютерный синтез нейротрансмиттерных образов

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Аннотация: *Рассматривается семантическая знаковая система, представленная двумя различными наборами элементов, посредством которых создаются объекты творчества, соотносимые с естественной деятельностью человека и Природы, воспроизводящей многочисленные виды живых организмов. Используя понятия и определения рабочих процессов в нейронных сетях, рассматриваются принципы создания нейронных трансмиттерных образов. Формализуя процессы создания объектов творчества, представлена топологическая вычислительная модель компьютерного синтеза нейротрансмиттерных образов, обладающих подобием форм.*

Ключевые слова: *нейронная сеть, компьютерная модель, вычислительная топология нейротрансмиттерного образа*

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Neural networks are among the most amazing Natural formations. A high concentration of neural networks is represented by complex mammalian brain structures (BSs). The human brain has well-defined abilities: thinking, logical choice of objects, and preservation of acquired knowledge. Studying the work processes of the neural network of the brain by means of computational topology contributes to the development of technical systems with artificial intelligence. Traditionally, when the thought processes in BSs are compared with Natural phenomena carried out according to a certain program, a high similarity index is noted. This allows declaring the presence of isomorphism properties. Typical examples of two isomorphism processes are literary works and the variety of Natural species of living organisms. In both cases, the results of creativity, in the broad sense of this concept, are created based on a set of symbolic programs. For literary creativity, this is a set of letters. For the creativity of Nature, this is a set of nucleotides.

The introduced concepts declare the presence of a neurotransmitter image as a mathematical object reproduced by means of computational topology and associatively perceived as a result of human or Natural creativity. Computer modeling of neural processes of living organisms that create complex images operates with the concepts of additive tracks of events in BSs. Similar models of the processes of generating event tracks, based on genetic material, are implemented in Nature when creating different types of living organisms.

Indeed, the presence of BSs in humans generates creativity, for example, writing various literary works based on an established sign set (alphabet). In Nature, similar processes implemented on the basis of a typical sign set (nucleotides) give rise to different types of organisms. This fact allows stating the presence of two processes in Nature that are different in etymology but have the same general property of generating the synthesis of associative images. The concept of such an understanding of the laws of Nature, in terms of the physiology of neural activity of BSs, was formed at the beginning of the twentieth century.

General ideas about the work of human BSs were introduced by Sechenov in 1891 [1]. The scientific content of the work on the mechanisms of memory formation in BSs highlights the presence of nerve centers. The modern anatomical paradigm identifies this natural phenomenon with the presence of brain regions responsible for the physiology of neural processes of perception of many factors. In his scientific work, Sechenov highlighted the general concept of the reflex reaction of the body and paid attention to the processes of excitation and inhibition. At the current stage of the development of BS research technologies, the connection between these processes has been established, which contributes to the development of ideas about the formation of associative memory, long-term and short-term memory. The actual ability of BSs to operate with a variety of concepts is formed naturally in the process of the evolutionary development of the organism. The neural network of the brain is considered a physical basis for the implementation of memory procedures.

The theoretical foundations of cerebral physiology were developed by Pavlov, who in 1904 presented a scientific work on the congenital nervous system activity of the organism [1]. This scientific potential was highly appreciated by the world community, and the author received the Nobel Prize. A series of scientific papers studying nervous processes demonstrated a method of sequential approximation to solving a large list of questions about the formation of human memory. In the first stages of studying BSs, researchers considered the theoretical issues of organizing an experiment for the selection of disturbing factors that to a certain extent create agreed images. Taking into account the presence of natural reactions available in the body, obtained on the basis of the long-term development of the species, the digestive system – the autonomic nervous system – was considered. This nervous system has a connection with BSs. In order to form numerous reliable descriptions of the experiment, a mammalian species was considered as a research object – an ordinary dog. In this kind of living organism, a memory apparatus has been formed in the process of evolutionary development. These are separate fragments of BSs, which recorded conditioned reflexes correlated with motivation. Such an arrangement of arguments in favor of choosing the type of living organism and organizing experiments for the physiological control of the motivational factor demonstrated the presence of a new technology in the study of BSs.

Having established a stimulating factor in the form of a light signal, the request of the autonomic nervous system for food intake was synchronously satisfied. The combination of these factors triggered a complex mechanism for the formation of an associated image identifying the event – the act of eating. In the theory of physiology, such an act corresponded to satisfying the need for nutrition. From the physiological point of view, the associated image was created subject to the presence of a light signal. Manifold repetition of the feeding scheme with a light stimulus created a stable response effect of the autonomic nervous system. The associative image has become a stimulus to trigger the autonomic nervous system, waiting for the act of nutrition.

During the experiment, it was noted that the absence of food in the presence of a light signal initialized the start of the working process of the autonomic nervous system. In fact, this meant that a living mammalian organism was able to learn and independently form important associated images in BSs.

The associated image, created on the basis of a network of neurons naturally connected to BSs, allowed the formation of long-term memory.

A logically sound judgment about this fact has been repeatedly tested experimentally. In the modern interpretation of this judgment, the presence of a statistical and systematic approach to the collection and analysis of experimental results is clearly visible. This fact is used in many modern methods of teaching different types of organisms. A single neural network mechanism associated with BSs makes it possible to create long-term images of signals.

Neural network workflows are created on the basis of special chemicals – neurotransmitters. Neurotransmitters are transmitters that implement the key functions of switching electrochemical flows. Electrochemical impulses from a nerve cell, through a network of synapses, propagate between neurons. Transmitters have the property of selecting specific areas of the cell membrane surface, initializing the creation of a unique electrochemical flow.

This effect creates a specific set of action potentials (APs) arising on the surface of several cells. By selecting APs on a group of cells, a track of events is created, the image of which is stored in BSs. Such an image as a mathematical object is isomorphic to a model of track events on a neural network. This phenomenon, established by Sechenov and Pavlov, launches the processes of searching for associative images that perform the functions of constructing a response – the reaction of a neural system to a similar group of APs.

Tracks of propagation of APs on a network of neurons create a transmitter image. According to the theory of neurophysiology, there are images created at the birth of an organism, as well as images formed in the process of vital activity. It is natural to believe that the images created by Nature are specific to each organism type. This concept is constantly supplemented by new results of numerous studies in the field of genetics. The constant renewal of the cellular populations of the body results in a modification of the neural network that generates neurotransmitter images. This is how the body adapts to the environment, and at the same time, the learning process is carried out, in the broad sense of understanding this term.

Developing these ideas, the scientific community has formed a thesis about the complex structural organization of many physiological processes in living organisms. These ideas are generalized in the concept of a dissipative system that is able to maintain a set of stable states. A low level of variability of functional states in living organisms is supported by a set of control signals – neurotransmitter images.

In terms of biophysics, the state of a living organism is characterized by a set of physiological processes. The mathematical model of any physiological process is compared to the image. Each organism type has a unique set of physiological processes. Taking this into account, it becomes clear that there is a need for a variety of Natural images for different physiological processes. It is due to the presence of a set of reference images that a series of reactions of the body to activating and inhibitory factors that contribute to the formation of a stable state, known as the law of homeostasis, is created. At the same time, the presence of Natural regulators of the functional state of the organism is explained by the long evolutionary development of each species with a unique genetic code.

The genetic code is a format for recording unique processes in the body, some of which act constantly, and the other part works in strictly defined periods of life. As an illustration, examples can be given: the age period of growth of BSs, skeletal limbs, teeth, or temperature regulation of the body surface in humans. These are regulatory program modules of the organism, which are activated in the presence of genetic associative patterns. The group of associative images of the regulation of the body's functional state is variable when the environmental conditions change. This thesis can be considered in the field of concepts of modern computer technology and intelligent systems. Note the presence of software products in the computer that have different functional descriptions of the action. For practical tasks solved using a computer, it is important to have memory blocks: long-term and random access memory (RAM). Long-term memory is characterized by random access, in which the act of requesting requires specifying the address of a memory cell. Associated computer memory (ACP) is created subject to the presence of a rule of reference, which is often specified in the format of a word or image. In this case, a successful search query in ACP implements a selection of several word forms or images that have common indicators. In the absence of an associated request image in the ACP structure, the "refusal" procedure is implemented.

It should be noted that the organization of storing and searching associated images on a computer is difficult to implement and requires special high-cost hardware modules. For each field of concepts and definitions of a process or phenomenon, it is required to create a specific image of requests implemented on a unique electronic block.

The execution of the procedure for searching for an associative image from an available set requires a formalized rule. The presence of such an algorithm makes it possible to create a group of objects with a unique signal image. In such a generalized image of a group, the order of enumeration of objects is not important. This concept corresponds to a strict definition of associativity in terms of mathematics.

As an illustration, consider an identity in which there is no indication of the order of enumeration of objects:

$$(a + b) + c = a + (b + c) = a + b + c.$$

Let us supplement this concept with examples of texts. Assume the existence of a rule for creating an image of a literary work executed in terms and definitions of computational topology. Also, assume that the numerical values of individual signs, which naturally form a set of word forms according to the author's plan, are considered as parameters of the associative image model.

A set of word forms is created in the basis of the selected alphabet. The creative process of creating a set of word forms is carried out by a reasonable object created by Nature. A human as a creative synthesizer of scientific and literary sets of word forms creates an iconic array of data. A similar process is observed when Nature creates living organisms, but from a set of nucleotides. Such a process is unique – it has a genetic code of the organism type. The genetic code of the organism is represented by a symbolic array and is installed by Nature.

The distinct closeness of the introduced concepts can be demonstrated by the example of literary creativity. It is obvious that literary works similar in format are associatively perceived as elements of the same group. Associative perception is created by BSs. Indeed, it can be assumed that the neurotransmitter model forms an idea of the kinship of the presentation forms of some of the author's ideas. In the mathematical model of the pragmatic process of recognizing the presence of associativity principles in a group of objects or elements, one can highlight the concept of a basic structure. This is important because to consider the issues of creating a group of associated objects, it is required to identify significant features that demonstrate a difference from the basic image.

The basic mathematical model of the associative image is represented in the form of the trochoid equation, as a special case of a cycloid. It will be assumed that R and d characterize the number of characters (n) of the created image:

$$x(t) = R - d\mathrm{Sin}(t);\ y(t) = R - d\mathrm{Cos}(t), \qquad (1)$$

where R is the power of a set of elements; d is the power of a subset of elements ($d \in R$); t is the event sweep parameter in the interval 2π.

Highlighting the concept of a subset in the model declares the possibility of creating related associative images. In this context of defining associativity, consider the ratio of the parameters R and d at which all available images are equivalent.

Let us create a basic image (Figure 1). For certainty, let us put $R = d = 50$. This condition, in terms of the trochoid model, declares the presence of a field of the same type of elements, which has a high entropy index. A trochoid as a cyclic image is created on the basis of a circle. The basic image created on the same type of elements according to expression (1) is represented as a half-circle [2]. The perimeter of the L_p image is determined by the ratio $L_p = 8R$, and the radius r of the circle by the expression:

$$r = \frac{\left(\frac{L}{2}\right)^2 + H^2}{2H}, \qquad (2)$$

where L is the size of the image base on the X coordinate; H is the maximum size of the image on the Y coordinate.

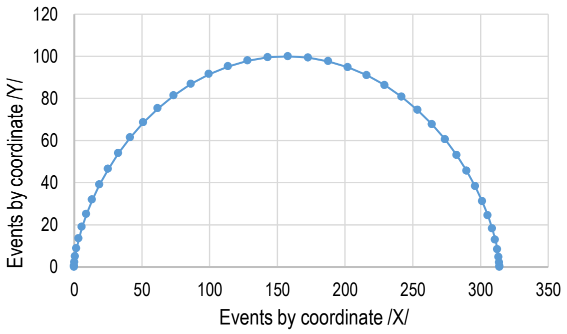


Fig. 1. Basic Image of a set of Equivalent Elements

Naturally, the image can be scaled taking into account the real indicators of R and r. So, for example, under the condition $P = d = 50$; $t = (0 \div 2\pi)$, we have: $L = 314.16$; $H = 100$; $r = 173.37$. The calculated numerical indicators $x_i(t)$ in $y_i(t)$ can be saved in the form of arrays $X(t_i)$ and $Y(t_i)$. Assume that ($x_i(t) \in X(t_i)$; $y_i(t) \in Y(t_i)$).

Obviously, under the condition $d < R$, the subset is positioned selectively. Keeping R = const, and setting an individual numerical indicator d_i for the indicator d, the track of events is reproduced in the model at an interval of 2π. By establishing a rule for the allocation of individual numerical indicators d_i, a partial or complete image is created on a subset d, for example, of a literary work arbitrarily selected from an information resource [3].

This principle of image synthesis can be reproduced on a set of nucleotides characterizing the genome of the selected organism. The NCBI information resource [4] contains a large number of sets of genomes of various organisms, including viruses.

The concepts introduced make it possible to implement computational procedures for creating neurotransmitter images using the trochoid equation. Let us consider the process of creating a neurotransmitter image by the example of poetry – Alexander Blok's "Aviator" [3]. Let us highlight the initial lines of the poem.

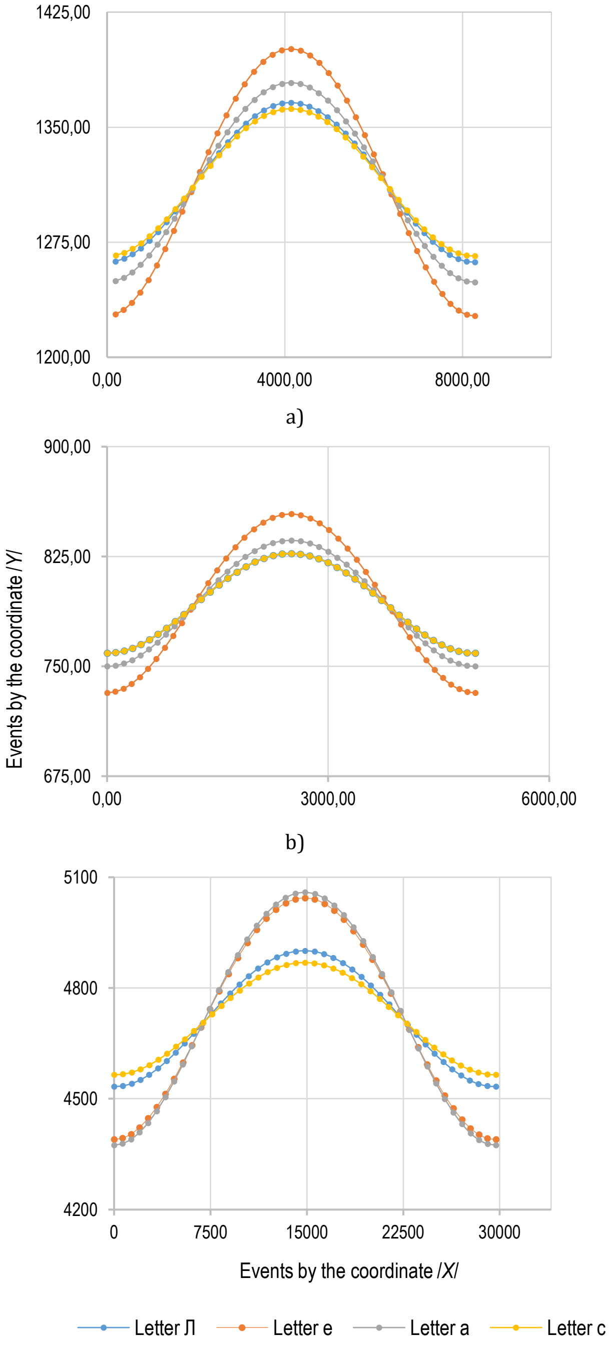
Летун отпущен на свободу.
Качнув две лопасти свои,
Как чудище морское в воду,
Скользнул в воздушные струи.

Его винты поют, как струны...
Смотри: недрогнувший пилот
К слепому солнцу над трибуной
Стремит свой винтовой полет...

Let us arbitrarily choose a sign set: "л", "е", "а", "с". and determine the numerical indicators of the sign set for a complete literary work in Russian (Table 1). Let us create an image of a literary work (Figure 2a) using the expression (1), R = const, $d = (d_1 = l, d_2 = e, d_3 = a, d_4 = c)$. The number of characters is determined by the text in Russian.

TABLE 1. Numerical Indicators of the Text

Parameters	A. Block "Aviator"	V. Bryusov "In the Spring"	A. Chekhov "Living Chronology"
Full number of characters, R	1314	793	4717
Number of characters:			
"л", d_1	52	34	184
"е", d_2	87	61	327
"а", d_3	65	43	342
"с", d_4	48	34	152



a)

b)

c)

Fig. 2. The Image of the Literary Work: a) "Aviator" by A. Blok; b) "In Spring" by V. Bryusov; c) "Living Chronology" by A. Chekchov

Let us consider another text – a poetic work by Valery Bryusov "In the Spring" [3]. Let us reproduce the initial fragment of the work and determine the numerical indicators of the sign set for a complete literary work and present it in Table 1 and Figure 2b.

Не в первый раз твои поля
Обозреваю я, Россия;
Чернеет взрытая земля,
Дрожат, клонясь, овсы тугие
И, тихо листья шевеля,
Берез извилины родные.

Вот косогор, а вот река,
За лесом – вышка колокольни;
Даль беспредельно широка,
Простор лугов, что шаг, раздольней;
Плывут неспешно облака
Так высоко над жизнью дольней.

Let us create a simple literary text. Let us create an image of a literary work in which there is no poetic rhyme. Consider the prose: Anton Chekhov's short story "Living Chronology" [3]. Let us highlight the initial lines of the literary work. Let us determine the numerical indicators of the sign set for a complete literary work and present it in Table 1 and Figure 2c. Let us create an image of a literary work () using the expression (1), R = const, $d = (d_1 = l, d_2 = e, d_3 = a, d_4 = c)$. The number of characters is determined by the text in Russian.

Let us consider two theses. First, the collection of created images of literary works demonstrates the presence of the author's style of using word forms created on the basis of four letters. It can be confidently assumed that with an increase in the number of signs used in the construction of the image of a literary work, the author's style of creativity will clearly manifest itself. This remark correlates well with the postulate about increasing the size of the information description of a process or object: the more indicators of an object are allocated, the higher the level of identification.

Second, the analysis of literary works having different presentation forms, using the same model, reproduces typical topological tracks of events with different metric indicators on the plane.

The considered judgments about the analysis of literary works should be correlated with the process of human creativity, which is naturally identified with the object of Nature. Such an object demonstrating the ability to carry out independent creative processes is certainly unique.

At the same time, it should be recognized that Nature itself reproduces the processes of creativity by creating and supporting the evolution of living forms of matter. The basis in such processes is the genome of a living organism, recorded in every living cell. Two structures are distinguished here as basic forms: deoxyribonucleic acid (DNA) and ribonucleic acid (RNA), which are contained in the cells of all living organisms. Each DNA or RNA molecule is assembled from smaller simple compounds – nucleotides: adenine (*A*), guanine (*G*), cytosine (*C*), and thymine (*T*).

The simplest form of life is represented by viruses. A virus is a small particle of matter. The virus, as a molecular formation based on DNA or RNA, is located in a protein envelope (capsid). Viral particles are capable of infecting living organisms, which generates the problem of recognizing individual strains and creating disinfection procedures. The pragmatics of solving this problem is created in the field of concepts of computer data analysis.

The hereditary material of the virus is presented in a set of nucleotides. A large amount of genetic material of different viruses is posted on the NCBI information resource [4]. One can say that the material of Nature's creativity created on a set of nucleotides is instrumentally read and placed in a special text format. It is obvious that the comparison of the creative process of man and Nature can be carried out by means of modeling. A natural and essential requirement in this process of model matching is isomorphism, which manifests itself in the unity of metrological procedures for registering initial data and constructing an image.

In Nature, there are viruses with the RNA and DNA genomes. Consider coronavirus 2 Cov-19/Japan/SZ-NIG-4-C818/2022 RNA, complete genome.

LOCUS BS002432 29805 bp linear RNA [5]. Let us look at the fragment represented by a set of signs – nucleotides: adenine "*a*", guanine "*g*", cytosine "*c*", thymine "*t*".

1 *ggtttatacc ttcccggta acaaaccaac caacttttcga tctcttgtag atctgttctc*
61 *taaacgaact ttaaatctg tgtggctgtc actcggctgc atgcttagtg cactcacgca*
121 *gtataattaa taacaatta ctgtcgttga caggacacga gtaactcgtc tatcttctgc*
181 *aggctgctta cggttcgtc cgtgttgcag ccgatcatca gcacatctag gttttgtccg*
241 *ggtgtgaccg aaagtaaga tggagagcct tgtccctggt ttcaacgaga aaacacacgt*
301 *ccaactcagt ttgctgttt tacaggttcg cgacgtgctc gtacgtggct ttggagactc*
361 *cgtggaggag gtctatcag aggcacgtca acatcttaa gatggcactt gtggcttagt*

Let us determine the numerical indicators on the entire genome array for each sign. The results are presented in Table 2. Let us create an image of the virus (Figure 3a) using the expression (1), R = const, $d = (d_1 = G, d_2 = T, d_3 = C, d_4 = A)$.

Consider a fragment of another virus strain [6]: coronavirus 2 HCoV-19/Japan/SZ-N-4-C940/2022 RNA, complete genome

LOCUS BS002446 29809 bp linear RNA. The fragment is represented by the same set.

1 *gattaagtg aatagcttgg ctatctcact tcccccgtt ctctgcaga actttgattt*
61 *taacgaactt aaataaaagc cctgttgttt agcgtattgt tgccttgtc tggtgggatt*
121 *gtggcattaa tttgcctgct catctaggca gtggacatat gctaacact gggtataatt*
181 *ctaattgaat actatttttc agttagagcg tcgtgtctct tgtcgtctc ggtcacaata*
241 *cacggtttcg tccggtgcgt ggcaattcgg ggcacatcat gtcttcgtg gctggtgtga*
301 *ccgcgcaagg tgcgcgggt acgtatcgag cagcgctcaa cttgaaaa catcaagacc*
361 *atgtgtctct aactgtgcca ctctgtggtt caggaaacct ggtgaaaa ctttcaccat*

Let us determine the numerical indicators on the entire genome array for each sign. The results are presented in Table 2 and Figure 3b.

Taking into account that the presented images were created on etiologically similar material and almost simultaneously, one can note a slight discrepancy in the tracks of the image (Figures 3a and 3b). Let us complete these representations. From an evolutionary point of view, it is of interest to consider the coronavirus of the past years. For example, coronavirus 2c England-Qatar/2012, complete genome [7].

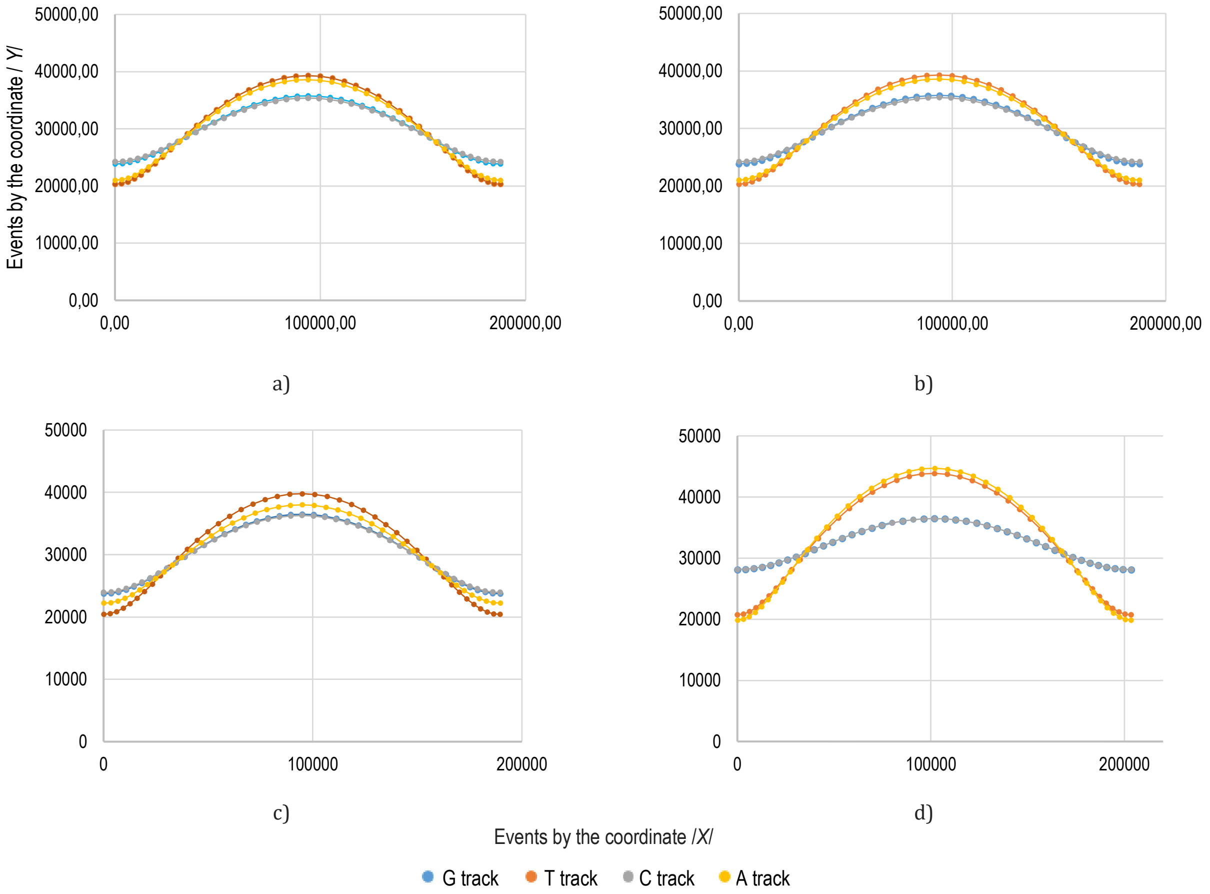
LOCUS KC667074 30112 bp linear RNA. Consider the fragment.

1 *gattaagtg aatagcttgg ctatctcact tcccccgtt ctctgcaga actttgattt*
61 *taacgaactt aaataaaagc cctgttgttt agcgtattgt tgccttgtc tggtgggatt*
121 *gtggcattaa tttgcctgct catctaggca gtggacatat gctaacact gggtataatt*
181 *ctaattgaat actatttttc agttagagcg tcgtgtctct tgtcgtctc ggtcacaata*
241 *cacggtttcg tccggtgcgt ggcaattcgg ggcacatcat gtcttcgtg gctggtgtga*
301 *ccgcgcaagg tgcgcgggt acgtatcgag cagcgctcaa cttgaaaa catcaagacc*
361 *atgtgtctct aactgtgcca ctctgtggtt caggaaacct ggtgaaaa ctttcaccat*

Let us determine the numerical indicators on the entire genome array for each sign. The results are presented in Table 2 and Figure 3c. The image of the KC 667074 virus strain, sample 2012, has differences from previous versions of the strains. However, in general, the image of the virus strain has not changed. This is a good sign of the adequacy of the model.

TABLE 2. Numerical Indicators of the Genome

Parameters	Coronavirus 2 Cov-19/Japan/ SZ-NIG-4-C818/2022 RNA		Coronavirus 2c England-Qatar/2012	Virus Sulfolobus islandicus 1, 2021
	LOCUS BS002432	LOCUS BS002446	LOCUS KC667074	LOCUS NC004087
Full number of characters, R	29805	29809	30,112	32308
Number of characters:				
"*g*", d_1	5955	5883	6380	4179
"*t*", d_2	9490	9553	9675	11563
"*c*", d_3	5571	5590	6166	4158
"*a*", d_4	8789	8783	7891	12408



a) b) c) d)

Fig. 3. Image of the BS002432 Virus (a), BS002446 Virus (b), KC667074 Virus (c), NC004087 Virus (d)

Now let us turn to the consideration of DNA-based viruses [8]. Consider the rod-shaped *virus Sulfolobus islandicus 1, 2021*, the complete genome. The virus belongs to the Rudiviridae family and is distributed in hydrothermal environments.

1 *ttgtagagca gtaagaaggt attgggagtt tttttcattt ttgcgtaaa tttcgcaact*
61 *aatgagataa attggaaatt ccaatttttt tcgttttttt cgtttttc gcaccaaagt*
121 *taataaattg aaaattccta aattcctaaa ttccaattat tcttcattt tgcgtaattt*
181 *tcgaaataaa gttaataaat tggaagttcc taaattccaa ttattctac accttgtaaa*
241 *attattccaa caaattaata aaattggaaa ttcctaagtt cctaattcc aataaattct*
301 *acatcttgga aatttattac aaaaagttaa taaaattgta aatccaaaa ttccaattaa*
361 *ttgtacatct tggaaaatta ttccaattag ttatgtaaat tggaattac aaaattccaa*

LOCUS NC004087 32308 bp linear DNA. Consider the fragment. Let us determine the numerical indicators on the entire genome array for each sign. The results are presented in Table 2 and Figure 3d. There is also a general pattern of creating tracks, but at the same time, there are differences. The differences are manifested in the clarity of the allocation of two tracks for two groups of *T–A* and *C–G* nucleotides. The pattern of detecting two groups of nucleotides isolated by means of the model corresponds to the Chargaff's rule (1951) [9]. It has been established that four types of nitrogenous bases are found in DNA: adenine, guanine, thymine, and cytosine [10]. The nitrogenous bases of one of the chains are connected to the nitrogenous bases of the other chain by hydrogen bonds according to the principle of complementarity: adenine connects only with thymine (*A–T*), guanine – only with cytosine (*G–C*). It is these pairs that make up the "rungs" of the spiral "ladder" of DNA. It should be noted that this property of the nucleotide DNA chain, in terms of modern research, is found only in a series of numerous statistical analysis procedures.

The presence in the mathematical model represented by the expression (1) of two parameters: *R* and *d*, declaring the presence of the conjugacy property of sets, is adequate to the concept of complementarity in genetics. An illustration of this concept is presented in Figure 4, where the paired combination of nucleotides on two event lines is a natural process in the synthesis of cell populations.

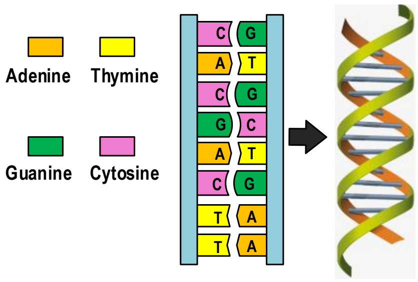


Fig. 4. Scheme of Nucleotide Combination According to Chargaff

The long-discovered effect of paired conjugation of nucleotides in modern research is considered an illustration of a little-studied natural scenario for creating a living organism. Naturally, the use of a mathematical model with two conjugate parameters correlated in biosynthesis with the tracks *T-A* and *C-G* declares the possibility of a formal study of DNA structures in different types of organisms. Taking this into account, let us create a formal procedure for evaluating the conjugacy of the coordinates of the event sweep track.

The expression is represented as:

$$Q = \frac{\sqrt{(x_i - y_i)^2}}{\rho}, \qquad (3)$$

where ρ = 10,000 is the scale factor; $Q = (0 \div \infty)$ is the conjugation index.

Let us clarify the concept of conjugation in the nucleotide chain of events. Let us keep the initial conditions $R = 50 = d$ and the numerical indices of the arrays $X(t_i)$ and $Y(t_i)$ obtained during the construction of the base image (Figure 1). It is obvious that for $|(X(t_i) - Y(t_j))| \approx 0$, the exponent $Q \to \infty$ is the dimension of the exponent Q (radians). By expression (3), one can calculate the conjugation index Q and create an image of the scan of the events for the base image at an interval of 2π, equal to approximately 43 iterations (Figure 5). Obviously, for p = const and any values of $R = d$, a tautochrone curve is obtained, which has a "short descent" profile.

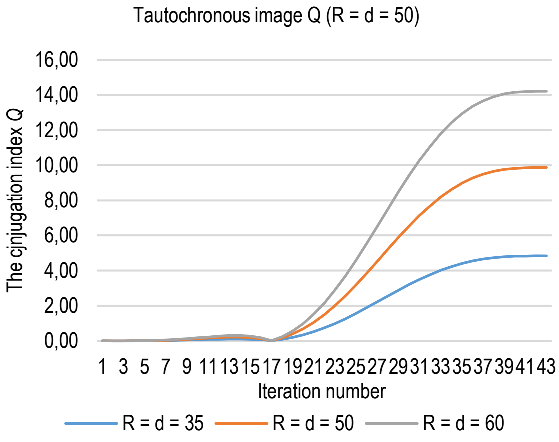


Fig. 5. The Basic Image of the Indicator *Q*

Indeed, this judgment is fair and has the logical meaning of an information package. For biosynthesis problems, it is difficult to maintain mathematical equality of the number of nucleotides over a very long-time interval. That is why complex, but compact in length sets (nucleotides) of events are found in Nature. On average, a typical set of genes is about 30–35 thousand elements. At the same time, chromosomes, as larger objects of synthesis, can contain tens of millions of elements.

This thesis can also be applied to literary works. Having a certain quantitative indicator of signs in the text, a literary work is characterized by an indicator of conjugation. It can be said that a very large number of signs – word forms reduces the value of the indicator of the combination of chapters, paragraphs, and subsections of a literary work. It makes it difficult to form a logically connected chain of events described in a literary work.

In other words, it is possible to allow redundancy of the text, but this will reduce the semantic significance of individual fragments of the information array of signs (text). In order to maintain a significant level of conjugation in literature, the rule of dividing a literary work into chapters or sections is used. In living nature, this rule is implemented in the genome of an organism, which is represented by a set of chromosomes.

Let us consider the established concepts by the example of the previously presented texts. Let us create an image of the indicator of paired conjugation of events for the literary work by Alexander Blok "Aviator". It is poetry. Let us numerical indicators of arrays $X(t_i)$ and $Y(t_i)$. Calculate the conjugation index Q by expression (3). Create a graphical image (Figure 6).

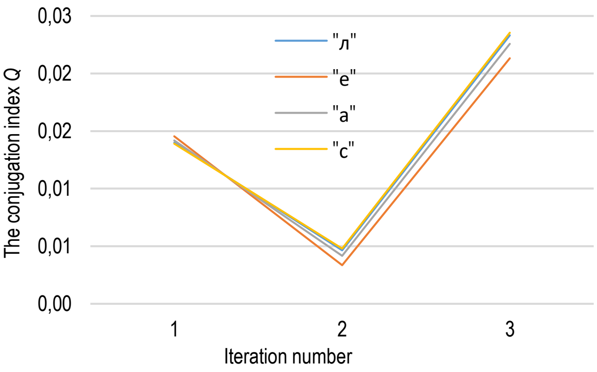


Fig. 6. The Image of the Indicator *Q* for the Poem by A. Blok "Aviator"

Let us carry out similar constructions for Anton Chekhov's literary work "Living Chronology". It is prose. Let us use numerical indicators of arrays $X(t_i)$ and $Y(t_i)$. Calculate the conjugation index Q by expression (3). Create a graphical image (Figure 7).

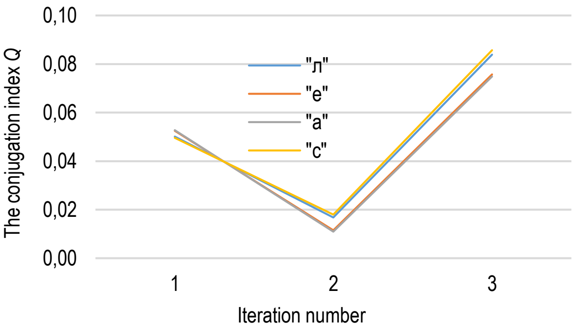


Fig. 7. The Image of the Indicator *Q* for the Work by A. Chekhov "Living Chronology"

The visual comparison of the images in Figures 6 and 7 demonstrates the difference: the Q index is higher in the first case. At the same time, there is a similarity: the minimum point is at the 7th iteration. Let us create a general judgment in which it is stated that relatively simple comparisons of images of conjugation indicators make it possible to detect differences in literary works. At the same time, it should be noted that the general appearance of images of different literary works remains the same.

Formally, the result obtained allows declaring the presence of a general form of the image of the indicator of the conjugation of literary works, but with an individually expressed set of tracks. It can be said that regardless of the genre of a literary work, a typical image is created in which the ranking of signs (letters) is observed. Let us write this judgment as an axiom.

Let us build an image of the conjugation index for genomes, using previously obtained data for a couple of viruses:

1) Coronavirus 2 HCoV-19/Japan/SZ-NIG-4-C818/2022 full genome LOCUS BS002432 29805 bp linear RNA;

2) Rod-shaped virus Sulfolobus islandicus 1, 2021, full genome LOCUS NC004087 32308 bp linear DNA.

In the calculations, numerical indicators of arrays $X(t_i)$ and $Y(t_i)$ will be used. Let us calculate the paired exponent Q of the conjugation by expression (3). Let us create a graphical image (Figure 8).

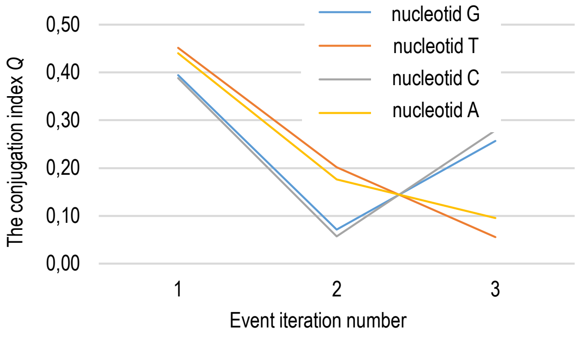


Fig. 8. Image of the *Q* Indicator for LOCUS BS002432/2022

By analogy, let us use numerical indicators of arrays $X(t_i)$ and $Y(t_i)$ for the rod-shaped virus. Let us calculate the paired conjugation index by expression (3). An illustration of the performed procedures is shown in Figure 9. A comparative visual analysis of the images presented in Figures 8 and 9 indicates a mismatch of the nucleotide tracks. There is also an intersection point, which indicates a "plexus" of nucleotide tracks. The presence of these features makes it possible to identify the genomes of organisms. Using thematic methods for analyzing images of various representatives of the living world, it is possible to establish evolutionary similarities.

The systematization of scientific knowledge presented by different sections of modern science about Natural processes creates the basis for establishing phenological patterns. Computer modeling makes it possible to determine the similarity of processes, objects, and events with different etymological characteristics. This is clearly seen when comparing different images as objects of creativity. The basis for computer modeling is information resources that allow creating unique rules for analyzing different processes.

Postulating the existence of various creative processes in society, it is possible to distinguish a literary genre. The process of creating a literary work performed by a human is based on the possibility of using a set of symbols that generate word forms. In practice, using many different word forms, a unique text field of a literary work is created. Despite the possibility of repeating signs and word forms on the text field, each individual literary work is unique. The concept of uniqueness is established using a topological model that initializes the creation of a computer neurotransmitter image.

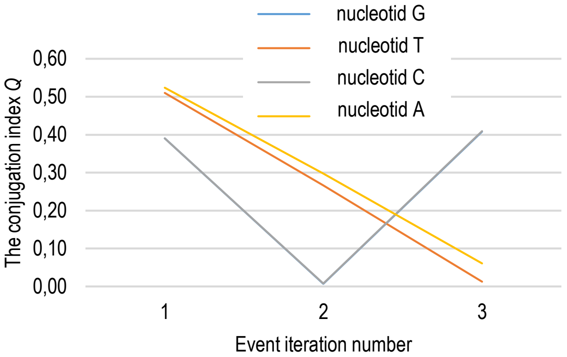


Fig. 9. Image of the *Q* Indicator for LOCUS NC004087/ 2021

The image structure reproduces a set of tracks that characterize the dynamics of changing elements of the text in question. It is noted that the manifestation of the compactness of the neurotransmitter image is characteristic of literary works. All the elements of the text array accepted for consideration form dense trochoid constructions. Similar constructions are observed in the creations of Nature – in the genome of living organisms. This allows declaring the existence of general principles of creativity.

The declaration of this judgment is based on the results of comparing transmitter images of different literary works and some genomes. This judgment is plausible because the additive composition of signs is considered both in the text field and in the field of genes of living organisms. The sequential allocation of individual signs, both for literature and for genetics, creates the concept of the unfolding of events. The compactness of the process of turning events in literary creativity is supported by the presence of a large number of signs and their numerous combinations. To organize a similar process in Nature, four nucleotides are used, which create less compact forms. This property of natural synthesis of living organisms is extremely important in evolutionary development. A smaller manifestation of compactness in the image of the conjugation index for living organisms makes it possible to adapt to different habitats.

This intuitive and well-explained judgment has strict rules for the formation of a mathematical concept. In terms of the general theory of topology, the com-pastness of an arbitrary data set is considered in terms of a closed and bounded space. Formally, this means that the selected data set is represented by a continuous series of values without missing any elements. An additional condition is the presence of a starting and finishing element or a group of elements in the data set.

These conditions, declaring the presence of compactness of both the literary work and the genome of a living organism, are clearly manifested in the analysis of a set of word forms and the genome.

Indeed, there are three parts in a literary work: the prologue (the beginning), the climax and the epilogue (the final part). Similarly, for the genome of a living organism, it is allocated. The first stage is the beginning, when DNA syn-thesis is initiated, which requires short (10-200 nucleotides) RNA sequences that perform the functions of primers (primers). Next, a series of procedures for the synthesis of the complete genome of the organism is carried out, which ends with the creation of the "finishing block" - the telomere.

The compactness of the data set is reproduced on a large theoretically developed material of mathematical theorems, computational topology. It is the mathematical definition of compactness that reproduces the exact and complete concept of compactness, created on the condition of "closure" and "limitation". In this sense, almost any literary production is unique, if only because it does not have an infinite number of elements (word forms) and has a "finishing block" of the narrative. In addition, in a literary work, individual parts are additions to the main set of word forms.

In this understanding, the genotype of a living organism is characterized by compactness, in which separate "information blocks" - chromosomes are clearly distinguished. The chromosome set for different living organisms has variability, which naturally contributes to the long-term preservation of the species in evolutionary development.

The use of computer technologies for modeling graphic images, in the field of concepts of mathematics and genetics, allows discovering the systemic principles of creativity, the foundations of which are always correlated with living objects of Nature.

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