

DOI: 10.26117/2079-6641-2019-26-1-78-93

MSC 76W05, 86A25

CHOOSING THE MODEL OF BIOLOGICAL NEURAL NETWORK FOR IMAGE SEGMENTATION OF A BIO-LIQUID FACIE *

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In the paper, the biological neural network models are analyzed with a purpose to solve the problems of segmentation and pattern recognition when applied to the bio-liquid facies obtained by the cuneiform dehydration method. The peculiarities of the facies' patterns and the key steps of their digital processing are specified in the frame of the pattern recognition. Feasibility of neural network techniques for the different image data level digital processing is reviewed as well as for image segmentation. The real-life biological neural network architecture concept is described using the mechanisms of the electrical input-output membrane voltage and both induced and endogenic (spontaneous) activities of the neural clusters when spiking. The mechanism of spike initiation is described for metabotropic and ionotropic receptive clusters with the nature of environmental exciting impact specified. Also, the mathematical models of biological neural networks that comprise not only functional nonlinearities but the hysteretic ones are analyzed and the reasons are given for preference of the mathematical model with delay differential equations is chosen providing its applicability for modeling a single neuron and neural network as well.

Keywords: biological neural network, hysteresis, facie, texture, image recognition.

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*This work was supported by the RFBR (Grants 19-08-00158-a, 17-01-00251-a, 18-08-00053)

Introduction

The problems of an earlier diagnosis and treatment at the earliest possible stage are always urgent and highly important for medical researches. Bio-liquids participate in the full range of the processes of intra- and extracellular metabolism and, thus, they are the source of comprehensive information on the condition of the entire organism. Biochemical, physical-chemical, immunological, and other methods of bio-liquid examination are of considerable current use in clinical science and laboratory medicine. Although the sensitivity of traditional clinical techniques is usually high enough, they give fragmentary data on the health condition disregarding the structural analysis of biological liquids. The structural concept used to be considered to be inapplicable to bio-liquids because of the extremely high variability of their molecular composition and their components interaction. Along with this, the information from such another modality as bio-liquid structuring could be very useful for practical medicine considering the fact that bio-liquids possess determinate, rather stable orderliness at the molecular and permolecular levels. Therefore, the structural analysis of a bio-liquid being brought into solid phase by dehydration shows not only the concentration of its constituents but also their interrelation character [1, 2]. At present, the most promising method to obtain a biological liquid dehydrated facie is the cuneiform dehydration method [3].

Materials and methods

Studying chemical and physical processes in liquid drops in the course of their dehydration is a site of special research interest for a number of reasons. A drop of liquid while being dehydrated can be considered as a system with liquid-solid transition, where the external forces, different both by nature and binding force, reveal their cumulative energy at a three phases interface. This transitional process and its accompanying phenomena appeal for research due to miscellaneous technological problems occurring when substances with varying surfactant characteristics interact, for instant, for complex assessment of a liquid's multicomponent composition: to show the behavior dynamics of chemicals in the time domain (under various storage conditions), to estimate the pipeline hydraulic fluid with different surface-active admixtures, to diagnose bee-farming products, and so on. Also, peculiarities of the drop dehydration process are crucial when it refers to such bio-liquids as blood serum, lymph, cerebrospinal fluid, secretory products, urine, etc. The cuneiform dehydration method exposes structure-specific character of a bio-liquid that is determined by the entire set of qualitative and quantitative parameters of the substances dispersed in the liquid. During the dehydration process, molecules and permolecular complexes are distributed in strictly defined places within the drying drop so to form the specific zones all over the dehydrated surface, with the structures being ordered according to the biochemical composition of a substance [4].

The first attempts to use the results of the crystallization phenomenon for various liquid substances in their liquid-solid transition took place in pharmacology and pharmacy in early 1930s [2]. The top priority of these researches was identification of the biochemical composition of the medications studied on the assumption of the particular character their crystallization results in. A bio-liquid drop, when drying free on a solid base, undergoes a series of complex physical, chemical, and mechanical processes named dehydration self-organization. The cuneiform dehydration method visualizes self-organization

of the components of a bio-liquid drop which results in structural pattern of the facie derived. Structural patterns of the facie (a dehydrated film of a bio-liquid drop) reveal information of the whole range of bio-physical and chemical peculiarities of the bio-liquid itself and, thus, their recognition can be used for the bio-liquid properties qualitative and quantitative estimation. Structural analysis of bio-liquid facies obtained by the cuneiform dehydration method has been used successfully in medical studies in miscellaneous areas: ophthalmology, therapeutic dentistry, cancer science, gerontology, neuroscience, surgery, obstetrics and gynecology, phthisiology, neonatology, nephrology [3].

The cuneiform dehydration process is a result of cooperative impact of the factors that differ by nature. A bio-liquid drop drying on a solid base is an open system with a permanent external interchange of energy. Inside of the drop the metabolic processes are also followed by energy transformation. Being dehydrated, the drop is undergoing the cooperative impact of number of different external forces coming with internal biochemical interaction inside of the drop. Mostly, the dehydration structuring depends on initial conditions: drop diameter and volume that determine its free surface curvature and evaporation velocity, such environmental factors as temperature, humidity, air pressure, etc., and dynamics of these factors throughout the dehydration. The structural pattern is a diagnostic tool as it undergoes changes if any pathology occurs, even in the very early going. There are physiological, physical, and procedural factors affecting the dehydration process and the facie structuring resulted, therefore, the cuneiform dehydration is to be running under the required conditions so to reduce uncertainties through the contingencies coming with the procedure. Providing this, the pattern recognition of the bio-liquid facies affords facilities for preclinical diagnostics.

The results obtained indicate high sensitivity and innovativeness of the cuneiform dehydration method for bio-liquids study and its diagnostic applicability as a progressive cutting-edge technique. Being a low-cost technology with no demands for expensive technical equipment, this method possesses non-invasive character for a number of bio-liquids, which is a plus in clinical testing. Combined with its high-detectivity, that allows revealing range of health disturbances at early stages to provide preclinical diagnostics; these particular features make this method valuable and advantageous for medical practices.

The bio-liquid facie analysis relates to the problems that are typical to structural imaging techniques. Such techniques are widely utilized in clinical practice to examine anatomical or biochemical abnormalities caused by disease (e.g. computed tomography, magnetic resonance imaging, etc.) where anatomical features are more significant than cellular activity. In the case of bio-liquid structuring accompanying the cuneiform dehydration process the very cellular activity is a characteristic feature, which stipulates the necessity of development of a dehydrated patterns recognition algorithm in the fashion of a structural imaging scanner for CT or MRI images, which would provide information on the biochemical crystallography of bio-liquids revealing the pathology. Being combined with traditional clinical research, structural analyzing leads to a higher research sensitivity and give an opportunity of pre-clinical diagnostics of abnormalities at the earliest stages.

Results and discussion

Currently, when being utilized in medical practice, the dehydrated facie pattern recognition has basically a qualitative character, e.g. visual comparison of textured patterns with some samples, while the quantitative estimation can be found in few researches [4] with no comprehensive bio-liquid texturing analysis. Still, the textured pattern comes with a number of specific features holding the diagnostic information. The key specifics of structural patterns of a bio-liquid facie are the following:

- a bimodal texture comprising low- and high-frequency structural components;
- spatial inhomogeneity of the pattern;
- dividing into particular zones depending on a bio-liquid type that imposes a specific character of structuring;
- periodic and non-periodic structural components within the same facie;
- shape, outline, size, optical density, grouping and layout, fractal dimension are the unique traits of structural components;
- in the case of abnormal clinical findings, the facie's structural pattern undergoes changes that affect all zones of the facie.

Digital image processing is affected by the input data detail levels. Thus, pixel characteristics are the input data for the pixel level, for the local feature level they are the pixel based detailed imaging data, the structural level and boundary detection uses relative position and layout elements features as input data, the object level relays on the single objects characteristics, the objet group level is fed by information of interposition and mutual arrangement of the elements to be recognized, the scene description level comprises an image comprehensive visual analysis including lighting, background, etc. [5].

The image processing steps in machine vision systems could be divided in technic group (low level - the pixel level and the feature level) and an intelligent one (high level - as from the structural level). Among the latter one the most critical stage is image segmentation. Its contribution increases in the case of big data, e.g. in medicine, geography, air photography, etc. Image segmentation is directly followed by pattern recognition, it mainly defines the performance progress of the next steps for object identification and image recognition in the whole. Therefore, the intelligent problem of machine vision technically amounts to segmentation problems and pattern classification.

Image segmentation is one of the computer vision methods popular in medicine and pharmacy, geography, and other areas demanding big data handling. It implies dividing digital images into segments (or sets of pixels) according to their color, brightness, disposition, etc. [5]. For pattern recognition, the specific facie zones and patterns layout are observed and identified by experts (clinicians). These areas of where the structural objects are located are considered to have specific configuration for all the facies within the same bio-liquid type in health and contrasting configuration in the case of disease. In other words, a precise segmentation is needed because even small errors in segmentation can distort the calculation of the pattern features affecting quantitation and possibly diagnostic decision-making.

The state-of-the-art segmentation methods using for a facie patterns could be divided into the following groups: manual segmentation and ground truth reconstruction, thresholding-based, stochastic and learning-based, region-based, boundary-based, and multi-modality methods [6, 7, 8]. Without loss of generality, image segmentation can be thought of as two related tasks: recognition and delineation. Recognition means determination of where exactly the object is and then distinguishing it from other object-like entities in the image; and delineation is to define the spatial extent of the object region in the image. Delineation, which is the second step of segmentation, aims for precise separation of the specific regions from the background and non-significant details. Some of intrinsic and extrinsic factors affecting significantly the cuneiform dehydrated image segmentation are the following: resolution related issues, large variability in the shape, texture, and location of pathologies, noise. These factors handicap image segmentation.

The pattern recognition problem is one of the most sought-after technology-oriented tasks. Its solution primarily relates to artificial intelligence and computer vision systems, where artificial neural networks set the leading position. The efficiency and capacity of current computer-based man-machine systems designed for solving intellectual challenges and expert decision-making are powerful enough to enable engaging neural models that are as close as possible to their biological prototype - the human brain.

Artificial neural networks (ANNs) are involved in image processing mostly on the low-level steps and are rare on the high-level ones. Herewith, ANNs can be used for all the steps in image processing [9, 10, 11, 12]: cellular neural networks (CNNs), Hopfield neural networks, neuro-fuzzy systems, etc. are applicable for background processing; feedforward networks, radial basis function networks, convolutional networks, and quantized neural networks are useful for image compression and data extraction, data coding/decoding; various ANN types could be applied for image segmentation and recognition, among them are pixel-based and based on local object properties convolutional networks, semantic neural networks, radial basis function networks, probabilistic neural networks, and biological neural networks based on the modeling of functional operation of biological neuron and neural ensemble [13].

When a pixel-based ANN is used for image segmentation, its learning is grounded on texture classification or combines textures and local contours. For the contiguous pre-segmentation and post-segmentation steps ANNs are fed by the contour detection algorithms, surface identification algorithms, a pixel segment membership test, the segmented image defuzzification, pixels clustering, and interactive segmentation. The shortcomings of this group of methods lay in their low response to the versatility of the image processed (e.g. its rotation or so), which results in their implementation impairment.

When using the topology-based ANNs, their learning implies recognition of textures diversity, combinations of textures and local contours involving the thresholding methods, such as simulated annealing method, histogram mapping method, the optical flow method, connecting edges and lines algorithm, contour growing method [11, 12].

The quantitative algorithms of image segmentation are in numbers nowadays but still, they are very far from human natural ability for object identification in the case of big data. Here is why the neural network modeling proves to be one of successful segmentation techniques as it matches up with algorithms of human brain operation [13]. Hysteretic characteristics of the neurons functioning naturally improve the effectiveness of the neural networks application for pre-processing and graphic data reduction to simplify their further treatment, etc. The term 'neural network' comprises a wide range

of different models, which have been, now and then, the subject of exaggerated claims regarding their biological plausibility. From the perspective of practical applications of pattern recognition, however, it ought to restrict attention to the specific class of neural networks with high practical utility.

The efficiency of practical use of ANNs depends on their technical parameters (architecture, organizing methods, learning algorithms) and their affinity to such functional abilities of human biological neurons as plasticity, self-training, short-term memory, selective memory, and total memory, which determines human skills to fix both local and total scene information as for the object researched. These features could be embodied in ANNs due to nonlinear (hysteretic) activation functions implemented [14]. Hysteretic character of neuronal operation raises naturally the practical use of ANNs in handling of such applied problems as data preprocessing and its further treatment in machine vision system operation.

The key specifics of the neuronal network models are the neuronal functional-linking and response of a neuron to the excitation signal. The research has shown that a neurone is surrounded by the cell formations (clusters) that enable the endogenic (internal) processes to start up within the neurone along the hysteresis curve and to entail a spike hereby. A neuronal response to the excitation signals was studied by A. N. Radchenko [15]. According to the analytical interrelations obtained by A. N. Radchenko, a neural network operation can be arranged so to solve urging problems of clustering, identification, etc. The applicability of the biological neural network models for development of pattern recognition systems is also shown.

So far, there are a number of biological neural models with various degrees of biological substantiation and adequate mapping of a certain class of the processes studied. Choosing a specific mathematical model means to find the balance between highly detailed elaboration of the model (and its fineness degree as a consequence) and the problems derived from the complexity of its practical use. Thus, for instance, the Hodgkin-Huxley model [16] relates to the row of the most specified models of high-order fitting to the biological data but, over its fact-laden and complexity, it has some implementation problems being not easily tractable in practical modeling of complex neuronal systems. That is why the analyzing problem of the biological neural network models with hysteretic characteristics stays one of the topical issues.

Mathematical modeling of biological neurons

By the early XXth century it was known that excited areas of neurofiber morphs into the electrical generator; then, electrical current, pervading the neighboring areas of neurofiber, makes them to generate current, which, in its turn, excites the new ones and so on. Thus, the nerve and muscle fibres electrically are resemble to some extend to electrical cable: they have a relatively high conducting core (protoplasm) surrounded by the high-impedance and high-capacity fibre membrane (H. Helmholtz, B. Verigo, N. Bernstein, L. Hermann et al. [17]). Thereat, membrane is the keynote in electrical impulse forming and propagation: the fibre area is getting excited when potentials difference on either side of membrane get the threshold level, in such a way, the difference of the membrane potentials is the very parameter that determines the current generation mechanisms cycling on and off.

The Radchenko model

The conductive receptors wherethrough incoming signals go to a neuron involve ionotropic and metabotropic receptors [15, 18]. Being located in synaptic gaps, ionotropic receptors form the ion channels for the charged ions to migrate through the membrane, which sums up in changing the membrane potential. Hence, ions collective migration results in initiation (or not) of a spike due to the external impact on a neuron. Metabotropic receptors are located in the extrasynaptic traps outside of the synapses, thus, they interact with ligands and make the neurotransmitter respond, which amplifies the initial signal massively (by a factor of 105). The eventual signal activates a neuron and initiates a spike even in the case of few ligands available. Due to such a mechanism sensor neurons reveal response to low-intensity environmental impact. Metabotropic receptors control the brain activity substantially. The case when a pattern of neuronal inputs coincides with a pattern of its synaptic sensitivity is an indicative stimulus for a neuron; the closer input signal to the indicative stimulus the higher frequency of the spikes generated by a neuron. This reaction is a so called evoked activity. It occurs only if a neuron responds to the current input pattern and makes a mere part of the whole brain activity; the main one is attributable to the background (spontaneous) brain activity, which is composed of isolated spikes. Neuronal spontaneous activity appears in a series of random spikes and, as research of a neural network reveals, has a unique overall electrical oscillatory rhythm (both of frequency and level) that differs from other zones rhythms. This is an endogenous type of activity induced by metabotropic receptors.

Across the plasmatic membrane of a neuron, all the receptors form the ionotropic (IRC) and metabotropic clusters (MRC) responsible for the transmembrane signal transfer. They perform two-level control of a neuron - both on subsynaptic and extrasynaptic levels [16]. The receptive cluster functions similar to the elastically supported wafer capacitor; it exhibits hysteretic characteristics and varies a distance between the elements of transmembrane dipole in response to the membrane potential dynamics. Interaction with a ligand leads to the changes in a receptor's conformation. As a result, the cluster could set one of three conformational conditions: depolarization, hyperpolarization, and immobilization. Each of these has its own energy level relating to the depolarization (DCT), chemical (CCT) or hyperpolarization conformational transition (HCT) correspondingly, or to the consolidation period. These conformational changes can be steady after removal of a neuromediator as well. Being in the altered state, a receptor could maintain its own activity (and sensitivity) in responding to the external impacts or be inactive (nonsensitive). The altered state of the receptor could be registered and saved (stored) by itself, but also it could be reset to the initial state (e.g. when strong changes in membrane potential occurs) [18].

The IRC provides a neuronal electrical reaction resulting in initiation of "evoked"spike. The MRC responds both to the electrical and chemical environmental impacts and generate "spontaneous"spikes. Thus, neuronal activity is not randomized but is determined by the inputs signals and, as a consequence, reveals determined outputs. Herewith, the MRC has higher efficiency then the IRC as an isolated postsynaptic potential of the latter is inadequate for a spike initiation. The MRC shows higher sensitivity and has intensified interactions between receptors within the cluster. A single MRC conformation is sufficient for a spike initiation.

Functionally, the MRCs can be thought as elements of the neuronal memory (a molecular trigger) based on the conformational mobility control of the receptors within a certain type cluster, where both, electrical and chemical, signals are able to induce spikes. The conformational transition dynamics can be described as follows [15]:

$$u_m = By \sqrt{\ln \frac{1-k}{y-k}} - Ay^2, \tag{1}$$

where u_m is a membrane potential, $A = \frac{\lambda_0 \rho}{\epsilon}$ and $B = \lambda_0 \sqrt{\frac{2Y}{\epsilon}}$ are the coefficients of chemical and electrical impact correspondingly; if $\lambda_0 = 1.4 \times 10^{-9}m$, $\epsilon = 10 \times 8.85 \times 10^{-12}F/m$, and $Y = 0.67 \times 10^6 N/m^2$, then $B = 0.12$. Setting chemical impact as missing ($A = 0$) allows building volt-conformational characteristics (VCC) $y = f(B, u_m, k)$ (Fig. 1).

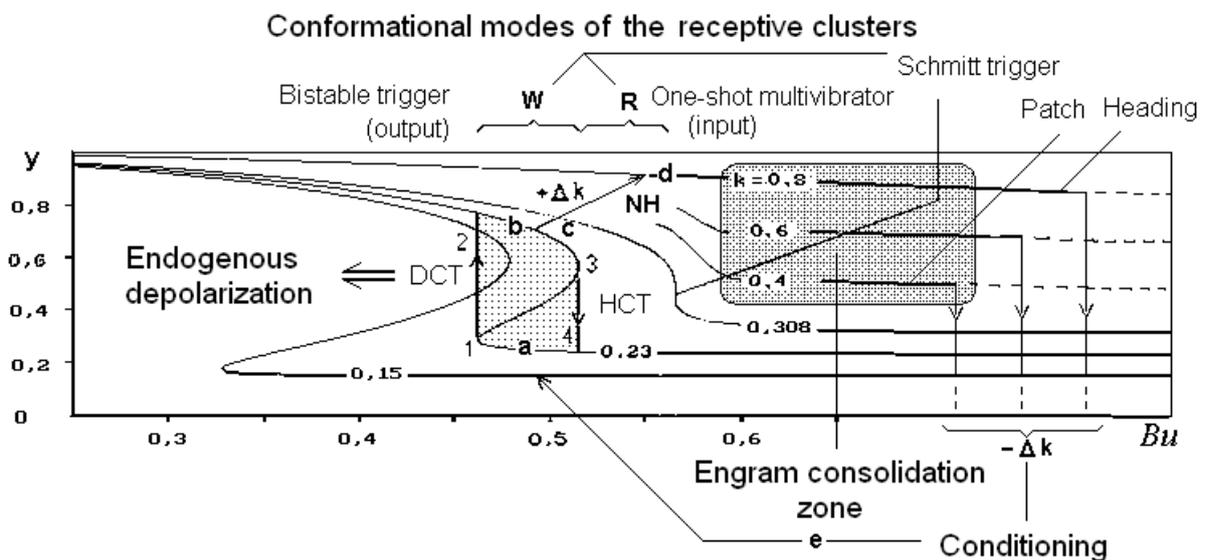


Fig. 1. Conformational modes of the receptive clusters of a neuron membrane

Then the equation (1) for the membrane potential with no chemical impact on it can be expressed as follows:

$$u_m = By \sqrt{\ln \frac{1-k}{y-k}}. \tag{2}$$

Parameter k describes the electrical mobility limitation ($0 < k < 1$); the threshold value of k , when the MRC loses its hysteretic properties, is equal to $k \approx 0.308$ [18].

Figure 1 shows that growth of the membrane potential u_m results in the MRC conformational changes in the cases of DCT or CCT. The membrane potential dynamics shifts the properties of the receptive cluster four times: zone 1 (Fig.1) relates to the gap between DCT and CCT, when the receptive cluster acts as a bistable trigger (output of one); in zone 2 it acts as a single flip-flop oscillator (output of zero); then in zone 3 - as a Schmitt trigger, there is a curve transition to the monotonous mode (up to the inflection point), and in zone 4 the MRC alternates to the monotonous mode (input of one), which relates to the cluster consolidation mode.

The chemical impact on the MRC is shown in Fig. 2. It is determined by the coefficient $A_0 < A_1 < \dots < A_n$, described by (1). The coefficient's values vary with different concentration of mediators and relates to different elastic characteristics of the MRC (when $B = 1.2$). Growth of concentration makes for the curve deformation. When the A_2 curve crosses with membrane potential u_0 (Fig. 2), CCT begins. It can be awoken for any abscissa value between DCT and the potential defined by the inflection point at $k = 0.308$, when these two curves are crossing.

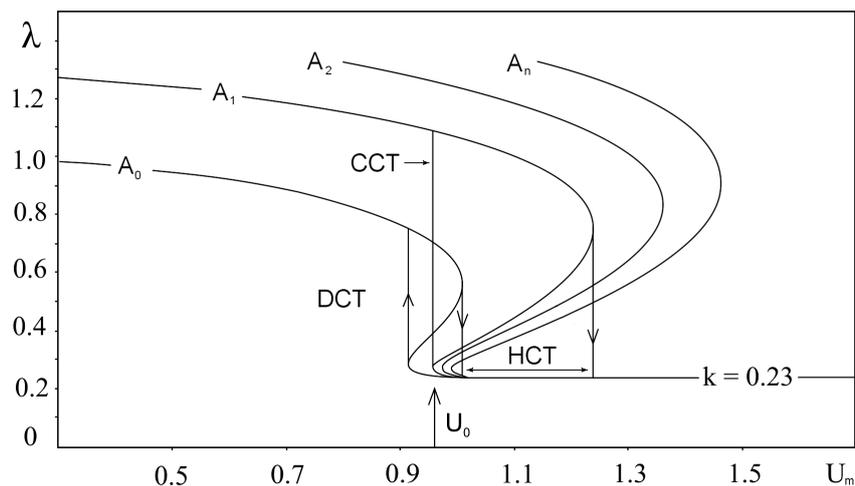


Fig. 2. The hysteretic curves shape variations corresponding to the MRC dynamics under the electrical and chemical impacts

Figure 1 presents energy processes accompanying transitions within the MRC, it is shown that HCT stores energy, DCT (or CCT) reveals energy, quantity of energy is proportional to the hysteresis loop area. The MRC features classified above determine its spike initiation capacity; they disappear, if the membrane potential immobilization takes place and the hysteresis loop is smoothing over. Herewith, the chemically-induced transition reveals more energy than the electrically-induced one and, therefore, plays the leading role in the endogenous neuronal excitation as it induces more intensive spike.

The Kashchenko-Mayorov model

Applicable and easy-to-use model of a biological neuron is considered in greater detail by S.A. Kashchenko and V.V. Mayorov [19]. The discussed results indicate that the dynamics of electrical processes running within a neuron is preset by its historical behavior, which determines utilizing delay differential equation for the mathematical modelling as the most adequate option. This phenomenological spiking neuronal model is based on delay differential equations and demonstrates good agreement with empirical biological data. Its algorithm implies solutions of a spiking neuron and neural ensemble equations with different environmental impact factored in as well as hysteresis qualities of a neuron. The mathematical description of the model reflects a neuron's capacity to generate narrow-pulse high-amplitude spikes with slow membrane potential dynamics during pulse spacing. Being modified, the model can comprise synaptic interaction of spiking neurons and excitation wave propagation in the circular neuronal structures, which corresponds to modeling the information memorizing and storing provided by

stable combinations of the neuronal activity coherent continuous waves with varied phases. Also, the Kashchenko-Mayorov model allows solving the design problem of the neuronal network generating the periodic pulse train with the specified interspike intervals, and the neuronal network implementing for the specific neuronal groups including synchronization modes in the circular neuronal structures, that simulates processes of information retention and storage in the central nervous system.

According to the model, a neuron condition is characterized by the potentials difference on its membrane (transmembrane potential). Outer surface of membrane is electropositive as related to inner surface except for spikes generation time. Most of the time membrane is strongly polarized. The transmembrane potential dynamics is driven by the ion currents, both sodium and potassium currents are described by the model, the latter one is delayed. The reference point relates to the membrane polarization maximum (hyperpolarization).

Mathematical model of a biological neural network

This model relates to the class of electrical input-output membrane voltage models that describe the relationship between neuronal membrane currents at the input stage and membrane voltage at the output stage. The research results presented in [19] give comprehensive analysis of a biological neuron and its mathematical model which is based on K-current and Na-current flowing through the neural membrane and could be described by a delay differential equation:

$$\dot{u} = \lambda [(-1 + f_K(u(t-1)) - f_{Na}(u))] \cdot u, \tag{3}$$

where $\lambda = \frac{h(b-a)}{c}$ is a coefficient that describes the velocity of the membrane capacity recovery (in a logarithmic scale), a, b, c are the constants reflecting biological features of membrane, h is a time delay between K - current and Na - current; $f_K(u) = \frac{f_K^*(u)}{b-a}$, $f_{Na}(u) = \frac{f_{Na}^*(u)}{b-a}$ are the functions of K - current and Na - current, $f_K^*(u)$ and $f_{Na}^*(u)$ are continuously differentiable function with zero limits as $u \rightarrow \infty$.

The activation function of a neuron with initial conditions is restricted by the following limitations:

$$\begin{cases} f_K(u) > 0, f_{Na}(u) > 0, \\ f_{Na}(u) \rightarrow 0, \text{ if } u \rightarrow \infty, \\ -1 - f_{Na}(0) + f_K(0) > 0, \\ f_K(u) < c \cdot u^{-1-\varepsilon}, \\ f_{Na}(u) < c \cdot u^{-1-\varepsilon}. \end{cases} \tag{4}$$

where c and ε are the constants, $\varepsilon > 0$, as a natural consequence of the model's biological preconditioning.

As it said above, a neuron undergoes the electrical or chemical impact, and if the neuron is excited electrically, its activation function (3) is given by:

$$\dot{u} = \lambda [-1 + f_K(u(t-1)) - f_{Na}(u)] \cdot u + g(v(t) - u), \tag{5}$$

where $g(t)$ is a degree of electrical impact; $g = g \cdot h/c$ - standardized conductivity factor, $g^* > 0$ - corresponding conductivity coefficient, $g^* = const$.

In the case of the chemically-induced excitation, a neuron's activation function is described as follows:

$$\dot{u} = \lambda(-1 + f_K(u(t-1)) - f_{Na}(u) - f_{Na}(u) + \chi_v(u, V)) \cdot u, \quad (6)$$

where $\chi_v(u, V) = \chi^*(u, V)(h/c(b-a))$ - chemical impact degree; other parameters are the same as in (3)-(4).

In the presence of mediator the expression (6) transforms into the following:

$$\dot{u} = \lambda[-1 + f_K(u(t-1)) - f_{Na}(u) + g_v(u_{rev} - u)] \cdot u, \quad (7)$$

where g_v is a conductivity coefficient, u_{rev} - stable positive level of the membrane potential in a mediator environment.

For the detective neurons a spike is a response to the environmental impact in the case of its strong intensity. If the impact has a periodic character ($v(t) = \lambda w(t)$), then the dynamics of the neuronal membrane potential (3) is subjected to the external influence frequency and the neuron can react in a complex multimodal way, a so called "shelf-structure"[19].

If the membrane potential of a neuron is at resting, the slight environmental influence doesn't induce a spike, because of a subthreshold character of the impact; a spike can be induced only if the depolarizing current passing through the membrane exceeds the threshold. The influence growth leads to the high-frequency series of spikes being generated (train pulse response). Permanent depolarizing electrical impact diminishes absolute value of membrane potential and forces a neuron to respond in spikes series. In the case of nonspiking change of the membrane potential equation (3) has a similar solution, but subthreshold environmental impact does not lead to the membrane resting, it induces stepwise dynamics according to the "shelves".

If $g = 0$, then equation (5) describes a positive stability of the membrane potential u_0 , but if the initial conditions $u(0)$ exceed certain constant value, its solution has an exponentially high amplitude spike with respect to λ (velocity of the membrane potential reduction). If the external impact v_0 in (5) has a small amplitude and corresponds to λ , then pause time (between the end of one spike and start of another) asymptotically tends to $\left(\frac{\sigma}{\alpha} + 1\right)$, where $0 < \sigma < \alpha_2$, $\alpha_2 = f_{Na}(0) + 1$ providing the exposure time T is high enough.

As it stated in [20], the chemical impact is effective for modeling connection and ensemble synchronization of neuronal network; the electrical impact is effective to impose a spiking period.

If the model is based on the MRCs considered, the activity pattern of the nearest-neighbor environment won't be described by its neurons by the only configuration (as in the case of synaptic memorizing), but in a multiple way due to such patterns are being held in numbers. Suppose that intrinsic random spike and high environmental intensity are the conditions for the obligatory memorizing of the environmental pulses pattern by a neuron [18]. Then, whenever the neuron meets the stored pattern again, it generates a single spike called a wave spike. Assume that neurons are incapable of spiking after the series of metabotropic spikes (e.g. wave spikes) for a refractory period. Therefore, the network activity will propagate in a pulsating source-diverging wave manner instead of a continuous wave, with a wave propagation character subjected to the unique randomized

pattern. Such a pattern is a synaptic pattern in the case of evoked activity, and is a response of the metabotropic receptors if the wave propagation takes place.

Thus, each networked neuron performs two functions simultaneously: it is a detector, as it aims for the specific character of the data via the variation of synaptic weights, and it is a data carrier as it records it in the MRCs. These functions efficiency is provided by the following: relatively flexible calibration of synaptic weights allows neurons to enhance the capacity to recognize the underlying factors and realize the big picture of the whole receptive area; object snapshot by the extrasynaptic MRCs, to the contrary, provides its statefulness, when environment of a neuron is recorded and copied scaled-down. Despite each neuron has the only one set of synaptic weights, it can store a quantity of identification matrixes ($\sim 10^4 \div 10^5$), thereat synaptic recognition provides evoked activity of a neuron (initiates a spike series), whereas few neuronal detectors create a pattern of this activity at the same time. Metabotropic recognition results in a single spike, ensemble if which forms the identification wave front. As soon as neurons are trained to neglect the nonregular, not recurring patterns, the more frequent ones will "train" the network to its own waves propagating while less-common combinations will create only local propagation areas, which, nevertheless, can grow according to these patterns frequency increase [20].

In view of the above, the biological neuron model (3) should consider the neuronal interaction as well as electrical or chemical environmental influence. The dynamics of a networked element could be specified by this model as followed [21]:

$$\dot{u} = \lambda[-1 + f_K(u_i(t-1)) - f_{Na}(u_i) + Y_i] + I_i, \quad i = 1 \dots N, \quad (8)$$

where I_i is an input effect (external) on the i -th neuron corresponding to the electrical impact; Y_i is a network environmental effect on the i -th neuron, corresponds to the chemical linkage between the network elements according to the Radchenko model; N - the total amount of neurons.

The activation function modeling the external impact in (8) can be written using the Bouc-Wen hysteretic model [22]:

$$\dot{z} = D^{-1}(A\dot{x} - \beta|\dot{x}| \cdot |z|^{n-1}z - \gamma\dot{x}|z|^n), \quad (9)$$

where A , n , β , γ are dimensionless coefficients that specify the hysteresis curve shape; $D > 0$, its value normally depends on the process origin and type. Setting $D = 1$ we arrive at a linear dimension of a $z(t)$ variable, which one is indicative of the hysteresis displacement [23].

Then equation (9) can be written as follows:

$$\dot{z} = A\dot{x} - \beta|\dot{x}| \cdot |z|^{n-1}z - \gamma\dot{x}|z|^n, \quad (10)$$

The range of the parameters in (10) is detailed in [23], suitable selection of particular values for A , n , β , and γ seems to be the problem for further research in the mathematical model specification for the bio-liquid image segmentation and pattern recognition regarding their unique structure features.

Conclusions

Analyzing the neural network methods for image segmentation, the biological neural network is offered for the bio-liquid facies segmentation with its feasibility grounded.

The advantages of the model are predictability of its response to the environmental impacts and functional adequateness even if the network elements are small in numbers [19, 20, 21, 22]. As a neuron can verify any state of the neuronal environmental activity due to its MRCs, then the neuronal network based on such neurons is up to great amount of operations in a single conditional informational cycle recording the activity patterns both for local and global neuronal activities. The proposed model is compact and useful for signal processing if the number of signals is not big and they form a set of finite values, which is corresponding to the problem of image segmentation and pattern recognition.

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Для цитирования: Semenov M. E., Zablotskaya T. Yu. Choosing the model of biological neural network for image segmentation of a bio-liquid facie // *Вестник КРАУНЦ. Физ.-мат. науки.* 2019. Т. 26. № 1. С. 78–93. DOI: 10.26117/2079-6641-2019-26-1-78-93

For citation: Semenov M. E., Zablotskaya T. Yu. Choosing the model of biological neural network for image segmentation of a bio-liquid facie, *Vestnik KRAUNC. Fiz.-mat. nauki.* 2019, **26**: 1, 78–93. DOI: 10.26117/2079-6641-2019-26-1-78-93

DOI: 10.26117/2079-6641-2019-26-1-78-93

УДК 004.93

ВЫБОР МОДЕЛИ БИОЛОГИЧЕСКОЙ НЕЙРОННОЙ СЕТИ ДЛЯ СЕГМЕНТАЦИИ ИЗОБРАЖЕНИЯ БИОЖИДКОСТНОЙ ПОВЕРХНОСТИ¹

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В работе рассматривается применение моделей биологической нейронной сети для сегментации изображения фации биожидкости, полученной методом клиновидной дегидратации. Выделены основные характерные особенности, присущие паттернам фаций биожидкостей, а также основные этапы их цифровой обработки в рамках задачи распознавания образов. Проведен анализ использования искусственных нейронных сетей для цифровой обработки изображений для разных уровней представления данных; сделан обзор основных нейросетевых методов сегментации. Описан принцип построения биологически достоверных искусственных нейронных сетей, использующих механизмы изменения мембранного потенциала нейронов и учитывающих при генерации спайка как вызванную активность, так и эндогенную (спонтанную) активность нейронных кластеров. Описан механизм инициации спайка для метаботропных и ионотропных рецептивных кластеров с указанием природы запускающего внешнего воздействия. Проведен анализ существующих математических моделей биологических нейросетей, содержащих помимо обычных функциональных нелинейностей нелинейности гистерезисной природы. Сделан выбор в пользу математической модели, использующей дифференциальные уравнения с запаздыванием, которые могут быть применены как для описания отдельного биологического нейрона, так и для описания работы нейронной сети.

Ключевые слова: биологическая нейронная сеть, гистерезис, фация, текстура, распознавание образов.

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¹Работа выполнена при поддержке РФФИ (Гранты 19-08-00158-а, 17-01-00251-а, 18-08-00053)