Research Article

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A Computational Model of Some Key Socially Significant Processes

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Abstract

This work deals with the tasks and relevance of mathematical computer modeling of biological systems and, in particular, simulation modeling. A discrete computer mathematical model presented is suitable for the ischemic stroke pathogenesis outlook engaged with an appropriate computer program described. For the first time, the results of stroke modeling performed by stochastic Monte Carlo method with the brain neurovascular units as elementary structures of the system have been proposed. Conclusions are drawn taking into account an applied pharmacological potential of the model for the current preclinical trails requirements.

Keywords: Mathematical computer modeling • Simulation modeling • Stroke • Monte carlo method • Discrete model • Neurovascular unit

Introduction

Medicine, and especially some of its areas, such as cardiology, neurology and oncology [1], most urgently needs adequate simulation and mathematical models at all levels of living matter organization [2], from the cellular to population ones. For natural reasons, there are a number of difficulties in conducting *in vivo* experiments on wildlife and, especially, on humans [3]. That is why structural, functional, simulation models *in Silico* are so relevant. Noteworthy, there are still no simulation mathematical models to operate with the ischemic brain stroke pathogenesis scenaria [4].

Stroke is the second largest death reason in the world according to WHO data [5], which is why research in the field of finding effective drugs for the treatment of this disease is of particular relevance. The development and introduction into circulation of pharmaceuticals is a complex and lengthy process that requires extensive preclinical and clinical studies. That is why the optimization of such scenarios by means of mathematical modeling using information and computer technologies is a separate extremely important task of a scientific and practical nature.

Stroke is the world's second leading cause of death, accounting for approximately 6,000,000 deaths each year. The lifetime risk of stroke is estimated to be between 8% and 10%. Stroke pathogenesis involves a diverse set of processes. Vessel occlusions (ischemic stroke) account for 85% of all strokes, with the remainder caused by primary intracerebral bleeding (hemorrhagic stroke). Embolisms are the most common cause of focally obstructed blood flow within the brain, accounting for approximately 75% of all cerebral vessel occlusions. Ischemia is defined as a decrease in blood flow severe enough to disrupt normal cellular function. Ischemia is so sensitive to brain tissue that even brief ischemic periods in neurons can set off a complex chain of events that can lead to cellular death.

The solution of this problem is possible *in silico* in the paradigm of a computational experiment. In this case, it is necessary to model not only the pharmacokinetics (i.e., the delivery of the drug to the selected organ),

but also the pharmacodynamics or, in other words, the therapeutic effect of its impact on the course of the disease under study [6]. And this means that in addition to the model of the disease itself (in our case, stroke), it is necessary to have a model of the pharmacokinetics of the study drug and a model of its pharmacodynamic effects.

Research is complicated not only by the lack of relevant descriptions of mathematical models of ischemic stroke in the literature, but also by the lack of pharmacokinetic models of innovative drugs under investigation, the pharmacokinetics of which can have a pronounced drug-specific character, especially when it comes to targeted delivery. At the same time, the rapidly developing branch of nanopharmacology offers a number of innovative drugs of the nano-group, the pharmacokinetics of which are fundamentally different from traditional drugs, but at the same time, the prospects for using them as neuroprotectors can hardly be overestimated [7].

Methodology

Here we present a two-dimensional discrete stochastic model developed by us for the evolution of elementary states of neurovascular units in the area of cerebral ischemia in stroke after occlusion of a small arteriole. This is a lattice model with a unit cell, which is a morph functional element of the brain tissue-a neurovascular unit.

Mathematical models of biological systems are usually divided into homogeneous and heterogeneous models (in their stationary or dynamic variants), and these models are obtained mainly within the framework of the following generally accepted approaches.

The first approach is to average variables over space and consider the system as homogeneous. Such models are called kinetic. Mathematically, they represent a set of systems of Ordinary Differential Equations (ODEs) with respect to the averaged values of the variables under study. In particular, in the works of Dronne, et al. presented a kinetic model of the behavior of brain cells under conditions of stroke [8]. The model well described the

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Received date: 01-Dec-2022, Manuscript No. CSRP-22-76831;Editor assigned:05-Dec-2022, PreQC No. CSRP-22-76831(PQ); Reviewed: 22-Dec-2022, QC No. CSRP-22-76831; Revised: 29-Dec-2022, Manuscript No. CSRP-22-76831(R); Published:06-Jan-2023; DOI: 10.3371/CSRP.FVAA.010623.

Clin Schizophr Relat Psychoses, Volume 16: S7, 2023

change in the state of cells in the epicenter of the affected area, under conditions of reduced blood flow. However, biomedical interest is not limited to these cells. It is also important to describe the spatial development of the lesion to neighboring areas, including those in which the blood flow is not disturbed. It is often necessary to determine the spatial characteristics of the affected area, and in this case kinetic models are not informative enough.

The second approach is applicable directly to heterogeneous models. In it, the dynamics of the system variables is described by a set of partial differential equations with boundary and initial conditions. Such equations are usually solved numerically using methods based on finite-difference approximations of partial differential equations. So, in the work of Chapuisat, et al. considered a finite-difference model of stroke development. At the same time, the general disadvantages of finite-difference models are their general complexity and complexity of setting boundary conditions, supplemented also by the fact that the cerebral cortex has a complex shape and consists of heterogeneous elements [8].

The third approach is based on the discretization of the system and the transition from variables describing concentrations to individual discrete elements. The methods used in such simulations include Monte Carlo methods [9], molecular dynamics methods, particle methods, etc. Currently, there are no discrete models for the development of ischemic stroke. The advantage of discrete models is the convenience of their implementation in the form of parallel programs, sufficient ease of implementation, good convergence. However, a large total number of elements can nevertheless make such models laborious.

Thus, in this field of science, it is important to create new adequate mathematical models that contain a relatively small number of parameters and variables and are easy to implement numerically [10].

Within the framework of our hypothesis, the elementary unit of the model might exist in one of the elementary states namely in physiological, ischemic, or destruction (implying apoptosis or necrosis) ones. Once ischemia is in the case, each cell of the lattice, as well as the neighbouring cells can change its state with a given transition rate. The possibility of transition to another state for each particular cell obeys a stochastic law which makes it treatable by the Monte Carlo method [4,11]. The model is implemented as a computer program driven in the Python 3.9 language which allows to run the parallel calculations to simulate the development of a stroke under various conditions.

Results and Discussion

On a 30 \times 30 grid of 900 neurovascular units, we have modeled the development of a "Perfect Stroke" in case of occlusion of a small arteriole, which is a section of a brain tissue area with a side of about 3 mm [12]. Figure 1 shows the visualization of data on changes in the structure of this section as a function of time.



Figure 1. Transition of the states of simulated areas. On the abscissa axis-the fractional content of neurovascular units in each of the elementary states in relation to their total number. On the y-axis-time in the format "hours: minutes: seconds".

On the graph, one can observe the growth of the L4 curve, which reflects the growth of the total number of damaged neurovascular units. This curve is cumulative with respect to the L3 curve (the number of neurovascular units subjected to destruction) and the L2 curve (lschemic Neurovascular Units). Line L1 reflects the content of undamaged lattice sites. Area A1, bounded by the lines L4 and L3, reflects the presence of a "Therapeutic Window", which, during morphological examination, is found as a penumbra around the core of the destruction of the ischemic area [14]. After the mark of 400 minutes (3 hours 20 minutes), there is a steady decrease in viable morph functional units (L1 and L2) with complete disappearance at around 600 minutes (10 hours). At the same time, 50% of the damaged cells of the studied area are formed by the hundredth minute from the onset of ischemia. The data obtained correlate well with published studies on the morphology of stroke development using biological models [12,13].

Conclusion

Thus, the model we developed can be used to study the influence of various conditions on the development of cerebral stroke. As a result of the study of the model under the conditions of the "Ideal" development of stroke, we obtained data that are significantly correlated with the clinical data published in the literature. By setting the appropriate parameters, the model can be used to study and predict the impact of external influences on the development of stroke, such as the administration of drugs, changes in the composition of the inhaled air, and changes in the composition of the blood.

Funding

The work was supported by the grant of the Ministry of Science and Higher Education of the Russian Federation No. 075-15-2020-792 (Unique identifier RF----190220X0031).

Conflict of Interest

The Authors declare no Competing Financial or Non-Financial Interests. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

Author Contributions

Dr. V.V. Fursov – general project management, experiment planning, *In Silico* research management, idea, hypothesis, structure, modeling, text; Mr. Aleksandr V. Ananyev – modeling, program code, text; Ryabov, V., Ananishnev, V., Tkachenko, A., Osmolovskaya, S., Frolova, T., Berestova L. – analysis and discussion of the data obtained

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How to cite this article: Fursov, Valentin V, Aleksandr V. Ananyev, Vladimir M. Ananishnev and Alexander V. Tkachenko, et al. "A Computational Model of Some Key Socially Significant Processes." *Clin Schizophr Relat Psychoses* 16S (2023). Doi: 10.3371/CSRP.FVAA.010623