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MATHEMATICAL AND PHYSICAL MODELING FORECASTING IN MEDICINE

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ABSTRACT

The main provisions of John Von Neumann's theorem of modeling living organisms using the method of physical and technical functional analogy outlined. Also studied in stages from 1895 to the present day is the development of mathematical and physical modeling and forecasting in medicine, where with the help of computational experiments they can predict new facts and predict the consequences of various extreme effects on the human and animal body.

Keywords

John Von Neumann, modeling, forecasting, medicine, mathematics, man, computer.

Mathematical modeling in medicine, in particular in morphology, has a long history. At the end of the 18th century, Otto Frank (1895) created a model of the circulatory system. In the early 70s of the last century, various aspects of modeling firmly and unobtrusively entered the medical and biological section.

John von Neumann in 1981, on the issue of modeling living organisms, formulated a theorem according to which all biological systems, due to their complexity and inaccessibility to understanding, should:

1 - Divided into morphological units, which are autonomous within certain limits.

2- To establish connections between these morphological units [1].

The main provisions of this theorem formed the basis for modeling living organisms using the method of physical and technical functional analogy, the essence of which was as follows:

1. The (structure) morphology and relationships between the morphological units of the simulated organ during its functioning are carefully studied;

2. Physical and technical objects are selected that perform functions similar to those of the selected morphological units;

3. From the selected technical units, a calculation diagram is drawn up, reflecting the connections between the morphological units and the functioning of the simulated organ;

4. Based on the compiled calculation scheme, a system of differential and algebraic equations is compiled, used in technology and physics and reflecting the functioning of the simulated organ;

5. Digital values of the coefficients are determined and calculated from the accumulated biophysical knowledge about the functioning of the simulated organ;

6. A language environment is selected to compile a program for the numerical solution of the compiled system of equations;

7. The compiled system of equations is solved step by step, and at each step new parameter values are substituted, used for the solution at the next step;

8. The solution is accompanied by the construction of graphs of changes in time of all parameters reflected by equations linking morphological units into a system of functioning of the simulated organ;

9. The resulting graphs of changes in the simulated parameters of a biological organ over time are compared with the parameters available in the biology of the simulated organ. Based on this comparison, a conclusion is drawn about the accuracy of the resulting model;

10. The discrepancies between the obtained results and physiological data are analyzed, and the calculation scheme or numerical coefficients of the equations are corrected;

11. After receiving results reflecting the normal functioning of the simulated organ, with acceptable accuracy, modeling of its pathologies begins;

12. To model pathologies, it is necessary to change the calculation scheme, add equations that reflect the change in the calculation scheme from the normal state model by introducing new dependencies or changing the coefficients of the equations;

13. Create a new program for solving equations that reflect the corresponding pathology;

14. Construct comparative graphs, taking into account the norm and new parameters reflecting the modeled pathology;

15. If there is a need to take into account a functioning that is not described in the existing model of an organ in the presence of experimental data, then it is necessary to construct a new calculation scheme that takes this organ into account;

16. Compose an appropriate mathematical description and determine the values of the coefficients based on the experimental data of this organ and introduce it into the existing model.

In this case, even very rough models have a very high order of description, but real modeling objects in their essence are much (several orders of magnitude) more complex than the constructed models [2].

V.V. Usik and R.B. Slobodskaya (2004) proposed a model of the vertebral body taking into account its geometry. This made it possible to increase the accuracy of diagnosing changes in the vertebral bodies that occurred as a result of disease or injury, to enable a specialist to predict the course of the disease and to study the response to ongoing therapeutic measures.

D.S. Alekseev (2009), who proposed a model of the ciliary apparatus of ciliated cells in the nasal mucosa, noted that the proposed model has sufficient flexibility in adjustable parameters and even types of cilium vibrations, which requires further refinement and complication of the model, which can increase as desired as development progresses. computing tools [3].

B.K. Buzdov (2011) proposed a model of cryodestruction of biological tissue (in particular skin), based on a complete numerical study, independent of dimension, of two-dimensional problems with nonlinear sources.

To estimate the age of a human fetus from fragments of the skeleton of the lower limb, A.E. Strizhkov (2011) developed a system of mathematical models that makes it possible to accurately estimate the biological age of a human fetus from fragments of its lower limb [3].

These models have found wide practical application in the practice of forensic medical examination. They also served as the basis for mathematical modeling of the age-related dynamics of growth of the bones of the lower limb in the fetal period of prenatal ontogenesis and the development of an algorithm for determining the biological age of the fetus based on the results of osteometry of the limbs [4].

A.I. Bunicheva et al. 2012 dealt with the problem of numerical modeling of blood flow in the human cardiovascular system taking into account gravitational influences. They proposed and studied a model of the functioning of the heart and the equation of state, and considered modifications of the graph of the cardiovascular system to simulate possible positions of an object under conditions of repeated gravitational overloads. Others – S.B. Ponomarev et al. (2000), based on Boolean algebra formulas, obtained a range of mathematical models and developed an information and analytical system that makes it possible to determine the expected localization of coronary stenoses with acceptable accuracy. In their studies, they clearly demonstrated the possibility of effectively using high information technologies in processing data from a non-invasive stress-inducing test to increase the accuracy of determining damage to the coronary system by stenosing coronary angiosclerosis.

I.B. Bukharov in 2005 developed a model for studying the structural and functional organization of the circulatory and external respiration systems, using the energy criterion of optimality.

Based on the method of physical and technical functional analogy, a hydromechanical model of the normal human cardiovascular system was obtained by I.S. Lebedenko, 2009, model of ventricular septal defect E.V. Blokhina, 2009, models of stenosis, mitral valve insufficiency (O.A. Bashkatova) and mitral valve prolapse (A.V. Tomashvili, 2010), model of tetralogy of Fallot (V.N. Kireeva, 2011) [5].

In 2012 A.M. Denisov et al. proposed a method for determining the projection of a point source of arrhythmia onto the surface of the heart based on solving the inverse problem of electrocardiography. Information about the position of this point is key for successful surgery to eliminate the source of arrhythmia. The required projection was calculated by A.M. Denisov based on solving the inverse problem of electrocardiography, which is a generalization of the Cauchy problem for the Laplace equation. To solve the inverse problem of electrocardiography, boundary integral equations and the Tikhonov regularization method were used.

V.A. Galkin and N.R. Urmantseva (2014) proposed mathematical modeling of hydrodynamic processes in the blood of the brain. The generated mathematical model makes it possible not only to visualize the movement of blood through the vessels, but also to expand the knowledge base about the circulatory system, which can be obtained without resorting to labor-intensive field experiments. The use of the proposed model and software systems that implement this model in healthcare will make it possible to modify and improve methods for diagnosing developmental defects and diseases of the cardiovascular system.

2013 data published by S.L. Plavinsky on the results of mathematical modeling of the spread of sexually transmitted infections. The practical significance of such a model for medicine, in particular for epidemiology, is simply enormous. Since such a model allows us to estimate the size of the epidemic, the features of its course and outline a prevention strategy taking into account the features of the development of the infectious process.

Yu.S. Nagornov (2013) proposed a model of an erythrocyte that allows one to calculate elastic properties and evaluate its morphology. In the future, the proposed model will make it possible to create calculation methods for atomic force microscopy to determine elastic stresses inside living objects.

O.Yu. Dolganova (2014) proposed a mathematical model of a growing biological body, built on the basis of a mechanical growth model, taking into account the possibility of controlling the deformed state of the system under study during its growth. The use of this model allows, before the surgical stage of treatment of patients with congenital nonunion of the palate, to plan the duration of the impact of the orthopedic device on the separated palatal fragments in order to bring them closer together, to formulate the parameters for individual adjustment of the orthopedic device (size, configuration, mechanical properties), to visualize the results of treatment before it begins [1].

In the works of P.S. Andreeva et al. (2014) presented the results of mathematical modeling of rotational flexion osteotomy, on the basis of which a mathematical model of the hip joint was built, taking into account the main muscle group. The data obtained made it possible to improve the result of medical rehabilitation of children and adolescents with Legg-Calvé-Perthes disease using modern reconstructive interventions based on the concept of three-plane correction of the spatial pathological orientation of the proximal femur, taking into account the stage of the disease, the localization of the degenerative-dystrophic process and the severity of the lesion [6].

Of particular interest is the work of V.Ya. Yurchinsky (2015), who, using discriminant analysis, built mathematical models that reflect the design features of the thymus at both the macro- and micromorphological levels, for all representatives of the comparative morphological series. He determined the nature of the mutual influence of various morphological parameters of the thymus and established the degree of influence of each morphological indicator on the morphological structure of the thymus as a whole. Based on the discriminant models he obtained, it becomes possible to determine the extent of differences and similarities in the structure of the thymus in vertebrates that differ in the level of organization, biological features, and degree of specialization to various environmental conditions [4].

As mentioned by N. Rashevsky (1966): For many scientists it is becoming more and more obvious that nowadays the question of creating biological mathematics arises with all urgency, which requires the closest cooperation and complete mutual understanding of biologists and mathematicians. Naturally, the first stage in this direction is for biologists to master the capabilities provided to them by the already existing arsenal of mathematical methods. Only after this is real progress possible in the further development of mathematics, directly aimed at helping biologists understand the complex patterns of the life process, starting from the subcellular level and ending with the relationships between populations in their real life environment [7].

In our era - the era of widespread computerization of all fields of science, creating the theoretical foundations of the phenomenon or process being studied means creating an appropriate computer model. This process is of particular importance for biomedical sciences, where new computer technologies come to the aid of research scientists, allowing them to replace real physiological experiments with computational experiments performed using computer modeling methods [8-9]. Their capabilities are very wide and sometimes they can provide the researcher with more information than real physiological experiments. Developing the theoretical foundations of a particular branch of science means creating a perfect mathematical model that generalizes the entire set of disparate empirical facts, and its implementation in the form of a computer model. This model allows, with the help of computational experiments, not only to reproduce a real physiological experiment, but also to predict new facts and predict the consequences of various extreme effects on the human and animal body. The task of a scientist is not only the accumulation of experimental facts, but also their mathematical generalization in the form of mathematical models. Mathematical modeling and computational experiment are the future of medicine.

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