

Regulatory Mechanisms Of Human Cellular Communities At Anomalies: Mathematical Modeling

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ABSTRACT:

The modelling approach used in this paper to represent the regulatory mechanisms of the cellular community is based on the functional unit of cellular communities (FUES), which consists of dividing, growing, differentiating, performing specific functions, and ageing cellular groups that function in concert as a whole. Considered are regulators of the interrelated activity between the hepatocytes’ molecular-genetic systems and the hepatitis B virus (HBV). The following regimes of the process, which depend on HBV miRNA concentration, are identified by computing experiments using the built programme complex: clarification, symbiosis, regular and irregular fluctuations, sharp destructive alterations that define various clinical types of sickness.

Keywords:

modeling, regulatorika, cellular communities, functional-differential equations with delay,

miRNA, viral hepatitis, functional equation;

INTRODUCTION:

The success of its application to biology, medicine, and agriculture is correlated with the global development of the theory and practise of mathematical modelling of the regulatory mechanisms functioning (Regulatorika) of living systems at the primary hierarchical levels of the organisation. This is because it enables the selection of the most efficient

methods for the prevention and treatment of a variety of diseases, for agricultural techniques of cultivation and plant selection, and for the creation of various prophylactic measures. According to WHO predictions, there would be 22 million cases of genetic illnesses in the following ten years, up from 14 million in 2012.

A national plan for the study of rare genetic disease regulatory systems has been adopted in European nations, and the current “Horizon 2020” programme is seen as the start of a new age. have already begun an unparalleled magnitude of international scientific research on genetic illnesses. collaboration in the investigation of living systems’ regulatory mechanisms.

The number of studies devoted to the creation and practical use of mathematical modelling methods of various regulatory mechanisms of the cell has been rapidly increasing since the discovery of regulatory micro-RNA molecules at the dawn of this century [1–11]. The “Human Genome” project had a budget of more than \$3 billion, however despite the expansion of large-scale worldwide studies on cellular regulatory mechanisms, the interpretation of genome data is still pending and its regulatory mechanisms are not fully understood.

In this regard, it is crucial to examine the hierarchical connections between the cellular communities of living systems at various levels of their organisation, to create conceptual models of the regulatory mechanisms of cellular communities, to examine potential formation laws of functional communities, and to reveal the fundamental association regularities. to create a model to ensure the population dynamics of the important research on multicellular organisms, where cells in the cell community perform specific functions of the organisms.

cellular groups that make up the cellular community; the creation of simulation models for cells based on the spatiotemporal organisation of cells and intracellular processes; and the use of differential equations with delayed argument to develop mathematical models of the quantitative relationships between cells. a qualitative and comparative examination of mathematical representations of cell division and differentiation that takes

Volume dynamics into consideration;

Elimination of the quantitative relationship between the parameters of the cell division model and the change in volume; investigation of the mechanisms that sustain the overall health and performance of tissues and organs.

To solve theoretical and practical tasks on developing information technology tools for regulating mechanisms of living systems and cellular communities, it is necessary to create and improve models that account for complex regulatory processes of living organisms. To do this, researchers can use the theory of linear programming, stoichiometric modelling technology, methods of discrete, stochastic, and hybrid approaches based on ordinary differential equations, partial differential equations, and other techniques. Researchers like James D. Murray (University of Oxford), Andreas Gisel (Institute for Biomedical Technologies), Wojciech Karlowski (Institute of Molecular Biology), Bernhard Palsson (Systems Biology Research Group), Leon Glass (Centre for Nonlinear Dynamics), and Bernhard Palsson (Centre for Nonlinear Dynamics) are working to develop and improve models that account for the intricate regulatory processes of living organisms.

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CONCLUSION:

A functional unit of cellular communities (FUES) is a fundamental structurally functional arrangement of cells joined by the performance of universal cellular tasks that enables the investigation of regulatory mechanisms of multicellular organisms cellular communities from uniform places. The mathematical modelling of the most common, unique to all true cellular communities, and regulatory processes of animal species at the subcellular level of their organisation are made possible by the FUES formulation. Chaos is characterised by erratic fluctuations and abrupt chaos death ("black hole" effect).

According to research findings, the following regulatory mechanisms occur during the onset of diseases: the inhibitory mechanism, the mechanism for mobilising an organism's potential at anomalies, and the mechanism for system improvement through time.

Quantitative studies of the processes of the interrelated activity of the genetic systems of liver cells and the hepatitis B virus were conducted using the findings of scientific study. It has been discovered that there are the following regulatory regimes between hepatitis B viruses' molecular-genetic system and hepatocytes: stagnant condition, self-oscillations, monotonic reduction

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