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North Caucasus Center for Mathematical Research
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"Operator Theory, Differential Equations and their Applications"

Seminar Chairmen: Prof. Anatoly G. Kusraev, Prof. Marat A. Pliev
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Parameter identification for models of biological pattern formation from information about stationary solutions

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Pattern formation in biological tissues plays an important role in the development of living organisms. Since the seminal work of Alan Turing, many biological structures have been described using the reaction-diffusion mechanism, but more recently other hypotheses have been proposed. In many experimental situations, only final stationary regimes are available for observation, while the initial data and transient processes are unknown. In this case, the available information is incomplete, thus the fixed parameters of the biological model correspond to a certain family of structures, and not to one specific solution. This significantly complicates the calculation of the discrepancy between the prediction of the mathematical model and the experimental data.

In this work, a statistical method has been developed for identifying the parameters of models for the formation of biological structures based on information about their stationary solutions. The idea of the method is to map the vector of control parameters to some random variable obeying a multivariate normal distribution. Knowing a certain number of stationary solutions of the model for fixed parameter values, one can estimate the parameters of this distribution and define the stochastic residual function. By minimizing this function, a point estimate for the parameter vector is obtained, after which the accuracy of the result is estimated using Bayesian methods.

The correctness of the method is tested on several classes of pattern formation models: reaction-diffusion systems, mechano-chemical models, and models consisting of a reaction-diffusion equation and an ordinary differential equation. In addition, the parameters of the classical Turing model of the chlorite-iodite-malonic acid reaction are identified using experimental data. Concentration profiles of chemical structures are extracted from a digital image of a chemical reactor, where the concentration profile of one of the components (the activator) is highlighted using a color indicator.

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