Investigation and numerical solving of a mathematical model of intracellular HIV dynamics: from ODE to PDE

D. Yermolenko^{1, 2}*, O. Krivorotko^{1, 2}, S. Kabanikhin^{1, 2}

¹Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia ²Novosibirsk State University, Novosibirsk, Russia

* e-mail: ermolenko.dasha@mail.ru

Key words: mathematical model of HIV dynamics, ODE, PDE, immunology, epidemiology, parameter specification problem, inverse problem, optimization approach, genetic algorithm, confidence intervals, optimal treatment control.

Motivation and Aim: Mathematical models of HIV dynamics are described by systems of nonlinear ordinary differential equations (ODE) and partial differential equations (PDE) and characterized by a set of parameters. These parameters describe virus natural death rate, target cell production rate, treatment efficacy reduction, etc. It is necessary to find the set of parameters for constructing an individual treatment plan. For this, an approach of inverse problem theory [1] in which the unknown model parameters are determined from the available experimental data (observations) is used.

Methods and Algorithms: The problem of estimating the HIV-infection parameters and the immune response using additional measurements of the concentrations of T-lymphocytes, free virus, and immune effectors at fixed times for mathematical models of HIV dynamics based on ODE [2] and PDE [3] are investigated numerically. The stability of the inverse problem solution is analyzed using the singular value decomposition for linearized matrix of the inverse problem. The state variable observations are different from each other by orders of magnitude, intuitively, it is critical that the estimation scheme take this into account. One way to do this is by appropriately weighting the states in a least squares cost criterion. A genetic algorithm for solving a least squares minimization problem on iteration of least squares method is investigated. To determine the level of error in the solution of the inverse problem, the confidence intervals of all parameters are obtained and analyzed.

Results: The numerical solution of the inverse problem of determining four individual parameters of patient for the mathematical model of HIV dynamics are obtained and analyzed using the combination of least square method and genetic algorithm.

Conclusion: It is shown that the common relative accuracy error of the four parameters identification is sufficiently small for a good mathematical model that has a solution quite close to the additional noisy measurements. It is shown that system of PDE describes the HIV dynamic more precisely then the system of ODE.

Acknowledgements: This work was supported by the President Grant of Russian Federation (No. MK-1214.2017.1) by the Ministry of Education and Science of Russian Federation and by the grant No. 18-71-10044 of Russian Scientific Found (RScF).

References

- 1. Kabanikhin S.I. (2012) Inverse and Ill-Posed Problems: Theory and Applications. Berlin/Boston: de Gruyter.
- 2. Adams B.M., Banks H.T. et al. (2005) HIV dynamics: Modeling, data analysis, and optimal treatment protocols. Journal of Computational and Applied Mathematics, 184:10-49.
- 3. Chalub F.A.C.C., Souza M.O. (2011) The SIR epidemic model from a PDE point of view. Mathematical and Computer Modelling. 53:1568-1574.