

Mathematical modeling and identifiability aspects in epidemiology

Krivorotko O.^{1, 2, 3*}, Kabanikhin S.^{1, 2, 3}, Zyatkov N.¹, Sosnovskaia M.²

¹ *Institute of Computational Mathematics and Mathematical Geophysics, SB RAS, Novosibirsk, Russia*

² *Novosibirsk State University, Novosibirsk, Russia*

³ *Sobolev Institute of Mathematics, SB RAS, Novosibirsk, Russia*

* *krivorotko.olya@mail.ru*

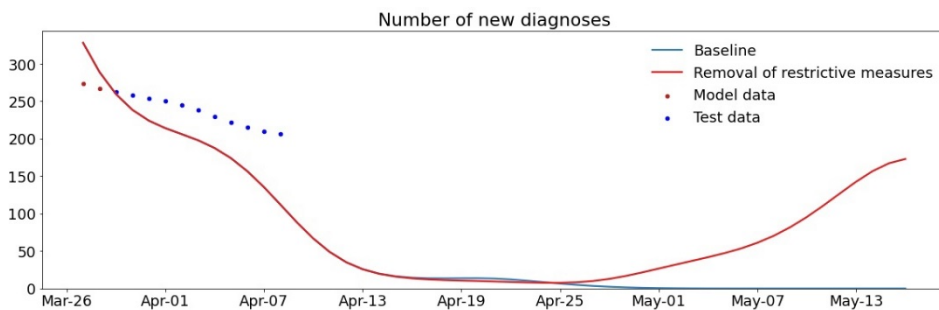
Key words: epidemiology, compartment models, agent-based modelling, stochastic models, data analysis, machine learning, optimization, regularization, identifiability, inverse problem, COVID-19, forecasting scenarios, high-performance computing

Motivation and Aim: Mathematical modeling of the spread of epidemics is an important tool for analyzing scenarios of infectious disease in the fixed region subject to external influences (restrictive measures, vaccination, virus mutation). Disease spread models are described by differential equations (compartment [1], reaction-diffusion and stochastic models), graph structure (agent-based models) with control and are characterized by their coefficients, individual for a particular disease and region. The aim of the work is to construct algorithms for identifying unknown parameters of compartment and agent-based models using additional information about the number of diagnosed, hospitalized, deceased cases at fixed points in time.

Methods and Algorithms: The problem of identification of parameters (the inverse problem) was reduced to the solution of the minimization problem of the misfit function. The inverse problem was solved by several methods and algorithms:

1. A sensitivity-based identifiability analysis of the selected model is performed [2, 3]. As a result, the intervals of variation of unknown parameters are reduced. The probability of hospitalization has been chosen from the web-site Invitro (concentration of IgG antibodies).
2. The regularization algorithm for solving of the inverse problem based on the identifiability analysis is developed using parameter variation limits, a priori information, etc.
3. The stochastic optimization: Tree-structured Parzen Estimator [4], nature-inspired algorithms (genetic, differential evolution, particle swarm), methods of data assimilation, big data analysis and machine learning are applied to solve the minimization problem.

Results: The agent-based model was constructed for describing the spread of COVID-19 and the scenarios of its propagation in the nearest 45 days in the Novosibirsk region with external influences [4, 5]. The parameters of agent-based model (infection rate, date of change in the infection parameter, test probability, and initial number of asymptomatic patients) were identified using additional data about number of daily diagnosed and deceased cases from March 12, 2020 to March 31, 2022 (red dots). The figure shows two scenarios of changes in the number of diagnosed cases in Novosibirsk region from April 1 to May 15, 2022: the baseline scenario (blue line) and a removal of restrictive measures (red line). Blue dots (April 1 to April 8, 2022) are the test real data that do not used in inverse problem solution.



Conclusion: It is shown that the number of diagnosed cases will increase from April 25, 2022 due to removal of restrictive measures, i.e. cancellation of wearing masks, social distance, isolation (red line). In this case, up to 150 diagnosed cases of COVID-19 are expected by mid-May 2022.

Acknowledgements: The study is supported by the Russian Foundation for Basic Research (project No. 21-51-10003) and by the Council for Grants of the President of the Russian Federation (project MK-4994.2021.1.1).

References

1. Krivorotko O.I., Kabanikhin S.I., Zyatkov N.Yu., Prihodko A.Yu., Prokhoshin N.M., Shishlenin M.A. Mathematical modeling and forecasting of COVID-19 in Moscow and Novosibirsk region. *Numer Anal Appl.* 2020;13(4):332-348.
2. Krivorotko O.I., Andornaya D.V., Kabanikhin S.I. Sensitivity analysis and practical identifiability of some mathematical models in biology. *J Appl Ind Math.* 2020;14(1):115-130.
3. Krivorotko O.I., Kabanikhin S.I., Sosnovskaya M.I., Andornaya D.V. Sensitivity and identifiability analysis of COVID-19 pandemic models. *Vavilov J Genet Breed.* 2021;25(1):82-91.
4. Krivorotko O., Sosnovskaia M., Vashchenko I., Kerr C., Lesnic D. Agent-based modeling of COVID-19 outbreaks for New York state and UK: parameter identification algorithm. *Infect Dis Model.* 2022;7:30-44.
5. Kerr C.C., Stuart R.M., Mistry D., Abeysuriya R.G., Rosenfeld K., Hart G.R. et al. Covasim: An agent-based model of COVID-19 dynamics and interventions. *PLoS Comput Biol.* 2021;17(7):e1009149.