Mathematical Methods and Models in Biosciences
June 18-23, 2023, Pomorie, Bulgaria
https://biomath.math.bas.bg/biomath/index.php/bmcs

Construction of a new infectious disease model using the time delay

Eunjin Eom[1], Siwon Ryu[2], Boseung Choi[3]

[1]Department of Economic Statistics, Korea University,
Sejong 30019, Republic of Korea
eej0417@korea.ac.kr

[2]Department of Economic Statistics, Korea University,
Sejong 30019, Republic of Korea
viewpit96@korea.ac.kr

[3]Division of Big Data Science, Korea University,
Sejong 30019, Republic of Korea
cbskust@korea.ac.kr

In this research, we developed a novel approach to construct a stochastic epidemic model based on the compartment of the SEIR model. This model is considered more realistic than the SIR model because it takes into account that an individual who has just been infected with the disease does not immediately transmit the disease to another individual. When it takes a longer time for an infected person to spread the disease to others, we constructed the infectious disease model that reflects this time interval as a time delay. In general, a time delay means that an infected person may not spread the disease to others for a certain period of time, rather than immediately spreading it to others after being infected. When we don't take into account the time delay in the epidemic model, the infected person immediately spreads the disease to others, so the predicted rate of spread can be excessively high. However, with the time delay considered, the infected may not spread the disease to others for a certain period of time, so the predicted rate of spread may be more realistic.

We considered a time delay distribution that estimates how long each infected person is not able to transmit the disease to another person. We performed the Bayesian method to estimate the epidemic model with time delay and applied it to the COVID-19 data in Seoul, Korea in 2020. The time delay-considered model showed a more accurate and explainable prediction for real disease spread data, especially for highly contagious diseases or when there are high numbers of infections.

Keywords: bayesian model, epidemiology, Gillespie algorithm, mathematical modeling, time delay