

A probabilistic description of the effect of vaccination in a Bayesian model of COVID-19 transmission dynamics

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Abstract

Bayesian probabilistic models for COVID-19 transmission dynamics have been very efficient to interpret early data from the beginning of the pandemics [1]. Using this approach, we showed that the impact of the non-pharmacological measures was clearly different in each country [2]. We further extended this initial model for the analysis of multiple periods of different transmission rates, enabling the inclusion of an arbitrary number of non-pharmacological measures. The algorithm computed the evolution of the daily number of infections by fitting a SEIR model to the observed daily deaths, in a Bayesian framework, using MCMC optimization to obtain the a posteriori distribution for the parameters that best described the impact on the transmission rate of each intervention measure. The model was successfully applied to a total of 30 European countries, obtaining good fit results and conclusions related to the impact of the different interventions that were consistent with results from other studies. Interestingly, the model also estimated the percentage of immune population required to reach the herd immunity in the different countries, which is a valuable tool to understand the evolution of the pandemics on the long term and help in future worldwide control strategies.

Here we show how we extended the model to include the effect of vaccination and the impact of the different virus variants on the transmission dynamics. Based on epidemiological evidence, we have used different probabilistic curves to estimate the degree and duration of the vaccination impact on the transmission, considering the different vaccine doses. We will discuss here the effect of using different vaccination parameters and probabilistic curves on the general transmission model.

The model successfully captures the positive impact of the vaccination on the evolution of the disease, takes into account the immunity of the recovered population and considers specific transmission parameters for the different virus variants.

References

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