Bayesian mechanistic model of COVID-19 transmission dynamics for the estimation of the impact of non-pharmacological measures

Javier Blecua, Juan Fernandez-Recio
Instituto de Ciencias de la Vid y del Vino (ICVV),
CSIC-Universidad de La Rioja-Gobierno de La Rioja
javier.blecua@alum.unirioja.es, juan.fernandezrecio@icvv.es

Brief description:

A new mechanistic model that describes the transmission dynamics of COVID-19 was applied to estimate the effect of the non-pharmacological measures by means of Bayesian analysis methods. The consistent results obtained for a total of 32 European countries, with data following very different patterns, confirmed that the model used is an appropriate method for describing the present and future evolution of the disease.

Keywords:

COVID-19 modelling, non-pharmacological measures, mechanistic model, Bayesian analysis,

Abstract:

COVID-19 (coronavirus disease 2019) is a pandemic disease caused by a new type of coronavirus called SARS-CoV-2, which has caused unprecedented medical, economical and social burden worldwide for the last two years. A variety of models to describe the transmission dynamics of the virus and the impact of non-pharmacological measures have been reported. Among them, Bayesian mechanistic models using MCMC optimization have shown good description of the transmission dynamics and have potential for accurate predictions of future evolution of the pandemics. In our group, we have been working on optimizing a previously reported COVID-19 transmission model, which has been extended here for the analysis of multiple periods of different transmission rates, enabling the inclusion of an arbitrary number of non-pharmacological measures. The algorithm computes the evolution of the daily number of infections by fitting a SEIR model to the observed daily deaths, in a Bayesian framework, to obtain the *a posteriori* distribution for the parameters that best describe the impact (positive or negative) on the transmission rate (R_t) of each intervention measure.

The model was successfully applied to a total of 32 European countries in which available data, such as daily cases and deaths as well as the measures imposed to the population to try to control the disease transmission, could be automatically downloaded and processed. In all these countries, the observed indicators for the evolution of the disease were following very different patterns, and a large variety of measures were imposed at different periods of time. The initial results showed good consistency in the estimation of the impact of the major measures, but there were many other measures with small, uncertain impact. After grouping similar measures to reduce the number of variables, results were more consistent with available information from other studies. For example, the results for the first wave of the pandemic indicate that the most effective measures were those related to the stay-at-home orders and recommendations (lockdown), the measures applied jointly in March 2020 and the mandatory use of masks. However, the results for more recent data have highlighted the need for further updates of the model, such as the inclusion of the effect of vaccination on the evolution of the disease. Interestingly, the model also estimates 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.

All details about this work are available in *http://jblecua.spdns.org:9095/* (user: *tfm*, password: *tfm*).

Figure:

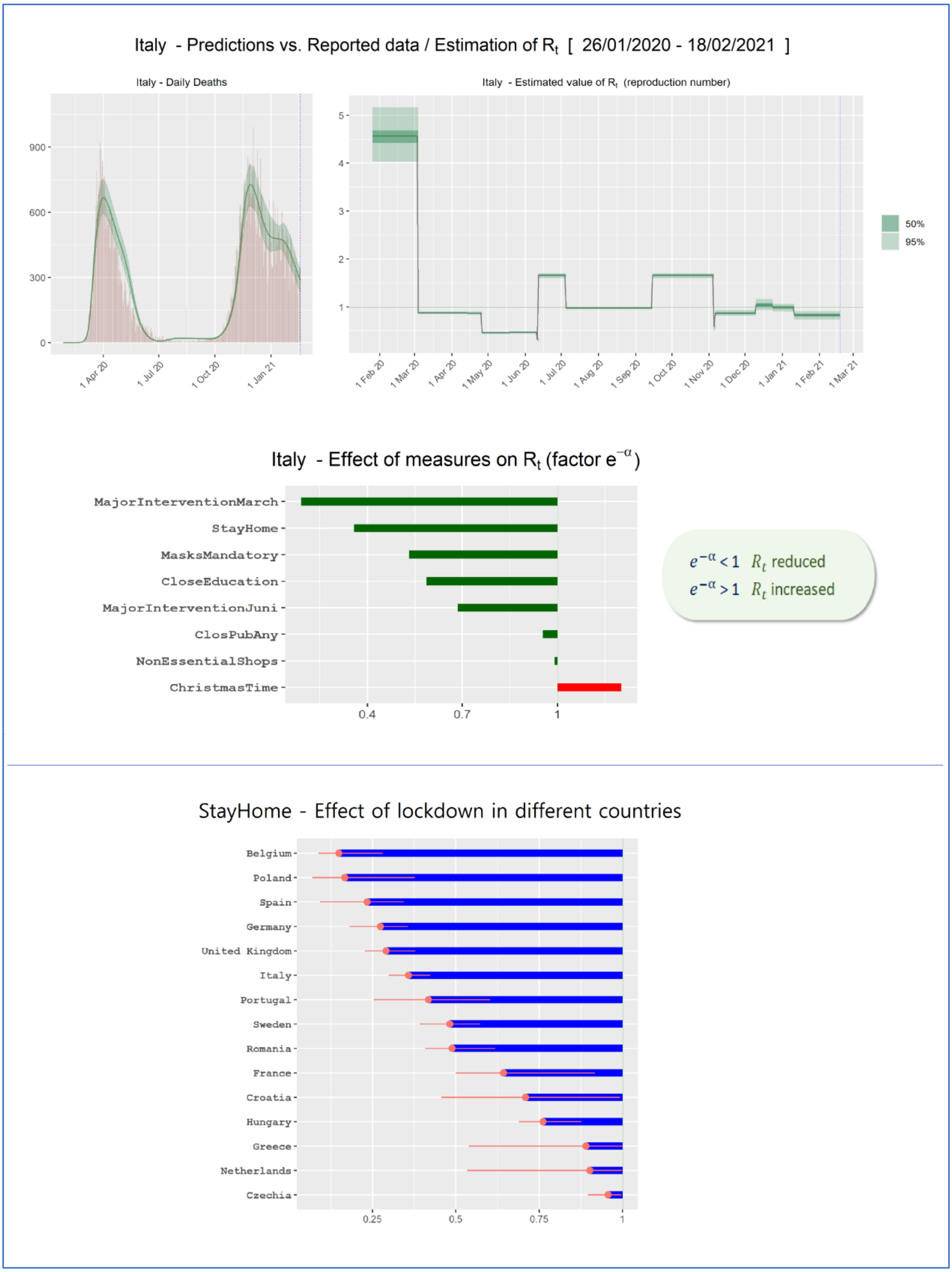

Figure 1 - Data fit / Estimations: Reproduction Number, effect of different measures, comparison between different countries