A SEIR model with time-varying coefficients for analysing the SARS-CoV-2 epidemic

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April 30, 2020

In this study, we propose a time-dependent Susceptible-Infected-Exposed-Recovered (SEIR) model for the analysis of the SARS-CoV-2 epidemic outbreak in three different countries, the United States of America, Italy and Iceland using public data inherent the numbers of the epidemic wave. Since several types and grades of actions were adopted by the governments, including travel restrictions, social distancing, or limitation of movement, we want to investigate how these measures can affect the epidemic curve of the infectious population. The parameters of interest for the SEIR model were estimated employing a composite likelihood approach. Moreover, standard errors have been corrected for the temporal dependence. The adoption of restrictive measures results in flatten epidemic curves, and the future evolution indicated a decrease in the number of cases.

1. INTRODUCTION

The use of epidemic models permits to simulate disease transmission dynamics to detect emerging outbreaks and to assess public health interventions (Unkel et al., 2012; Boily et al., 2007). With

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the scope to describe the dynamics of epidemics, standard methods, for example, the SIR model (Anderson et al., 1992), the population is divided into portions of subjects on the bases of their relation concerning the epidemic vector; the focus regards dynamic elements such as the depletion of the susceptible portion to the infected one or the possible evolution of the rate of immunization.

However, the standard SIR model, and other extensions as the SEIR model, do not take into account the time-varying nature of epidemics and several attempts were made to overcome this limitation (Dureau et al., 2013; Boatto et al., 2018; Kucharski et al., 2020). In particular, most extensions were conducted for adapting the SIR model to specific case studies (Liu and Stechlinski, 2012; Peng et al., 2020) or to include time-varying coefficients with the scope to estimate epidemic dynamics (Hooker et al., 2011; Chávez et al., 2017; Fang et al., 2020).

This paper considers a flexible extension of the SEIR model, which incorporates the temporal dynamic connected to the transmission rate parameter, one on the most critical indicators for epidemiologists and at the basis of the basic reproduction number R_O. Also, this method allows us to make considerations about both the trend and the prediction of the number of infected cases to evaluate how any possible influencing factors, i.e., the presence of a vaccine or restriction measures taken by the central authorities, can affect an epidemic outbreak (Haas, 2020).

The proposed method is applied to the 2019–20 coronavirus pandemic, the COronaVIrus Disease 2019 (COVID-19), caused by a Severe Acute Respiratory Syndrome CoronaVirus 2 named SARS-CoV-2 (World Health Organization et al., 2020). The World Health Organization declared the outbreak to be a Public Health Emergency of International Concern on January 30, 2020 and recognized it as a pandemic on March 11, 2020 (Team et al., 2020).

It is important to mention that with the scope of understanding what the epidemiological dynamics and the possible evolutions of the SARS-CoV-2 epidemic are, a consistent number of proposals has been presented, especially concerning SEIR models with different time-varying parameter specifications (Hong and Li, 2020; Petropoulos and Makridakis, 2020; Piccolomini and Zama, 2020; Wu et al., 2020; Zhang et al., 2020).

To study how country-based mitigation measures influence the course of the SARS-CoV-2 epidemic (Anderson et al., 2020), we have looked to the on-going epidemic in the three countries (Italy, Iceland and the United States of America) where the adopted mitigation measures have been different (Remuzzi and Remuzzi, 2020; Gudbjartsson et al., 2020; Dong et al., 2020).

The reference datasets are presented in Section 2, while the proposed model and the statistical

inference are illustrated in Section 3 and Section 4. In Section 5, we collect our results for the different countries with a proposal for the forecast. We end the paper with a brief discussion in Section 6.

2. COVID-19 DATASETS

According to the aim of this paper we used the screening data of daily new cases and the number of the total amount of positive cases of SARS CoV-2 according to three countries in different phases of an epidemic outbreak. For each country, we considered the data in a time window that starts about 15 days before the restriction measure is adopted and the sources of the data are described in the Appendix.

At the time of writing, the United States of America (US) was in the growing phase of the epidemic outbreak with an increasing trend of new cases. In the US every single state adopted a stay at home measures with a different starting date: the earliest state was Puerto Rico (March 15 2020), followed by California (March 19) and New York (March 20) where the highest increase of new cases was, subsequently, recorded. Every single state could adopt a different and inhomogeneous panel of restrictive measures. Data were analyzed from March 4, 2020, to April, 27 2020 for a total of 55 days of observation. At the end of the considered period we reported 820,514 current positive cases, 56,259 deaths, and a total of 988,197 confirmed cases nationwide.

Italy was a country in the middle phase where a first stabilization of the SARS-CoV-2 incidence was reported after the restriction measure, and, at the time of writing, we observed the beginning of a decreasing trend. The Italian Government adopted a national home lockdown restriction on March 9, 2020, for all the population followed by more severe measures on March 11, and ordered all nonessential businesses closed on March 22. Data were analysed from January 23, 2020, to April, 27 2020 for a total of 66 days of observation. At the end of the considered period, we reported 105,813 current positive cases, 26,977 deaths, and a total of 199,414 confirmed cases.

Finally Iceland was a country in the ending phase, where after a stabilization, the incidence of new cases was going down, and the epidemic outbreak was probably going to the end. The Iceland government adopted stricter measures to slow down the spread of SARS-CoV-2 on March 16, 2020, with an active searching strategy of new cases that lead to perform oropharyngeal swabs to about 10% of the entire population. We considered data from February 29, 2020, to April, 27 2020, for a total of 59 days of observation. At the end of the considered period, we reported 158 current positive cases, 10 deaths, and a total of 1,792 confirmed cases.

3. SEIR MODEL WITH TIME-VARYING COEFFICIENTS

3.1 SEIR model

We start introducing the SEIR model, which is one the most used extensions of the standard SIR model, an ODE-based epidemiological model (Kermack and McKendrick, 1927). Traditionally the SEIR model divides a population of hosts into four classes: Susceptible (S), Exposed (E), Infected (I) and Recovered (R). However in our framework, the last class should collect all the subjects which move outside the (I) status, i.e. recovered and deceased; for this reason, hereafter we denote (R) as Removed status. The model describes how the different portions of the population change over time t. In the standard SEIR model, deaths are modelled as flows from the S, E, I, or R compartment to outside, because natural deaths are normally not monitored. If S, E, I, and R refer to the numbers of individuals in each compartment, then these "state variables" change according to the following system of differential equations:

$$\frac{d}{dt}S(t) = \mu(N - S(t)) - \beta\frac{S(t)I(t)}{N} \tag{1a}$$

$$\frac{d}{dt}E(t) = \beta\frac{S(t)I(t)}{N} - (\mu + \sigma)E(t) \tag{1b}$$

$$\frac{d}{dt}I(t) = \sigma E(t) - (\mu + \gamma)I(t) \tag{1c}$$

$$\frac{d}{dt}R(t) = \gamma\, I(t) - \mu\, R(t) \tag{1d}$$

In the equations (1) N is the total population, μ is the mortality rate, β is the transmission rate, σ is the exposed to infectious rate, and γ is the removal rate that can broadly assumed to be the sum of $\gamma_R + \gamma_D$, where γ_R and γ_D are the recovery and the mortality rate, respectively.

In general, the parameters σ and γ are strictly dependent on the specific disease causing the epidemic and on the fraction of susceptible population. The parameter σ is set equal to η^{-1} where η is the incubation period which may be higher for asymptomatic subjects; γ is the recovery rate calculated as $\gamma = \rho^{-1}$ where ρ is the average duration of the disease.

Moreover, unlike the full specification, we do not consider the effect of births in model (1) and, therefore, $\sigma E(t)$ represents the number of new infected.

Based on this parametrization we can define the reproduction number, R_O, as

$$R_O = \frac{\beta\sigma}{(\gamma + \mu)(\sigma + \mu)}.$$

The index conveys the strength of contagious in an epidemic outbreak. In the case of both σ and $\gamma \gg \mu$, R_O can be approximated by β/γ.

3.2 Time-varying parameter specification

The standard SEIR model does not assume that the parameters μ, β, σ, and γ change over time. However, the characteristics of an epidemic suggest us that these parameters can vary. In particular, the overall mortality rate μ may increase if the number of deaths in a population directly or indirectly attributable to the disease (i.e., the insufficient capacity of health services) rises; the β rate may vary according to social distancing policies or, even, the isolation of infected people.

We aim to evaluate as the actions taken by the governments, and how a different degree of travel restrictions, social distancing or limitation of the people movement can affect the epidemic curve of the infectious population. Our working hypothesis is that if there is an effect of actions, they only affect the transmission rate of the epidemic, β. For this reason, we propose to modify this parameter over time, namely

$$\frac{d}{dt}S(t) = \mu(N - S(t)) - \beta(t)\frac{S(t)I(t)}{N} \tag{2a}$$

$$\frac{d}{dt}E(t) = \beta(t)\frac{S(t)I(t)}{N} - (\mu + \sigma)E(t) \tag{2b}$$

$$\frac{d}{dt}I(t) = \sigma E(t) - (\mu + \gamma)I(t) \tag{2c}$$

$$\frac{d}{dt}R(t) = \gamma\, I(t) - \mu\, R(t) \tag{2d}$$

The function $\beta(t)$ takes positive values between 0 and 1 and we consider the following $logit()$ specification

$$logit(\beta(t)) = \sum_{k=1}^{K} \psi_k N_k(t), \tag{3}$$

where $N_k(t)$, $k = 1, \ldots, K$, are K natural cubic spline basis functions evaluated at $K - 2$ equally spaced knots in addition to the boundary knots; the $logit()$ function is defined as $logit(x) = \log\left(\frac{x}{1-x}\right)$. The representation in (3) has the advantage that the estimation of $\beta(t)$ reduces to the estimation of the coefficients ψ_k. We refer to the next subsection for a short discussion about the number of knots and their positions. The time-dependent transmission rate $\beta(t)$ allows us to define a time dependent version R_O (the basic reproduction number) as follows

$$R_O(t) = \frac{\beta(t)}{\gamma}.$$

This index permits to evaluate the strength of contagious over a temporal window comparing $\beta(t)$ with the removal rate γ. In the same way of $\beta(t)$, a $logit()$ specification was also considered for γ

as $logit(\gamma) = \gamma^*$, which ensures to the rate γ values comprised between 0 and 1.

The system (2) is a system of nonlinear Ordinary Differential Equations (ODEs), which must be solved numerically. In this paper we use the ODE solver lsode (Hindmarsh, 1983) as it has implemented in the R package `deSolve`. If we suppose that μ and σ are known parameters, the (numerical) solutions $S(t;\theta)$, $E(t;\theta)$, $I(t;\theta)$, an $R(t;\theta)$ depend on the (vector of) parameters $\theta = (\psi_1, \ldots, \psi_K, \gamma^*)$.

4. STATISTICAL INFERENCE

The datasets of the different agencies in the world that publish epidemic data every day contain at least three time series: the total number of infected, the number of dead, the number of recovered (see section 2 for more details). We derive from these time series the daily number of current positive cases $Y(t)$ and the daily number of new positive cases $Z(t)$, recorded at day t, $t = 1, \ldots, T$.

Usually, the time series are supposed to be realizations of a stochastic version of the compartmental models. The different versions can be broadly classified into continuous models and discrete models. In the first group fall the continuous-time Markov chains (CTMCs) and the stochastic differential equations (SDEs) (Allen, 2008). In the second group a discrete-time approximation to the stochastic continuous-time model is considered (Lekone and Finkenstädt, 2006). There exists an extensive literature on calibrating the stochastic models against time-series with different inferential approaches (Finkenstädt and Grenfell, 2000; Ionides et al., 2006; Hooker et al., 2011; Andersson and Britton, 2012; Dureau et al., 2013).

Instead in this paper we follow the simplest idea that the solutions of the system (2) are actually the expectations at days $t = 1, \ldots, T$ of as many counting random variables. More precisely we model the observed counts $\{Y(t), Z(t)\}$, as

$$Y(t) \sim \text{Poisson}(I(t;\theta)) \tag{4a}$$

$$Z(t) \sim \text{Poisson}(\sigma E(t;\theta)). \tag{4b}$$

Then the estimate of the parameters $\theta = (\psi_1, \ldots, \psi_K, \gamma)$ are obtained by maximizing the independence loglikelihood (Chandler and Bate, 2007)

$$\begin{aligned} cl(\theta) &= \sum_{t=1}^{T} Y(t) \log I(t;\theta) - I(t;\theta) + Z(t) \log(\sigma E(t;\theta)) - \sigma E(t;\theta) \\ &= \sum_{t=1}^{T} cl(\theta;t). \end{aligned}$$

Note that $CL(\theta)$ is not a 'true' log-likelihood but an instance of a composite likelihood (Lindsay, 1988) since it does not seem reasonable to assume that $Y(t)$ and $Z(t)$ are mutually and temporally independent. However, even though the model is not correctly specified, the maximum composite likelihood estimator, $\widehat{\theta}$, is still a consistent and asymptotically Gaussian estimator with asymptotic variance $V(\theta)$ under mild conditions (Chandler and Bate, 2007; Jacod and Sørensen, 2018).

The variance $V(\theta)$ can be estimated by the sandwich estimator $\hat{V} = \widehat{B}^{-1}\widehat{M}\widehat{B}^{-1'}$. The 'bread' matrix is given by $\widehat{B} = T^{-1}\sum_{t=1}^{T}\nabla u(\hat{\theta};t)$ with $u(\hat{\theta};t) = \nabla cl(\hat{\theta};t)$. In the presence of time-dependence the 'meat' $\hat{M}$ is given by the heteroskedasticity and autocorrelation consistent (HAC) estimator

$$\hat{M} = T^{-1}\sum_{t=1}^{T}\sum_{s=1}^{T} w_{|t-s|}\nabla u(\hat{\theta};t)\nabla u(\hat{\theta};t)^{\top}$$

where $w = (w_0, \ldots, w_{T-1})$ is a vector of weights (Andrews, 1991).

With the aim of forecasting the spread of the epidemic outside the observed period, the number and the positions of knots in (3) play a crucial role. The higher the number of nodes, the less smooth the function $\beta(t)$. In this way, however, there is a risk of over-fitting the data. On the other hand, the trend of the $\beta(t)$ outside the observation time interval is mainly determined by the basis functions corresponding to the boundary knots.

We select the number of knots by maximizing the Composite Likelihood Information Criterion (Varin and Vidoni, 2005)

$$CLIC(\widehat{\theta}) = cl(\hat{\theta}) + \mathrm{tr}(\widehat{B}^{-1}\widehat{M}).$$

The criterion has strong analogy with the Akaike Information Criterion (AIC). In fact $cl(\hat{\theta})$ measures the goodnes-of-fit similarly to the log-likelihood and the penalty $\widehat{B}^{-1}\widehat{M}$ reduces to $-(K+1)$ if the model (4) is correctly specified, i.e if is the 'true' likelihood.

We could locate the internal knots to reflect policy interventions. However, it is very difficult to hypothesize the immediate effects of these policies and a simpler choice has been to place temporally equally spaced nodes. As for the boundary knots, it was chosen to place them at the beginning of the period and one week after the last observation available to obtain more stable estimates in the forecast period.

5. RESULTS

The epidemic outbreak showed different patterns in the selected time window: the current SARS-CoV-2 cases in the US were increasing reaching one million of infected, but a stabilization of the

number of daily new cases; in Italy, after an initial grow the number of newly infected, which reached 6.000 daily new cases, a drop up to 2,000 SARS-CoV-2 cases was been observed cases per day. In Iceland, the occurrence of new SARS-CoV-2 cases knew a modest peak, a decreasing trend and a limited number of new cases in the last considered day (Figure 1).

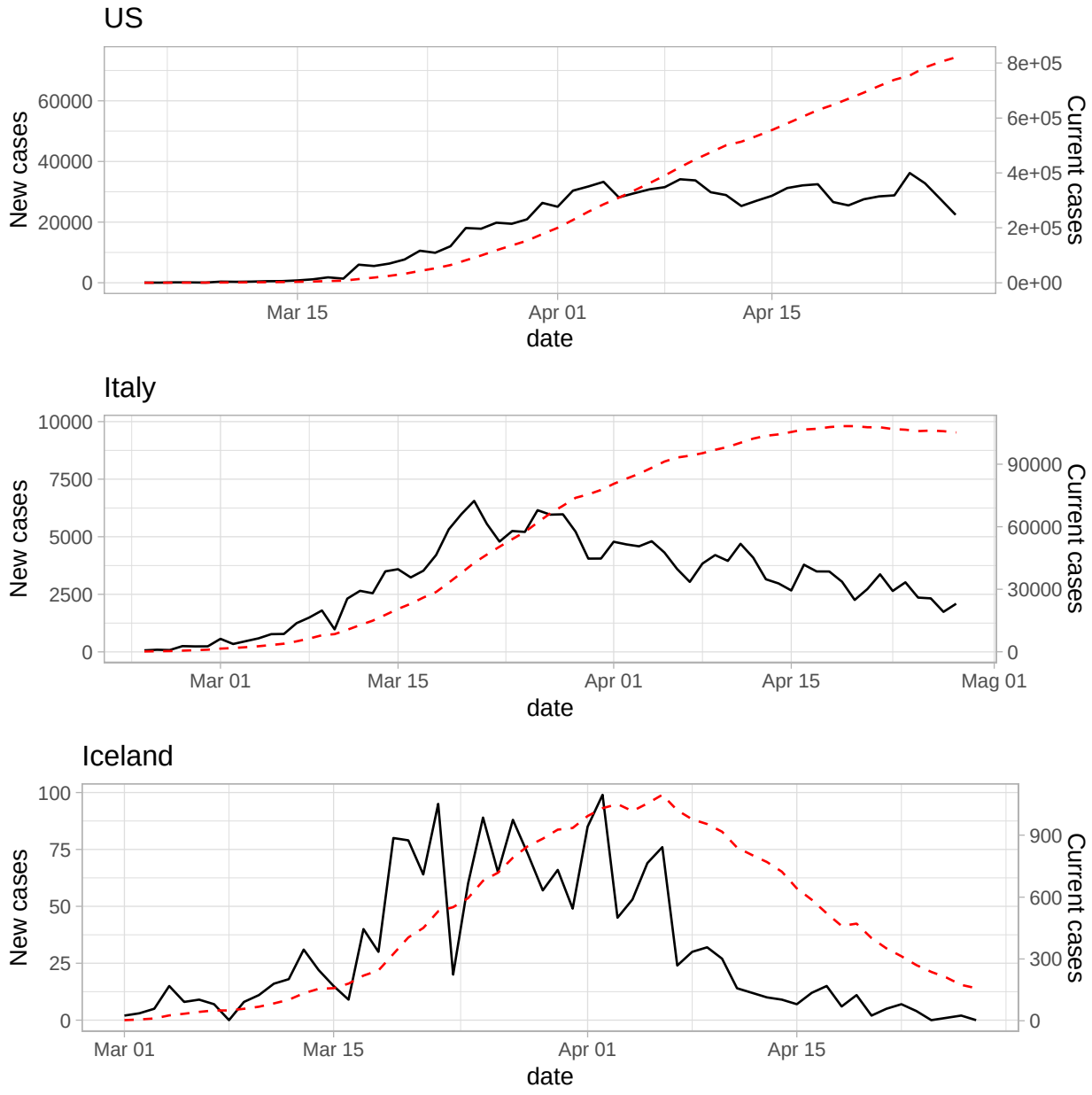

Figure 1: Daily new (solid black line) and current (dashed red line) cases of SARS-CoV-2 in (a) the US, (b) Italy and (c) Iceland.

In the literature the incubation duration of the SARS-CoV-2 was estimated as $\eta = 5.2$ (Wang et al., 2020) and therefore we set the specific parameter $\sigma = 1/\eta = 0.192$. The overall mortality

Country	γ	(95% CI)
the US	0.012	[0.009-0.014]
Italy	0.025	[0.023-0.027]
Iceland	0.084	[0.065-0.106]

Table 1: Estimated values of the γ parameter and its relative 95% Confidence Interval.

rate μ was calculated as $1/(\text{lifespan}) = 1/(365.25 \times \text{LE})$ where the Life Expectancy (LE) is 78.5 years in the US, 83.2 years in Italy and 82.2 years in Iceland, respectively. The total population (N) in 2020 was is 329.23 (US), 60.32 (Italy) and 0.36 (Iceland) millions of inhabitants. The starting values $S(0)$, $E(0)$, $I(0)$ and $R(0)$ for the numerical resolution of the system (2) were set as follows

- $I(0) = Y(1)$ i.e. the number of currently infected on the first day of the dataset (US: 142, Italy: 155, Iceland: 1);
- $R(0)$ equal to the number of currently recovered on the first day of the dataset (US: 7, Italy: 0, Iceland: 0);
- $E(0) = Z(1)/\sigma$ where $Z(1)$ is the number of new infected on the first day of the dataset (US: 68, Italy: 66, Iceland: 2);
- $S(0) = N - E(0) - I(0) - R(0)$.

On the basis of the CLIC we identified a different number of basis functions for $\beta(t)$, namely $K = 5$ for Italy and the US, $K = 3$ for Iceland.

The estimate of $\beta(t)$ (see Figure 2) showed an overall decreasing pattern of the transmission rate across the selected countries. In particular, in the US the estimate of $\beta(t)$ was closed to 0.8 in the initial period (about ten days) of the epidemic outbreak, denoting an uncontrolled situation, moving to values of approximately 0.1 after about 45 days of the epidemic, with a predicted scenario of a slightly increasing trend and a great amount of uncertainty. In Italy, the estimate of $\beta(t)$ was moving from initial values of 0.65 to value close to 0.05 after about 50 days of observations. The estimate of $\beta(t)$ were lower than those reported for the US. The estimate of $\beta(t)$ in Iceland showed a fast decreasing trend from values of 0.9 to about 0 at day 40. The 30-days prediction for $\beta(t)$ is pratically zero, denoting the end of the epidemic.

The estimates of γ ranged from a low rate in the US and Italy, 0.012 and 0.025 respectively, to a higher rate in Iceland, 0.084. Then the removal duration, i.e. the reciprocal of γ, was estimated

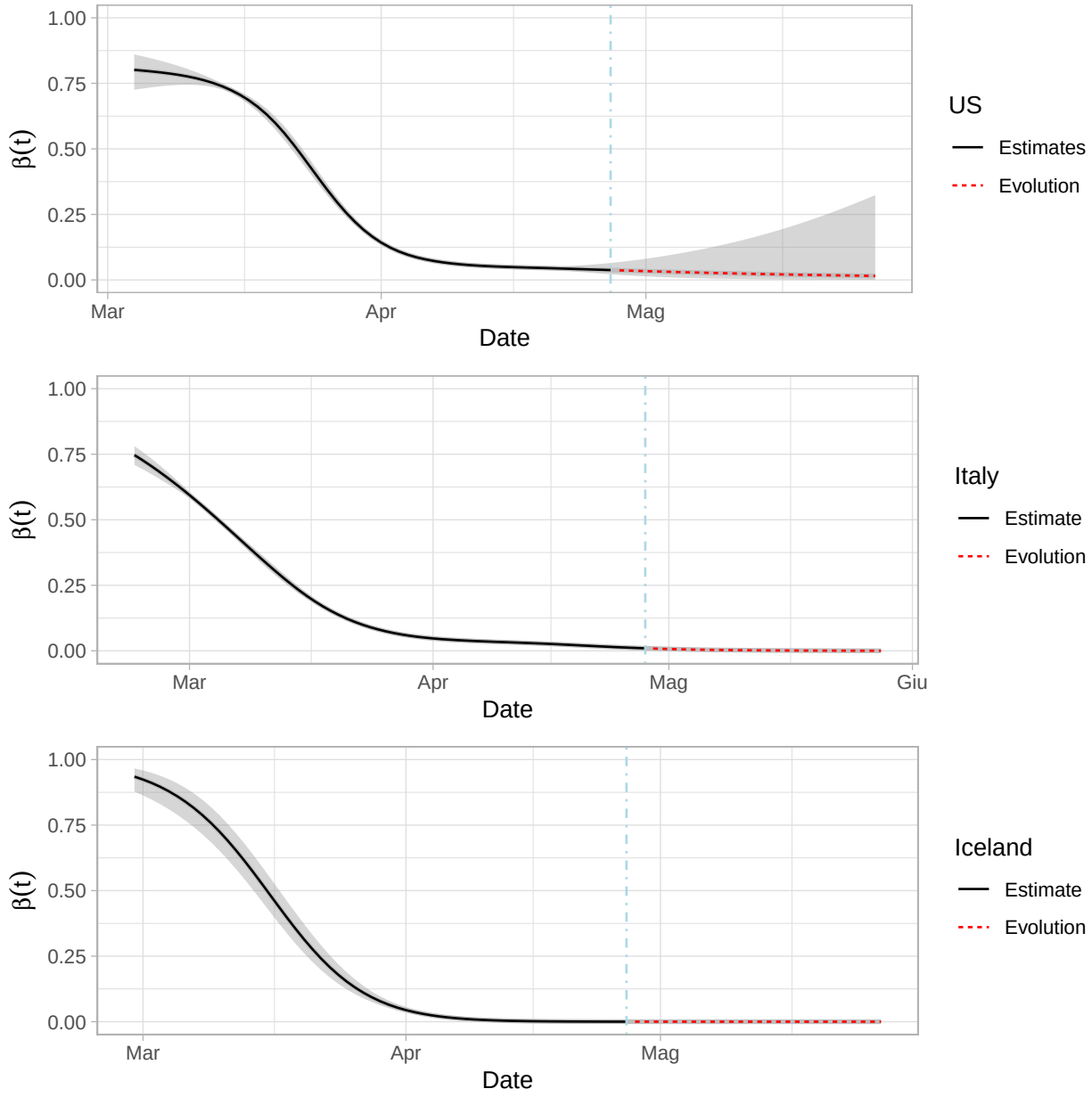

Figure 2: The estimate of $\beta(t)$ curves and 95% confidence bands (in grey colour) for the US, Italy and Iceland. The dashed line represent the 30-day predicted evolution.

at 86.9 days (95% CI: 70.7-106.8) for the US, at 40.2 days (95% CI: 37.6-43.1) for Italy and at 12.0 days (95% CI: 9.4-15.3) for Iceland.

The model fitting was deemed satisfactory (Figure 3 and Figure 4) both with respect to the number of new cases and to the cumulative positive cases. Our major findings were: in the US, the current positive cases were going to increase, reaching a probable maximum after the window of the next 30 days. In Italy, the epidemic outbreak had known its maximum in the number of

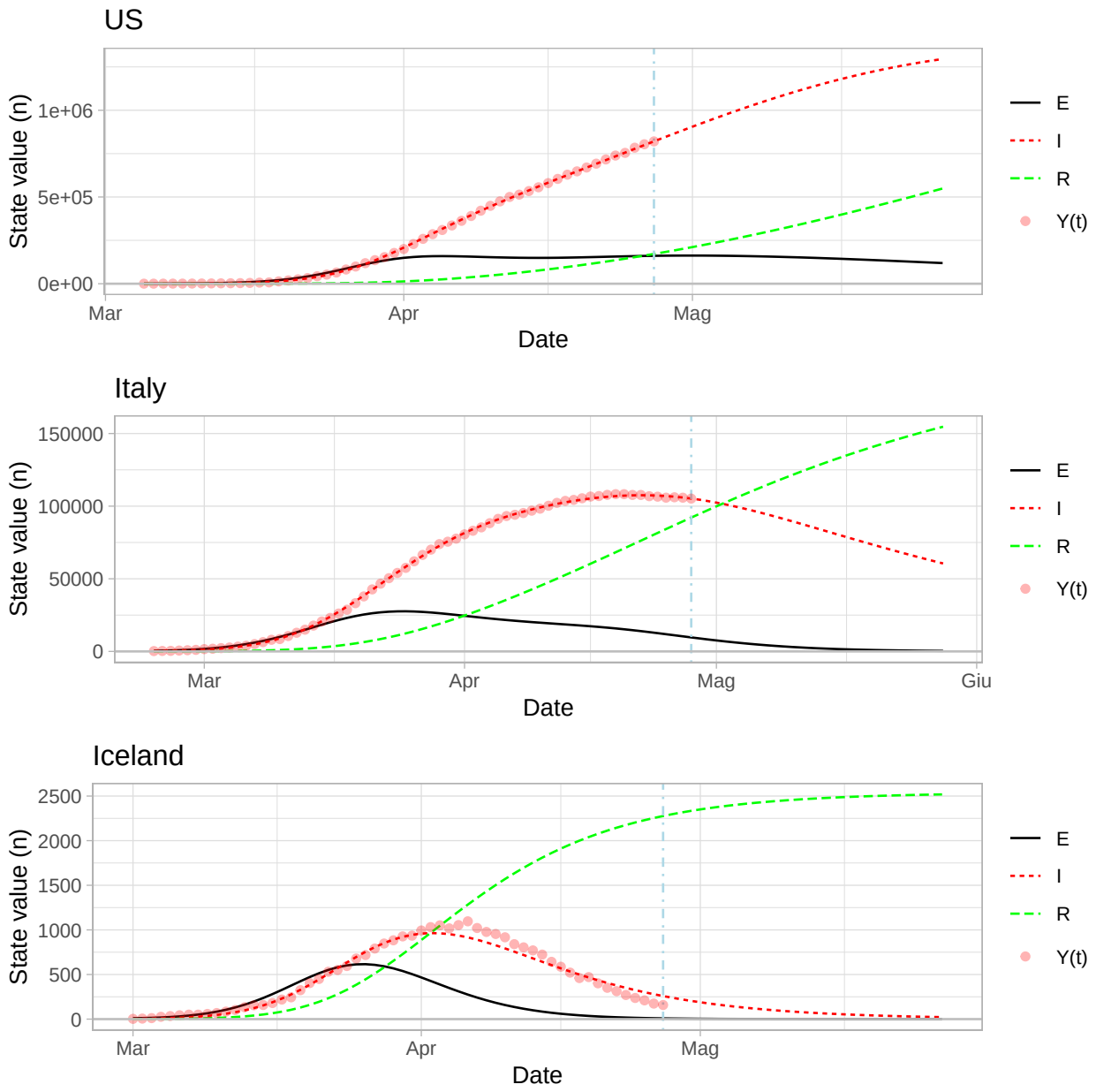

Figure 3: The expected number of Exposed, Infected and Recovered subjects for the US, Italy and Iceland, based on the model parameter estimates. The dotted points indicate the observed number of infected cases.

positive cases around April 20th, and the tendency was for a slight decline. In Iceland, the peak of positive cases was registered on April 10th, associated with a rapid decreasing phase and a low number of new cases in the last observed days; in this case, the SARS-CoV-2 epidemic was going to be overcome approximately at the end of May.

The estimated trend for $R_O(t)$ appears quite different among the selected countries (see Figure

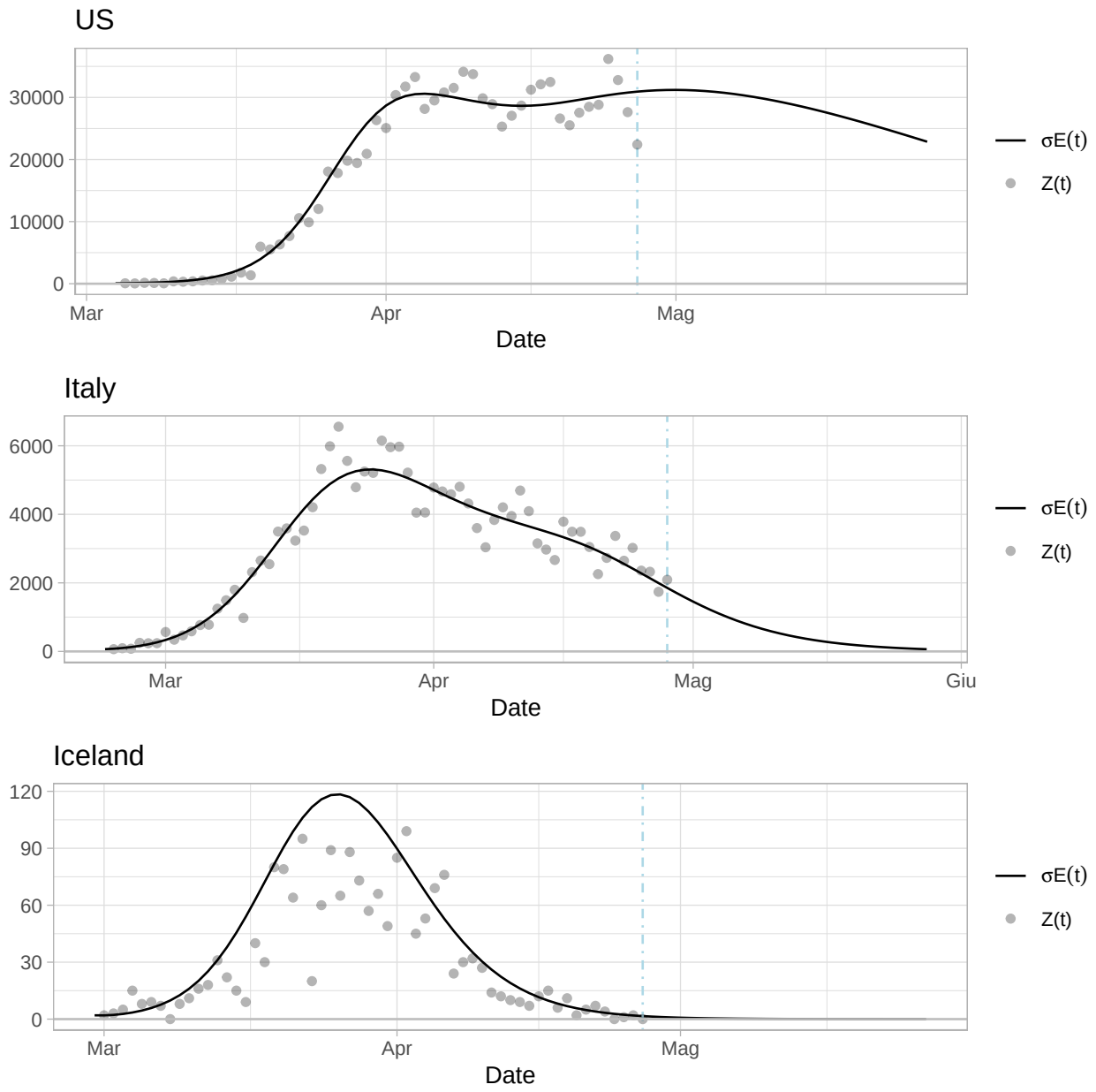

Figure 4: The expected number of new infected cases for the US, Italy and Iceland, based on the model parameter estimates. The dotted points indicate the observed number of new infected cases. The dashed line indicates the last day observed.

5). The value $R_O(t) = 1$ was reached on different dates in Iceland (March 28th) and in Italy (April 16th), while in the US is expected to be achieved only in the end of May.

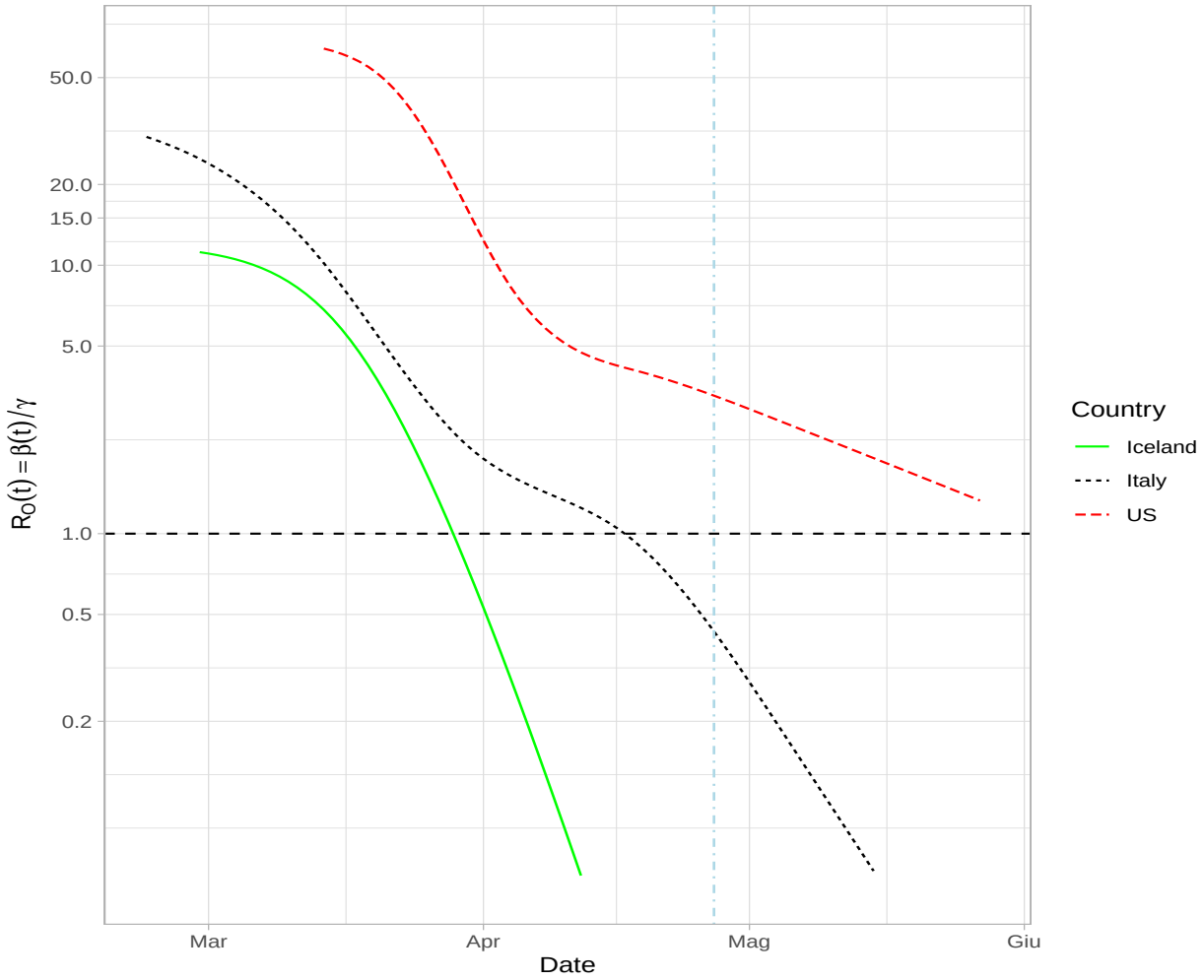

Figure 5: Estimated $R_O(t)$ values for the US, Italy, and Iceland and predicted evolution. The Y-axis is in the log-scale. The dashed lines indicate $R_O = 1$ and the last day observed, respectively.

6. DISCUSSION

International health organizations recommend to implement public health and social measures to slow or stop the spread of SARS-CoV-2, reaching the full engagement of all members of society (World Health Organization et al., 2020). Countries have adopted different public health and social measures depending on the local specific historical evolution of the SARS-CoV-2 pandemic and on their health system capacity. Our analysis considers data of three countries, the US, Italy and Iceland which have, on one side, different geographic and demographic characteristics and, on the other one, as many dissimilar approaches in terms of public health policies and restrictive measures concerning the on-going epidemic.

Our proposal allows us to estimate an epidemiological SEIR model with a time-varying trans-

mission rate ($\beta(t)$) with the scope to assess the timeline and the strength of the effects produced by the adopted restrictive measures. The removal rate, γ ,was estimated, considering both two different time series (daily new and current positive cases). We avoided considering estimates of clinical SARS-CoV-2 recovery rate and specific mortality rate calculated by others, with the scope to comment on the knowledge provided by the analysed data on the removal rate γ estimated by our model.

In the US, the transmission rate of SARS-CoV-2 was very high at the beginning of the considered temporal window, and its reduction appears to be later and slower in comparison with those observed in Italy and even more in Iceland. This difference may be viewed as a result of the approach adopted by the US in the epidemic onset based only on a containment strategy (Parodi and Liu, 2020).

It is essential, in this connection, to emphasise the importance that in the US, the COVID-19 onset began a few days later than Italy, where, on March 9, 2020, the Italian Government set Europe's first nationwide restriction on movement due to the incoming SARS-CoV-2 epidemic. The estimates on the Italian transmission rate confirming the control of the epidemic wave after approximately 20 days of home restrictions, but with a high mortality toll in comparison with the preceding Chinese epidemic (Rubino et al., 2020). A social distancing and passive testing of symptomatic cases was the Italian strategy to contain the epidemic. Positive cases with few symptoms were confined in home isolation. However, there was a consistent amount of asymptomatic, which remained undetected, contributing to spread the epidemic (Lavezzo et al., 2020; Flaxman et al., 2020).

Iceland has the advantage that the epidemic outbreak started later than Italy; we observed that the Icelandic transmission rate quickly moved to values close to 0 after only 15 days of the restrictive measures (Gudbjartsson et al., 2020). These results were mainly attributable to an active searching strategy of asymptomatic positive cases organized by the national health service, which lead to be tested about 6% of the Iceland population at the date of April 2, 2020. However, the presence of a free voluntary private screening program estimated that the fraction of undetected infections by the Icelandic health service ranged from 88.7% to 93.6% (Stock et al., 2020).

The estimated values for γ reflects both the locally adopted swab policy and the specific phase of the epidemic wave: in fact, the active monitoring in Iceland provide a reliable value for the removal rate that is of about 12 days in line with that measured in China (14 days, (Wang et al., 2020)); in

Italy, the controlling strategy implies that after a positive swab test, a control swab will be repeated after a period of home isolation implying a longer time to obtain the healing confirmation; in the US the low number of removed subject in comparison with the high increase in the incidence makes challenging a reliable estimation of the removal rate.

The proposed methods has become a standard approach to estimate the transmission rate in a dynamic context (Hong and Li, 2020; Petropoulos and Makridakis, 2020; Piccolomini and Zama, 2020; Wu et al., 2020; Zhang et al., 2020). The method has the double scope of having a real-time monitoring and of supplying possible evolution scenarios. The estimated fluctuations of $\beta(t)$ were driven by gradual changes in the behaviour of the population at risk as a consequence of the adopted restrictions. Respect to other specifications, our approach has the advantage of employing a basis of splines that allow us a high grade of flexibility for the estimation; we estimated the parameters for $\beta(t)$ and γ through a composite likelihood loss function considering the information provided by both the occurrence of new SARS-CoV-2 cases and the current positive cases; in order to cope with the possible presence of heteroscedasticity and autocorrelation in the data, we estimated consistent standard errors combining a sandwich variance estimator and a HAC correction.

There are several other limitations to our analysis. We used plausible biological SARS-CoV-2 parameters for the SEIR model based on updated numbers (i.e., σ), but these values may be refined as more comprehensive data become available. The predicted values for $\beta(t)$ are valid only in the absence of future changes to the restrictions, which is not likely to happen if an intermittent social distancing measures will be adopted (Ferguson et al., 2020).

Our results demonstrate that the transmission rate in the US, Italy, and Iceland showed a decline after the introduction of restriction measures. Despite this common trend, some differences in terms of timeline and impact are present. In particular, US experts argue that more helpful tools are needed in order to reach the control of the epidemic wave (Parmet and Sinha, 2020).

The adoption of restrictive measures results in flatten epidemic curves and thus the distribution of the SARS-CoV-2 cases in a more extended period, respect to an uncontrolled epidemic outbreak. In the absence of a specific vaccine, the high number of susceptibles and the relaxation of restrictions taken represent a cause of future outbreaks.

APPENDIX

Data sources

Iceland: John Hopkins University (`github.com/datasets/covid-19`), CSSE (2020).

Italy: Italian Civil Protection, (`github.com/pcm-dpc/COVID-19`), Morettini et al. (2020).

US: John Hopkins University (`github.com/datasets/covid-19`), CSSE (2020).

Software

The statistical analysis was carried using the R software (R Core Team, 2019). Results and figures can be reproduced using the companion code in `github.com/Paolin83/SARS-CoV-2_SEIR_TV_model`.

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