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Monitoring Covid-19 contagion growth in Europe

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Abstract

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Keywords: Contagion models, Covid-19, European countries, Poisson Autoregressive models, Reproduction number.

JEL classification: C21, C58, E44, G21.

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Abstract

We present an econometric model which can be employed to monitor the evolution of the COVID-19 contagion curve. The model is a Poisson autoregression of the daily new observed cases, and can dynamically show the evolution of contagion in different time periods and locations, allowing for the comparative evaluation of policy approaches. We present timely results for nine European countries currently hit by the virus. From the findings, we draw four main conclusions. First, countries experiencing an explosive process (currently France, Italy and Spain), combined with high persistence of contagion shocks (observed in most countries under investigation), require swift policy measures such as quarantine, diffuse testing and even complete lockdown. Second, in countries with high persistence but lower contagion growth (currently Germany) careful monitoring should be coupled with at least "mild" restrictions such as physical distancing or isolation of specific areas. Third, in some countries, such as Norway and Denmark, where trends seem to be relatively under control and depend on daily contingencies, with low persistence, the approach to restrictive measures should be more cautious since there is a risk that social costs outweigh the benefits. Fourth, countries with a limited set of preventive actions in place (such as the Netherlands, Switzerland, and the United Kingdom) may revise their positions if high values of contagion remain.

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1 Background

The spread of the COVID-19 virus at the beginning of 2020 caught many governments by surprise and unveiled a widespread lack of pandemic preparedness at the global and national level. In the absence of a pharmaceutical therapy or a vaccine for the virus, governments have inevitably focused on so-called Non-Pharmaceutical Interventions (NPIs), such as quarantine or isolation requirements for infected individuals, in the attempt to reduce the reproduction number (the average number of secondary cases each case generates), and thereby limit the number of new cases by preventing human-to-human transmission (so-called "suppression" strategy). In some countries, these measures have been very rigidly enforced, bringing entire cities in lockdown and generating very significant costs for the local economy, in the form of both a supply-side and a demand-side shock. Other countries have initially considered an alternative option (so-called “mitigation”), which entails allowing a partial continuation of economic activity, in the hope to mitigate the overall cost for society and achieve “herd immunity”, assuming that 60% of the population becomes infected with the COVID-19. Soon, also thanks to evidence produced by researchers in the form of an impact analysis of alternative scenarios (see [1]), this latter policy option appeared impractical, since the ensuing cost in terms of lives lost (an estimated 260,000 deaths in the United Kingdom only) would have been prohibitive.

In the current circumstances, given the absence of a vaccine and the incomplete information about several aspects of the virus (i.a., the reservoir and intermediate vehicles of the virus, the role of different risk factors, the dynamics of transmission and especially the role of asymptomatic transmission), governments operate under significant uncertainty. Against this background, data from countries where the virus has initially spread (notably China) are a precious source of information for the 188 countries that are currently fighting against the virus. The more data becomes available, the more policies can be formulated with the backing of evidence as regards the “curve” and the “peak” of the contagion. Comparative analysis of the spread of the virus in different countries is also essential to start drawing lessons on which policy mixes proved more effective, and which ones did not achieve the desired results. To the contrary, research on past pandemics is not particularly useful in this case, since the rate of contagion and the mortality rates of COVID-19 are different compared to HIV, SARS, H1N1, or Ebola.

Early attempts to model the contagion curve of the COVID-19 include ([2]), which predicted that the outbreak would peak 126 to 147 days (around 4 months) after the start of person-to-person transmission in England and Wales, at a time in which the virus had been found in just 25 countries; and ([3]), which combines a stochastic transmission model with data four datasets on cases of COVID-19 originated in Wuhan to estimate how transmission varied over time, and calculate the probability that newly introduced cases might generate outbreaks in other areas. In [1], researchers modified an individual-based simulation model developed to support pandemic influenza planning to explore scenarios for COVID-19 in GB. In [4] researchers have used early data from the spread of the disease in Wuhan to nowcast and forecast the evolution of the contagion in the region and throughout China, estimating a basic reproductive number for 2019-nCoV of 2.68, and an epidemic doubling time of 6.4 days.

A particularly relevant paper is [5] which, while mathematically expressing the current practices in the modelling on the global spread of diseases, draws policy making suggestions. We follow the same line of research, combining mathematical rigour with attention to drawing results that can be useful for policy makers. Specifically, our contribution is a new statistical model for disease spread which, by taking dependence between daily contagion counts into account, can better capture the contagion curve dynamics and, thus, can draw further light on the understanding of its possible future path.

To better understand our specific contribution, we recall that the reference epidemiologic model, the Susceptible Infected Recovered (SIR) methodology (see, for example, [5] and [6]), is essentially based on the determination of the reproduction rate R_0, calculated as:

$$R_0 = \frac{f * (1-a) * E(T)}{h} \tag{1}$$

where, for any individual in a population: f is the probability of becoming infected (infection rate); $E(T)$ is the mean incubation time of the disease, in case of infection; h is the probability of detecting the infected case (confirmation rate); a is the probability of isolating the contacts of the infected case (quarantine rate). Using what available in the SIR modeling literature, [5] proposes how to set these parameters to study a possible evolution of the COVID-19 outbreak in France: T is based on a Gamma distribution, with expected value equal to $E(T) = 7.5$, estimated from the Chinese contagion data; b is obtained assuming $a = 0$ and $h = 1$ in Equation 1: this, setting R_0 at the observed initial reproduction rate of China ($R_0 = 2.6$) leads to $f = 0.34$. Then, [5] shows how R_0 could change when a and h take a range of possible values, related to alternative policy measures to be adopted.

A first problem with the above approach, and others available in the literature and on media discussions about the COVID-19, is that it introduces a bias on the measurement of f. In other words, what is being estimated is not the infection rate f but the "instantaneous" reproduction rate $b = \frac{f*(1-a)}{h}$, which "incorporates" a and h when they are different from zero. A second problem is that, while $E(T)$ and f may be considered as quite stable across different countries so that estimates from China could be extended to other countries, a and b vary a lot, depending not only on the adopted prevention policies but also on how people are compliant with them.

To address the first problem, we opt for a model capable of learning b, not f, directly from the data. Within this framework, the effect of policy making can be evaluated not in absolute terms, but relatively to the existing measures. To cope with the second problem, we estimate the instantaneous reproduction rate of a country, b, directly from its observed evidence, taking into account the need to incorporate sudden changes in contagion counts ("shocks") that may be due to changes in a and h.

Before introducing our model, we frame our previous two propositions within the context of the exponential growth models employed in the SIR literature ([6]). The exponential growth model assumes that the contagion process follows a Poisson distribution, with an intensity determined by:

$$\lambda(t) = \lambda_0 * exp(\gamma t), \tag{2}$$

which describes the mean intensity $\lambda(t)$ as an exponential function of time, starting from a base level λ_0, with growth parameter γ. The parameter γ is usually estimated regressing the logarithm of the cumulative number of cases up to time t, $N(t)$, on the number of days since the start of the epidemic (conventionally set at an appropriate time, t_0):

$$logN_t = \kappa + \gamma * t, \tag{3}$$

where κ is an intercept term, estimated by $\kappa = log(N_0)$, and γ is a regression coefficient.

Alternatively, γ can be obtained regressing the number of daily new cases, $n(t)$, on the same time variable:

$$logN_t = \kappa' + \gamma * t. \tag{4}$$

where κ' is an intercept term and γ the same regression coefficient as before. It can be easily shown that the two formulations are equivalent, taking $\kappa' = \gamma\kappa$.

Once an estimate for γ is obtained, b can be calculated as the ratio between the new fitted cases at t and the total number of fitted cases in the previous $(t-l, \ldots, t-1)$ days, in line with the expected incubation time (7.5 days for COVID-19), we take $l = 8$. Formally:

$$\hat{b} = 7.5 * \frac{\hat{\gamma_t}}{\sum_{t-l}^{t-1} \hat{\gamma_t}} \text{with } l = 1, \ldots, 8. \tag{5}$$

Following the previous step, a baseline level of R_0 can be calculated as follows:

$$R_0 = E(T) * \hat{b} \tag{6}$$

which, assuming $E(T) = 7.5$, gives $R_0 = 7.5 * \hat{b}$.

Epidemiologically, the higher the R_0 the higher the number of people that will be infected and, eventually, will be hospitalised in severe conditions, or will die. A value of R_0 less than 1 indicates that the epidemic is under control, and is leading to an upper bound of cases. From our proposed definition of b, it is clear that policy making (and its compliance) can affect it by changing a, h, or both.

The exponential growth model in Equation 6 has the advantage of being a parsimonious model: it is based on one parameter, γ, simple to interpret. On the other hand, it has the disadvantage of being fit "globally", on the whole distribution, with a limited account of "local" shocks (e.g., daily changes in the contagion counts that depend on specific issues, such as the outburst of a cluster of cases in a new location, the application of a new policy measure, the diminished compliance to measures, and so on).

From a mathematical point of view, the effects of a and h on b can vary, not only across countries but also over time: a correct measurement model must take into account the dependency of temporal variations in counts. These observations motivate the development of a model of the contagion process that dynamically learns from the data both the contagion growth and how to correctly measure the b, taking into account the temporal variations of a and h, in particular. Such a model, not yet available in the literature, could greatly improve the predictive accuracy and the results which can be obtained from a SIR model. Besides, it can better shape information for policy-makers and the general public on the need for certain policy actions and the need to comply with them.

In this paper, we address the shortfall and propose a dynamic contagion model that can readily adjust the b estimate to account for dependence on past shocks. In this regard, NPIs can be designed and timed with enhanced precision, especially when implementing a suppression strategy. We use an autoregression model, that is, a time series model that uses observations and estimates from previous time steps as input to a regression equation to predict the value at the next time step. We show that our proposed model is able to take contagion shocks into account, not only in the short term (day to day) as it is usually explained and understood by most communication on the virus, possibly giving imprecise information as data is subject to random variation. Instead, our model embeds a component that measures long-term dependence on contagion shocks, more difficult to measure, but more effective in enabling a thorough understanding of the contagion dynamics.

The paper is organised as follows. Section 2 introduces the methodology. Section 3 describes the considered data, from nine European countries. Section 4 applies the model to the data. Section 5 concludes by outlining some implications for policymakers.

2 Methodology

To develop a model for the contagion growth of the COVID-19 which can properly take into account time variations of the epidemic counts, we consider the daily counts of new infections for each country, as in Equation 4. However, differently from Equation 4, which uses a simple regression line over time, we consider an autoregressive model, that can take both short-term and long-term dependence on past contagion shocks into account. Such a model has first been introduced by [7] in the context of financial contagion. Nonetheless, [8] have recently proposed to apply the approach to COVID-19 contamination to China, Italy, Iran and South Korea to identify the trend that each country is experiencing, trying to anticipate its peak. Given the rapid spread of the disease, we now propose a more comprehensive model, that can complement and improve the SIR model, and we apply it to selected European countries.

Formally, resorting to the log-linear version of Poisson autoregression, introduced by [9], we assume that the statistical distribution of new cases at a time (day) t, conditional on the information up to $t-1$, follows a Poisson law, with a log-linear autoregressive intensity, as follows:

$$Y_t|\mathcal{F}_{t-1} \sim Poisson(\lambda_t)$$
$$\log(\lambda_t) = \omega + \alpha \log(1 + y_{t-1}) + \beta \log(\lambda_{t-1}), \tag{7}$$

where $y \in \mathbb{N}$, $\omega \in \mathbb{R}$, $\alpha \in \mathbb{R}$, $\beta \in \mathbb{R}$. Note that the inclusion of $\log(1 + y_{t-1})$, rather than $\log(y_{t-1})$, allows to deal with zero values.

In the model, ω is the intercept term, whereas α and β express the dependence of the expected number of new infections, λ_t, on the past counts of new infections.

The sum of the α and β parameters expresses the degree of dependence of the process on its history (its persistence). In other terms, the closer $\alpha + \beta$ to 1, the higher the persistence of shocks in the counting process. Indeed, the value of $\alpha + \beta$ determines the sign and the magnitude of the autocorrelation of the count series. When the sum of α and β is positive, the count time series shows a positive autocorrelation at lag 1. The closer the sum to 1, the slower the decrease of autocorrelation after the first lag. The level of persistence, $\alpha + \beta$, also affects the unconditional mean of the process, that, for a given value of ω, increases with it. [9] show that, as long as $|\alpha + \beta| < 1$, Y_t is stationary and the model parameters can be consistently estimated through the maximum likelihood method.

For a given level of persistence, the values of α and β define the process dynamics. The α component represents the short-term dependence on the previous time points. The higher α, the higher the unconditional variance of the process. The β component expresses instead the long-term dependence on all past values of the observed process. The inclusion of the β component is analogous to moving from an ARCH ([10]) to a GARCH ([11]) model in Gaussian processes and allows to capture long memory effects, particularly important in the disease contagion context.

To help interpret parameters and understand their role in the process, it is useful to express the log-intensity process as a function of all the past observations:

$$\log(\lambda_t) = \omega \frac{1-\beta^t}{1-\beta} + \beta^t \log(\lambda_0) + \alpha \sum_{i=0}^{t-1} \beta^i \log(1 + y_{t-i-1}) \tag{8}$$

where both λ_0 and y_0 are assumed to be fixed.

One may readily note that the long-run tendency of the process is determined by β, while α determines the magnitude of the correction based on the observed events.

To give further insight, we simulate six series all following the dynamics of Model 7, but characterised by different values of the parameters. The simulated series are plotted in Figure 1. They were obtained by generating 1000 data points starting from the initial values $y_0 = 10$, $\lambda_0 = 10$ and discarding the first 200 observations to make sure that the process has reached the stationary region. In all cases we set $\omega = 0.1$.

In particular, we considered the following scenarios:

1. α+β=0.6, with $\alpha = 0.5$, $\beta = 0.1$: persistence not close to 1, short-term dependence prevailing;

2. $\alpha+\beta$=0.6, with $\alpha = 0.1$, $\beta = 0.5$: persistence not close to 1, long-term dependence prevailing;
3. $\alpha+\beta$=0.98, with $\alpha = 0.85$, $\beta = 0.13$: persistence close to 1, short-term dependence prevailing;
4. $\alpha+\beta$=0.98, with $\alpha = 0.13$, $\beta = 0.85$: persistence close to 1, long-term dependence prevailing;
5. $\alpha+\beta$=0.98, with $\alpha = 1.72$, $\beta = -0.74$: persistence close to 1, short-term dependence prevailing and higher than 1, with negative long-term dependence;
6. $\alpha+\beta$=0.98, with $\alpha = -0.74$, $\beta = 1.72$: persistence close to 1, long-term dependence prevailing and higher than 1, with negative short-term dependence.

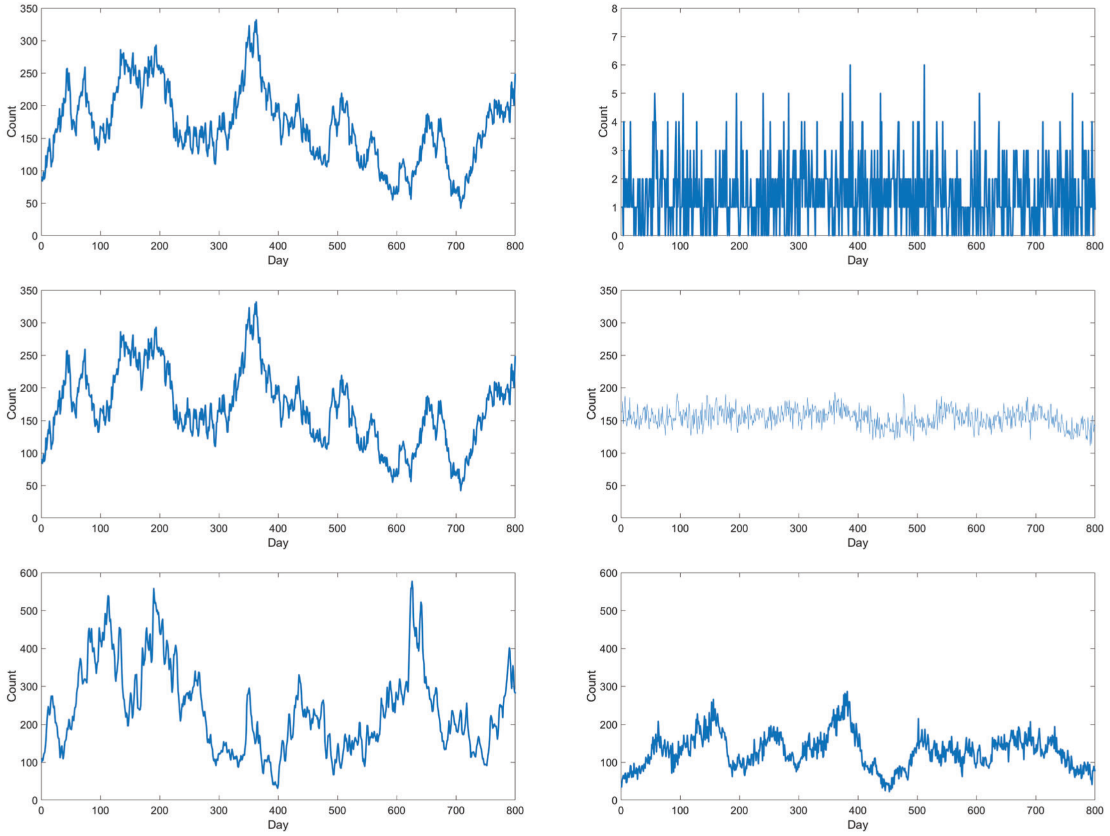

Figure 1: Simulated time series following the specified PAR model, from left to right and bottom down: (1): $\alpha = 0.5$, $\beta = 0.1$; (2): $\alpha = 0.1$, $\beta = 0.5$; (3): $\alpha = 0.85$, $\beta = 0.13$; (4): $\alpha = 0.13$, $\beta = 0.85$; (5): $\alpha = 1.72$, $\beta = -0.74$; (6): $\alpha = -0.74$, $\beta = 1.72$. In all cases we set $\omega = 0.1$, $y_0 = 10$, $\lambda_0 = 10$.

It can be noticed from Figures 1(1) and 1(2) that, when the persistence is low, the series is noisy, with a higher variability when the process is dominated by α. When the persistence is high and close to 1 (Figures 1(3) and 1(4)), the high dispersion and path dependence of the situation when $\alpha > \beta$, due to the fact the process is more influenced by recent shocks rather than its long memory, is particularly evident. We also show (Figures 1(5) and 1(6)) two cases, that will be helpful when analysing our empirical results, in which one of the two parameters is higher than 1, while the other is negative and lower in magnitude. In these cases, the previous considerations about the higher dispersion of the situation when $\alpha > \beta$ is confirmed, but also the process dominated by β shows relatively high path dependence, as the impact of past shocks increases with time.

3 Data

We have applied our proposed model to the available data retrieved from the daily situation reports communicated by the World Health Organisation (WHO) (see [13]) complemented, for a few cases, with data from the Robert Koch-Institut for Germany (see [14]), and from the Office Fédéral de la Santé Publique for Switzerland (see [15]).

Since our analysis explores the dynamic of the COVID-19 contamination, identifying the first day of our sample for countries under investigation is of particular importance. Indeed, while we focus on domestic contagion of the disease, the first recorded cases were considered "imported" cases in all countries. Therefore, to the extent possible, we retain the first day of local transmission in each country as the first date of our time series. Table 1 reports the first day local contamination occurred in each country, as well as the first day of measures implemented to counter the spread of the virus.

Table 1: Countries' first date of local transmission

Country	First day of local transmission	First day of implemented measures against the spread of COVID-19
France	End of January*	March, 17th (quarantine)
Germany	End of January*	March, 23rd (physical distancing and isolation)
The United-Kingdom	End of January*	March, 23rd (quarantine)
Italy	February, 20st	March, 10th (quarantine)
Spain	February, 26th	March, 14th (quarantine)
Norway	February, 29th	March, 12th (physical distancing and isolation)
The Netherlands	February, 29th	March, 16th (physical distancing and isolation)
Switzerland	March, 1st	March, 18th (physical distancing and isolation)
Denmark	March, 1st	March, 11th (quarantine)

Source: Author's elaboration. Information regarding the first day of local transmission are retrieved from the daily situation reports issued by the World Health Organisation.
*Note that for France, Germany, and the United Kingdom, no accurate day is reported.

For the sake of clarity and interpretation, we decide to group the countries according to three different waves of contagion, which occur only a few days apart. That is:

- the first wave focuses on Italy, for which the data spans from February, 20st to March, 28th;
- the second wave includes France, Germany, Spain, and the United Kingdom. The data cover the period from February, 26th to March, 28th. It is worth mentioning that despite early local

contamination in France, Germany, and the United Kingdom, the contagion was somehow "controlled" with only a very few cases reported before February, 26th (see Figure 2);

- the third wave looks at Norway, the Netherlands, Denmark, and Switzerland. The data runs from Feb, 29th to March, 28th.

Although some countries registered their first local transmission only a few days after the chosen starting date, the number of new daily reported cases over these days is still low and does not qualitatively alter the analysis.

Following the above assumptions on the start of the series, Figure 2, built on the data reported by WHO, presents the observed evolution of daily new infections for each country included in the analysis.

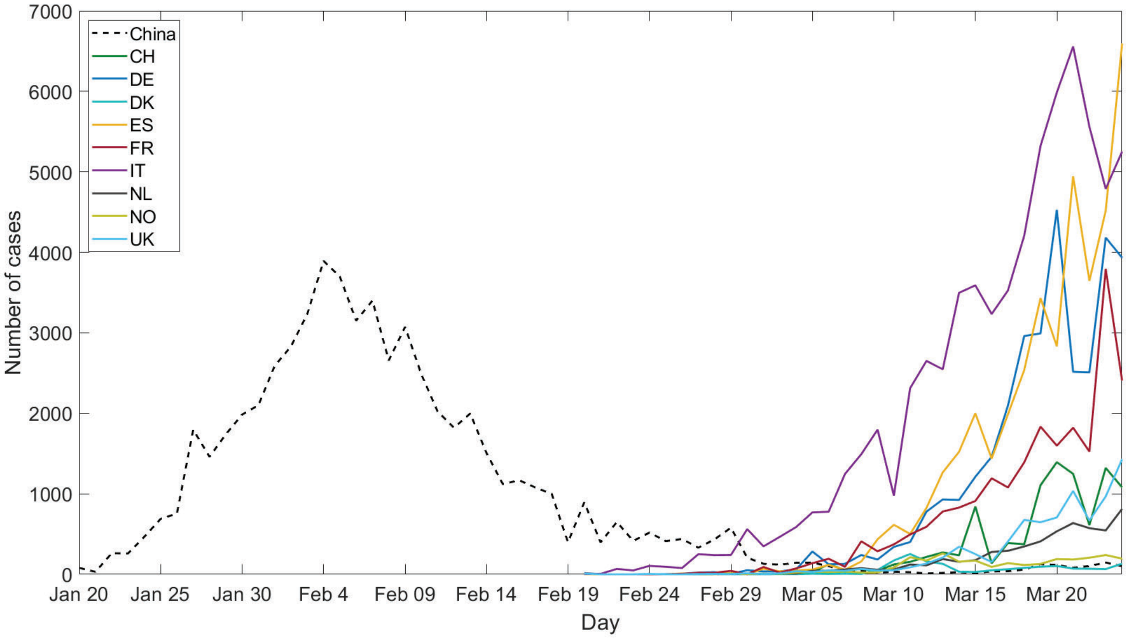

Figure 2: Observed new daily infection counts in all countries

While [8] shows that China has completed a full cycle with an upward trend, a peak, and a downward trend, Figure 2 indicates that, overall, European countries seem to face the ascending phase of the contagion. Prima facie evidence suggests that some European countries are being hit more severely than China has been.

4 Results

The application of our model can confirm the above insights through a dynamic estimation of the growth curve. As put into perspective in Section 1, the key components of our model are the coefficients α β, which can be seen as an extension of the γ parameter in the SIR growth model. In particular, β is the long-term component and is able to express the sign and grasp the velocity of the contagion growth. In this section, we derive the estimated coefficients for the European countries and employ them to estimate b and R_0.

In particular, in a first step, the model estimates parameters on the whole available sample, for each country under investigation. In other words, it leads to coefficients that are the most updated estimates. We report these results according to each country and wave of contagion. These estimates are crucial to understanding whether a country has a trend and, if so, to determine the type of trend each country is experiencing on the contagion curve.

In a second step, bearing in mind the still relatively short time series, we aim to further interpret the estimated parameters. To this purpose, we tailor the model to each European country data series repeatedly, using an increasing amount of data in a retrospective way. More specifically, we first fit the model over the first 15 days (a minimal requirement for statistical consistency of the results), then over the first 16 days, and so on. Therefore, from day 15 onwards, the model estimates one parameter pair (α, β) per day, allowing us to grasp the contagion dynamics. While the first step gives an overall insight into the process each country is experiencing, the second step is key to understand the dynamics of the trend.

In a third step this section aims at interpreting the results within the SIR model context, allowing comparison, and a better interpretation of our proposed model. In this regard, we estimate a dynamic R_0 for each country as defined in Equation 6, thereby incorporating the effects of policy making and compliance to it in the estimated b parameter.

Finally, in a fourth step, we examine what could be the effects of a modification of policy measures, on the current levels of R_0, thereby obtaining a useful scenario analysis, in line what presented in [5], but with a more solid parameter estimation background.

4.1 Overall sample estimates

The results of the first step, shown in Table 2, Table 3 and Table 4, illustrate three different patterns, mostly driven by the value of the β. The most salient one lies in the similarity between the estimated parameters for Italy, France, Spain, Switzerland, the Netherlands, and the United-Kingdom, with a strong positive β, greater than α, as in scenario (6) in Figure 1. As such, it implies that overall and until the date accounted for, the process is still growing, and with a steep growth. On the other side of the spectrum, Denmark and Norway can form a second cluster: these two countries record a negative or insignificant β, but important and positive value of α, as in scenario (3) and (1) in Figure 1. For the time being, in those countries, there appears to be only a short-term dependency of contagion cases. This could be explained by the measures introduced very promptly in light of the evolution of the new daily infected cases (see Table 1). Note also that the value of ω is high and prevails over α and β, which may indicate unexplainable randomness in the data and thus, further confirming that new daily counts of infected cases are much less dependent on time than it is for the previous cluster. Finally, Germany seems to be in an intermediate situation, with high persistence but less prevalence of β over α, with respect to the countries in the first cluster, similar to scenario (4) in Figure 1.

Overall, note that the identified clusters of countries are not necessarily based on waves of contagion, although this may help interpretation. Instead, it seems that other factors, such as country characteristics, as well as the various policy actions implemented to control the spread of the virus, may explain the difference in the estimated coefficients for the European countries

	Italy	
Parameter	Estimate	S.E. (p-value)
ω	0.766	0.113 (0.000)
α	0.281	0.314 (0.188)
β	0.633	0.322 (0.028)

Table 2: Model estimates for Italy with standard errors and p-values.

	France		Germany		Spain		The United-Kingdom	
Parameter	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)
ω	0.076	0.020 (0.007)	0.587	0.211 (0.004)	0.551	0.202 (0.005)	-0.204	0.011 (0.000)
α	-0.414	0.014 (0.000)	0.252	0.469 (0.297)	0.056	0.152 (0.357)	-0.244	0.020 (0.000)
β	1.420	0.007 (0.000)	0.690	0.492 (0.085)	0.893	0.177 (0.000)	1.297	0.018 (0.000)

Table 3: Model estimates for France, Germany, Spain and the United-Kingdom with standard errors and p-values.

	Switzerland		Norway		The Netherlands		Denmark	
Parameter	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)	Estimate	S.E. (p-value)
ω	-0.109	0.013 (0.000)	0.963	0.509 (0.034)	0.241	0.005 (0.000)	1.495	0.658 (0.015)
α	-0.362	0.034 (0.000)	0.548	0.147 (0.000)	-0.450	0.021 (0.000)	0.972	0.171 (0.000)
β	1.386	0.025 (0.000)	0.280	0.209 (0.095)	1.431	0.018 (0.000)	-0.287	0.100 (0.004)

Table 4: Model estimates for Switzerland, Norway, the Netherlands, and Denmark with standard errors and p-values.

covered by this study.

4.2 Dynamic sample estimates

In the second step, we focus more closely on the dynamics of the estimated parameters, rather than at a specific point in time[1]. Figure 3 provides information on the daily estimated pair of coefficients, (α, β), from 15th day in the sample onwards.

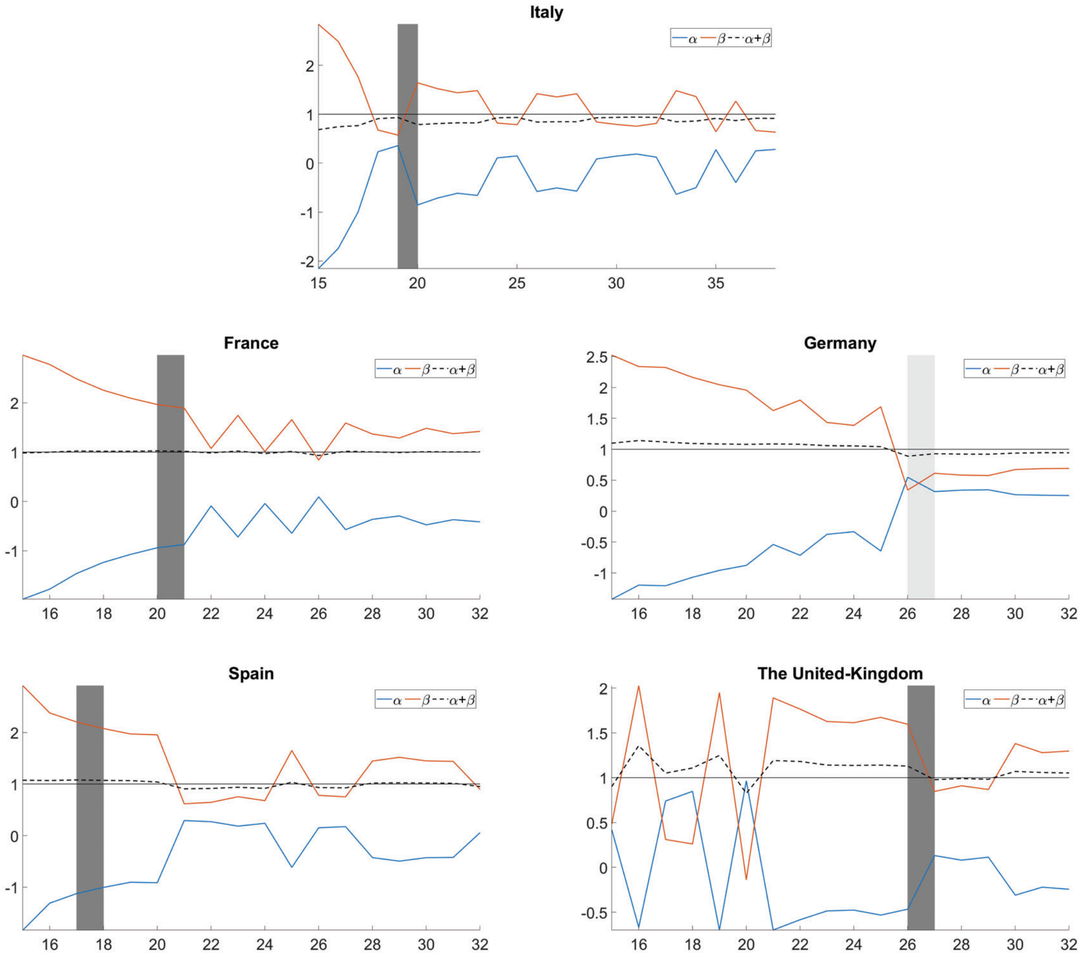

Figure 3: Evolution of the ω, α and β parameters for European countries. Note that the dark grey area corresponds to the first day of "stringent" implemented measures, while the light grey area denotes "soft" measures, as described in Table 1. The dashed line reports the sum of α and β.

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[1] Note that the values in Table 1 reflect the latest estimated parameters for each country in Figure 3, as they correspond to the values estimated over the entire sample, i.e. up to 28 March.

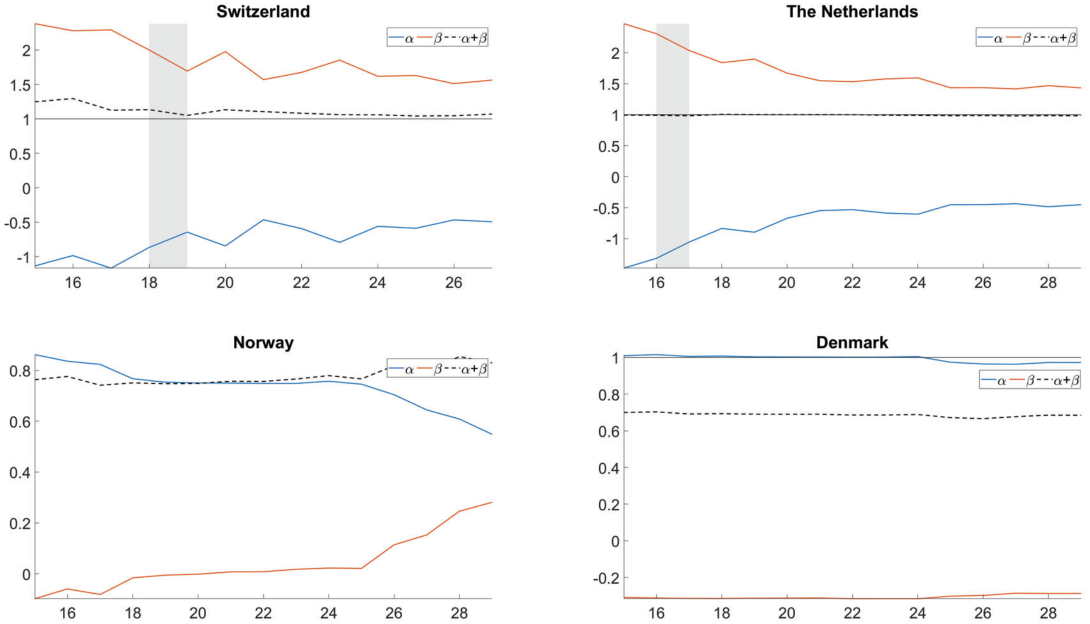

Figure 3 (continued): Evolution of the ω, α and β parameters for European countries. Note that the dark grey area corresponds to the first day of "stringent" implemented measures, while the light grey area denotes "soft" measures, as described in Table 1. In the case of Norway and Denmark, policy measures were enforced before the 15th day. The dashed line reports the sum of α and β.

For the first identified cluster (i.e., Italy, France, Spain, United-Kingdom Switzerland, and the Netherlands), the value of the β is persistently large (above 1), suggesting that in these countries, there is high transmission of variations of the daily counts. In other words, this persistent and substantial value may reveal a change in policy measurements of the number of new cases, that affect h (e.g., the number of tests varies) and late and/or overly relaxed isolation measures, that affect a. This result must be confirmed over time, as one of the caveats is the need for longer observations to properly interpret the long-run effects of policy measures that are slow to appear. To this aim, recall that the incubation time is a random variable and is usually expected to hoover from 1 to 21 days, with an average of 7.5 days.

The graphs in Figure 3 are indeed quite useful to monitor changes in the curve over time; note for example, the recent tendency to "close the gap" between α and β for some countries, such as Italy, Spain, which suggests that a peak is in sight.

We remark that it is important to mention that when $|\alpha + \beta| > 1$, as it occurs for the United-Kingdom at the beginning of the period, and before policies are implemented, the contagion process diverges and indicates that the estimates are not reliable. This suggests an important monitor check on data quality: when the persistence diverges, more data should be accumulated. To a lesser extent, this fact is also observed in Germany, where the process stabilises at the same time as policy action is taken.

We also remark that, although in some countries the dynamic graphs indicate that the gap between α and β is narrowing, this is particularly striking in the case of Germany where the β relaxed in the past few days. From the Chinese experience (as shown in [8]), it is tempting to say that the closing of the gap could signal the appraisal of the peak. Nonetheless, this conclusion should be pondered looking at the value of ω (see Table 3) which, for Germany, is relatively high with respect to α and β, indicating that a degree of unexplained randomness may be present, and which may indicate a low dependency on time, making the trend difficult to predict.

Finally, the experience of Norway and Denmark contrasts with that of the other countries. The first difference lies in the value $|\alpha + \beta|$ which is far from 1, indicating that these countries are undergoing a slower growth process. The second outstanding discrepancy is the inversion of alpha and beta. In this regard, the estimated parameters feature a no memory process. That is, they show a contagion rate of newly infected cases that mainly relies on daily contingencies. Hence, this process is driven by variations of the previous day due, for instance, to a workload capacity reached in hospitals, a lack of conducted tests, favourable weather that makes people decide to go out, and so on.

Overall, the dynamic sample estimates can constitute a useful tool for decision makers. In each country, once a minimal series of data is collected (we suggest at least 15 days) the values of α and all β can be monitored along time, to identify the current stage of the contagion cycle.

4.3 Reproduction rate estimates

We now insert our obtained estimates into the frame of the SIR model, the most used epidemiological tool to assess contagion growth. Following what suggested in Equation 6, we can calculate R_0 for each of our time points. Figure 4 presents the results for each surveyed country and shows that, while the previous findings reconfirmed, more conclusions can be drawn.

Specifically, Figure 4 confirms what we observed for Norway and Denmark. The growth rate of infected cases, R_0, is somewhat under control. This phenomenon is even more impressive once the measures, both mild and strict, have been applied. Indeed, for the two countries, the R_0 respectively skyrocketed at around 3 and 4.5 but was promptly monitored.

The cases of France, Spain, and Italy illustrate a significant value for R_0 at the beginning of their cycle. More recently, the countries have managed to squeeze the reproduction rate, especially in Italy, where they have been implemented for a longer time. Repeated government actions, as well as increasing public awareness of compliance, could explain the flattening of the value of R_0.

The case of Germany is similar to those of Switzerland and the Netherlands. The R_0 is lower than for previous countries (for Germany and Switzerland), but the decline is sluggish. In the same token, one may observe the effects of endorsed actions, although, for Germany and the Netherlands, their "mild" nature might explain the slower compression of the reproduction rate. The swifter decay in Switzerland, instead, hints at a higher degree of compliance with isolation requirements.

Finally, the evolution of the reproduction rate in the United Kingdom is currently alarming, with R_0 displaying substantial values, well above 1. Following [5], when R_0 is above 1, the case is qualified as "*supercritical*". Whilst almost all the countries in our sample project such a high value, the case of the United Kingdom catches particular attention because of the persistent stationary evolution of the reproduction rate, which exhibits no signs of decline over the period. However, the late introduction of confinement could eventually trigger a fall in R_0 over the forthcoming days.

Overall, the presented reproduction rate estimates, calculated along time, can constitute a very important monitoring tool, which can be used to strengthen or to relax policy actions, along time.

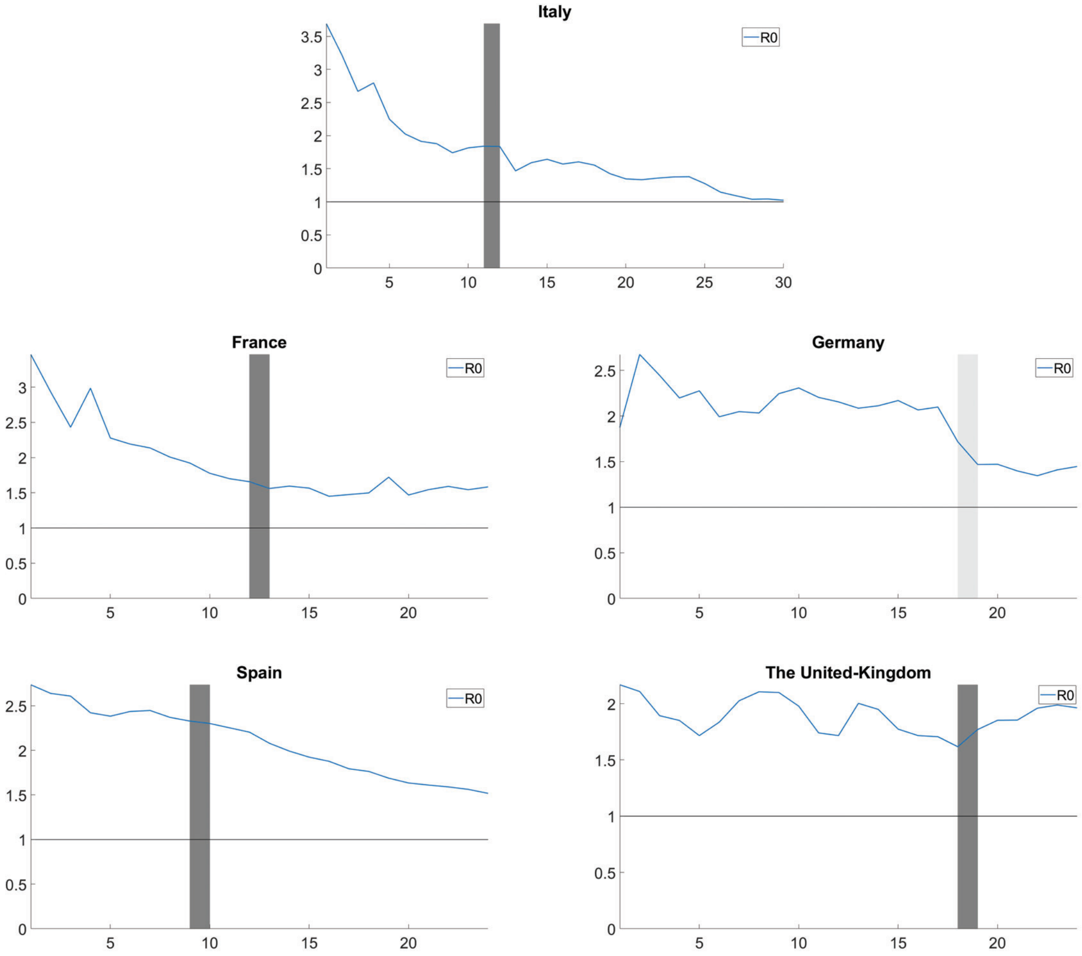

Figure 4: Evolution of the R_0 parameter for European countries. Note that the dark grey area corresponds to the first day of "stringent" implemented measures, while the light grey area denotes "soft" measures, as described in Table 1.

When the estimated R_0 goes below the value of 1, for a sufficient length of time (we suggest a time period that, for precautionary reasons, coincides with the incubation time), actions can be relaxed. Our current estimate indicates that this may be the case for Italy very soon if the downward trend for R_0 is maintained. Conversely, when the estimated R_0 shows persistent high values (as it is currently shown by the United Kingdom), actions should be strengthened.

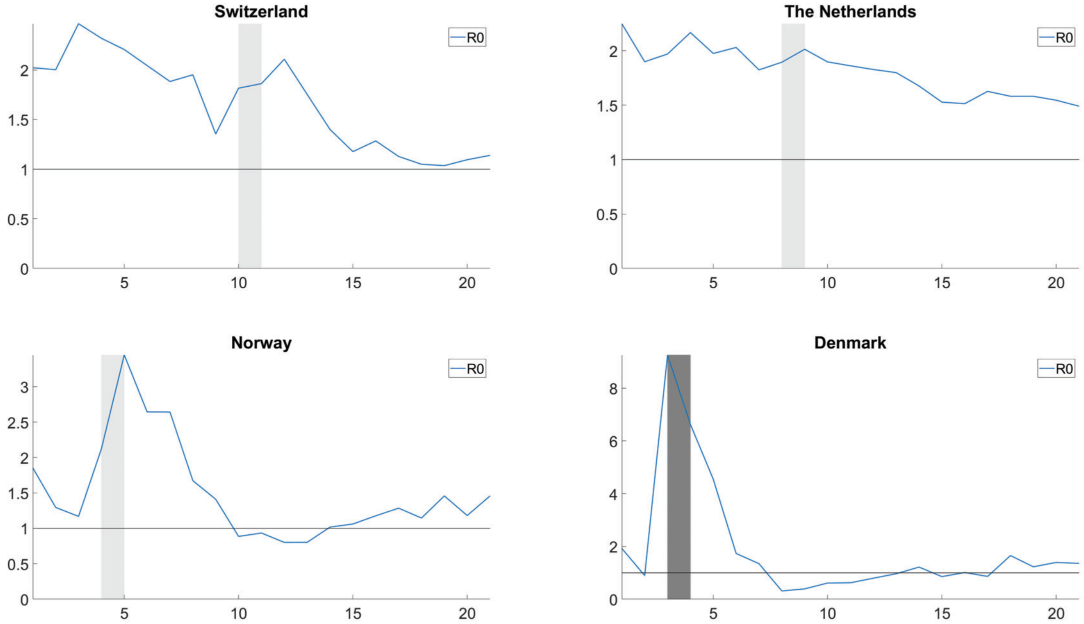

Figure 4 (continued):Evolution of the R_0 parameters for European countries. Note that the dark grey area corresponds to the first day of “stringent” implemented measures, while the light grey area denotes “soft” measures, as described in Table 1. In the case of Norway and Denmark, policy measures were enforced before the 15th day.

4.4 Scenario analysis

It is important to recall that our methodology to compute R_0 assumes that the probability to be subject to quarantine and of a case to be detected (respectively, the parameter a and h in Equation 1) are retrieved along with the infection rate f from the data, through the estimated b parameter. In other words, the process followed by the reproduction rate of positive cases in Figure 4 is “learning” all these three parameters together from the newly observed number of infected cases.

For scenario analysis, we can assume, without loss of generality, that the estimated R_0 are consistent, with a mix of policy measures such that $1 - a = h$. We can consider this as a ”baseline” scenario and evaluate how R_0 could evolve, if more stringent policy measures were implemented, in alternative scenarios.

The scenario values for the parameter a can be related to the work carried out by [5], in which they consider different levels of rule tightness to cope with the COVID-19. They consider a policy measure as strong when $a = 0.8$. Although this rate may be realistically applied to China, we do see a room in Europe for harsher measures. Accordingly, we propose a scenario that can reach $a = 0.6$ in countries featuring stringent measures such as quarantine, and $a = 0.4$ in countries enacting “mild” measures such as social distancing (as may be the current case in Europe). Concerning the parameter h, we recall that it expresses the probability that an infected case (even if asymptomatic) is confirmed by a test as a positive case. Ideally, this rate should be equal to 1. However, there is an inherent risk that, for instance, tests are limited or too costly, that the test fails, or that it is applied to an individual with symptoms, that are those of the classic flu, and not of the COVID-19, with a waste of time and resources. While [5], targets this rate at 0.9, we assume that the average value for Europe is currently around 0.6. Indeed, [16] indicates that this assumption is reliable: they estimate h for Italy at different time points and show that it is rather low in the early stages of virus spread (i.e., until the beginning of March) and, then, it increases to recently reach 0.8.

Following the previous considerations, Table 5 summarises two different scenarios that can be used as a complement of the dynamic estimations illustrated in Figure 4. These scenarios are divided between countries having implemented (so far) strong measures (Scenario 1a & 2a) and the countries having opted (so far) for "mild measures (scenario 1b & 2b). Scenario 1a & 1b are considered as the baseline scenarios, under which R_0 is equal to our estimated values, assuming $a = 0.4$ and $h = 0.6$ for countries adopting stringent measures and $a = 0.6$ and $h = 0.4$ for countries adopting "mild" measures. We then assume that all countries can strengthen their measures by a third. Thus, while in Scenario 2a, h shifts to $h = 0.6$ for countries enacting stringent measures account, in Scenario 2b a shifts to 0.6 for countries that have adopted "mild" measures.

Accordingly, the latest R_0 values in Figure 4, in line with Equation 1 can be multiplied (divided) by the ratio between the shifted value and the assumed current value of $1 - a$ (h), equal to 2/3, to obtain new values for R_0.

Taking into account both an increased testing and a strengthening of policy interventions, the value of R_0 becomes lower for all countries, proportionally to their starting point. Countries with an important R_0 under Scenario 1 are more likely to further compress the reproduction rate of infected cases under Scenario 2. For all countries, heightening the measures would definitely help reducing the growth of newly infected cases.

Having said that further measures may be useful, their marginal benefit (as shown, for example, by the reduction of R_0) should be weighted against their costs. To this aim, we believe that our research should be complemented with research work that aims to measure the socio-economic costs for controlling the COVID-19 pandemic, as in the recent work of [17].

We finally remark that we have presented one possible scenario configuration, but that many others can be easily obtained, by a straightforward application of Equation 1, as we have shown.

5 Conclusions

Faced with a pandemic for which they were hardly prepared, European countries have adopted a plethora of rushed policy measures, ranging from mere reliance on the population's responsible behaviour, to complete country lockdown coupled with relatively harsh enforcement measures. Some countries have acted more rapidly than others, as in the case of Denmark and Norway, where measures were adopted in the first two weeks from the first significant evidence of contagion on the national territory; countries like Germany and the United Kingdom have adopted measures significantly later than others. Some countries (e.g. Germany, the Netherlands) were able to rely on an advanced healthcare infrastructure and spare capacity in terms of intensive care hospital beds, as well as availability of medical equipment such as ventilators, tests, and respirators. Countries have adopted different criteria for testing, a variety of technological means to track the spread of the virus, and different ways to report cases. All this is important in order to assess the effectiveness of the response to the pandemic in different countries.

A few weeks from the spread of the COVID-19 virus in Europe, it is still very difficult to assess which measures have proven effective, and whether the peak of cases is near, at least for

Table 5: Estimation of the overall R_0 under the alternative scenarios

Stringent measures		
Country	Scenario 1a ($a = 0.6$ and $h = 0.4$)	Scenario 2a ($a = 0.6$ and $h = 0.6$)
Italy	1.023	0.682
France	1.583	1.055
Spain	1.517	1.011
The United-Kingdom	1.963	1.308
Denmark	1.356	0.904
Mild measures		
Country	Scenario 1b ($a = 0.4$ and $h = 0.6$)	Scenario 2b ($a = 0.6$ and $h = 0.6$)
Germany	1.446	0.964
Norway	1.528	1.018
The Netherlands	1.458	0.972
Switzerland	1.139	0.759

Source: Author's elaboration. The parameters a and h respectively denote the probability to be under quarantine and the rate of confirmation once the virus is detected.

some countries. The difficulty of interpreting available data increases further, if one considers that some countries have changed their policy approach several times in the course of a fistful of weeks. Still, relying on a solid approach to data monitoring and prediction is important to avoid spreading disinformation and creating false expectations among the population: a common approach to different national experiences is also essential in order to start drawing lessons for the future, as the outbreak reaches other parts of the world (e.g., the United States, but also many African countries), where an effective response does not seem likely.

This paper proposes a model that allows for the identification of short-term and long-term components in data relative to COVID-19 contagions. Our intention is to propose a dynamic model, rather than a set of definitive results: as the timeframe becomes longer, we expect the model predictions to evolve, particularly as a result of the adopted policies. The results of the model can be updated on a daily basis and can offer governments a basis for forecasting the peak, a monitor on the evolution of contagion, as well as approach policy choices for the "post-lockdown" period. As a matter of fact, once the peak is reached, countries will start considering a mix of new policy measures, gradually lifting restrictions to relaunch the economy, such as i.a. the obligation to wear masks in public places, the development of apps for self-reporting of symptoms, or a widespread, randomized testing strategy. These measures, depending on the circumstances, may also trigger a return of the COVID-19 contagion, which can be detected by the proposed model. The model can also be used to monitor the spread of the virus in the post-lockdown phase, enabling a comparative analysis of the effectiveness of alternative policy measures.

The model proposed must be analysed with a number of caveats in mind. First, the dataset still covers a relatively limited timeframe, especially for some countries. Second, the model relies on officially data on reported contagion cases, which may represent only part of the total cases, both due to limited testing and also to the fact that part of the infected population (although apparently a small proportion) remains asymptomatic throughout the infection period. Third, countries have followed different approaches to testing, and some countries (or some subnational governments) have changed approach to testing during the period analysed. Although the model can capture these aspects into its autoregressive dynamics, more detailed data could help to better explain the underlying causes behind the model estimates.

That said, the dynamic estimates presented in this paper suggest that countries that have imposed early measures to limit the spread of the contagion (e.g., Norway and Denmark) have been relatively successful in controlling the reproduction rate, despite the fact that R_0 was initially very high in both countries; countries in which the action has been relatively targeted and based on extensive testing, like Germany (and to some extent Switzerland and the Netherlands), obtained significant results in containing the reproduction rate even before adopting mild social-distancing measures; countries like Italy, Spain and France seem to be still in an upward trend, but are close to bringing the reproduction rate back under control. And the United Kingdom, where several policy changes have been implemented in the first weeks, until a lockdown policy was finally implemented, seems on the verge on an explosive trend, with the reproduction rate remaining at a “supercritical” level.

The proposed model can prove useful beyond the monitoring of the spread of COVID-19. Beyond extending the data to subnational governments (e.g. Italian regions, German Länder) and to other countries (e.g. other EU Member States, the United States), the model enables a comparison of the spread of the contagion in light of different policy approaches chosen by different governments, both in terms of timing and scope of future policy reforms.

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