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Supplementary information

Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe

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ACCELERATED ARTICLE PREVIEW

Contents

List of Supplementary Figures

List of Supplementary Tables

Supplementary Methods.

Death model

We observe daily deaths $D_{t,m}$ for days $t \in \{1, \dots, n\}$ and countries $m \in \{1, \dots, M\}$. These daily deaths are modelled using a positive real-valued function $d_{t,m} = \mathrm{E}(D_{t,m})$ that represents the expected number of deaths attributed to COVID-19. The daily deaths $D_{t,m}$ are assumed to follow a negative binomial distribution with mean $d_{t,m}$ and variance $d_{t,m} + \frac{{d_{t,m}}^2}{\psi}$, where ψ follows a half normal distribution, i.e.

$$D_{t,m} \sim \text{Negative Binomial}\left(d_{t,m}, d_{t,m} + \frac{{d_{t,m}}^2}{\psi}\right),$$

$\psi \sim N^+(0,5)$.

Here, $\mathrm{N}(\mu, \sigma)$ denotes a normal distribution with mean μ and standard deviation σ. We say that X follows a positive half normal distribution $\mathrm{N}^+(\mu, \sigma)$ if $X \sim |Y|$, where $Y \sim N(\mu, \sigma)$.

The expected number of deaths d in a given country on a given day is a function of the number of infections c occurring in previous days.

At the beginning of the epidemic, the observed deaths in a country can be dominated by deaths that result from infection that are not locally acquired. To avoid biasing our model by this, we only include observed deaths from the day after a country has cumulatively observed 10 deaths in our model.

To mechanistically link our function for deaths to infected cases, we use a previously estimated COVID-19 infection-fatality-ratio *ifr* (probability of death given infection)[9] together with a distribution of times from infection to death π. The *ifr* is derived from estimates presented in Verity et al[1] which assumed homogeneous attack rates across age-groups. To better match estimates of attack rates by age generated using more detailed information on country and age-specific mixing patterns, we scale these estimates (the unadjusted *ifr*, referred to here as *ifr'*) in the following way as in previous work.[2] Let c_a be the number of infections generated in age-group a, let N_a be the underlying size of the population in that age group and let $AR_a = c_a/N_a$ be the age-group-specific attack rate. The adjusted ifr_a is then given by

$$\mathrm{ifr}_a = \frac{AR_{50-59}}{AR_a}\,\mathrm{ifr}'_a,$$

where AR_{50-59} is the predicted attack-rate in the 50-59 year age-group after incorporating country-specific patterns of contact and mixing. This age-group was chosen as the reference as it had the lowest predicted level of underreporting in previous analyses of data from the Chinese epidemic[1]. We obtained country-specific estimates of attack rate by age, AR_a, for the 11 European countries in our analysis from a previous study which incorporates information on contact between individuals of different ages in countries across Europe.[3] We then obtained overall ifr estimates for each country adjusting for both demography and age-specific attack rates. The attack rates for our study and populations are show in table 4. Details of this calculation can be found in Verity et al [cite] and Walker et al [cite]

From the above, every country has a specific mean infection-fatality ration ifr_m. In our model, we will allow the ifr_m for every country to have some additional noise around this. Specifically, we assume

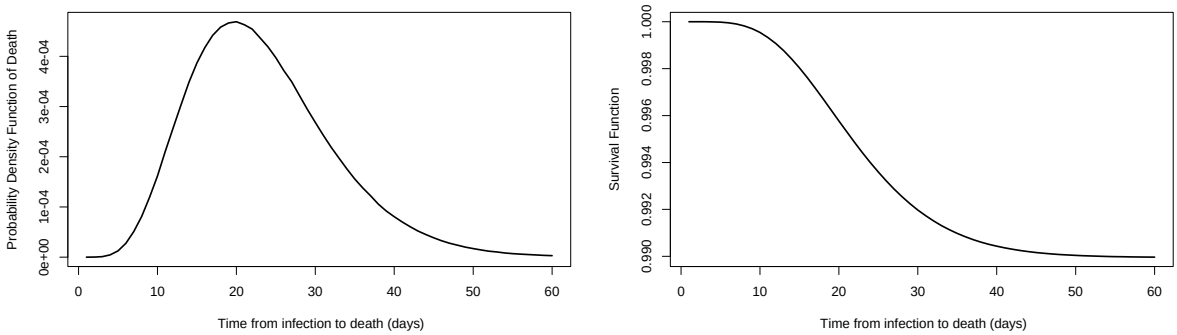
$$\mathrm{ifr}^*_m \sim \mathrm{ifr}_m \cdot N(1, 0.1).$$

Using estimated epidemiological information from previous studies,[1,2] we assume the distribution of the time between infection and death, π, to be the sum of two independent random times: the incubation period (infection to onset of symptoms or infection-to-onset) and the time between onset of symptoms and death (onset-to-death). The infection-to-onset distribution is Gamma distributed

with mean 5.1 days and coefficient of variation 0.86. The onset-to-death distribution is also Gamma distributed with a mean of 17.8 days and a coefficient of variation 0.45. The infection-to-death distribution is therefore given by:

$$\pi \sim \text{Gamma}(5.1,0.86) + \text{Gamma}(17.8,0.45)$$

Supplementary Fig. 1 shows the infection-to-death distribution and the resulting survival function that integrates to the infection fatality ratio.



Supplementary Fig. 1. Left, infection-to-death distribution (mean 22.9 days). Right, survival probability of infected individuals per day given the infection fatality ratio (1%) and the infection-to-death distribution on the left.

The expected number of deaths $d_{t,m}$, on a given day t, for country, m, is given by the following discrete sum:

$$\mathrm{d_{t,m}} = \mathrm{ifr_m^*} \sum_{\tau=0}^{t-1} \mathrm{c_{\tau,m}}\, \pi_{t-\tau,m}^*,$$

where $c_{\tau,m}$ is the number of new infections on day τ in country m (see next section) and where π is discretized via $\pi_{s,m} = \int_{s-0.5}^{s+0.5} \pi(\tau)\, d\tau$ for $s = 2,3, \ldots$ and $\pi_{1,m} = \int_0^{1.5} \pi(\tau)\, d\tau$, where $\pi(\tau)$ is the density of π.

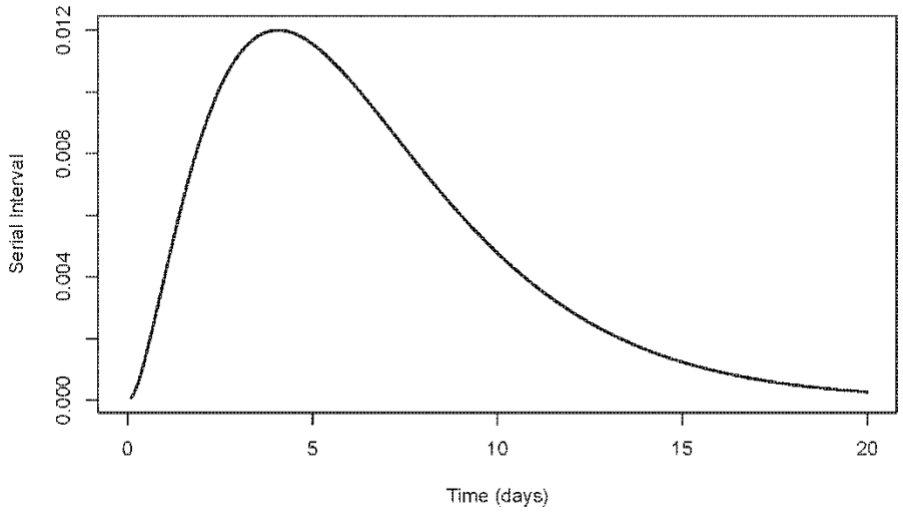
The number of deaths today is the sum of the past infections weighted by their probability of death, where the probability of death depends on the number of days since infection and the country-specific infection-fatality ratio.

Infection model

The true number of infected individuals, c, is modelled using a discrete renewal process. This approach has been used in numerous previous studies[4–7] and has a strong theoretical basis in stochastic individual-based counting processes such as Hawkes process and the Bellman-Harris process.[8,9] The renewal model is related to the Susceptible-Infected-Recovered model, except the renewal is not expressed in differential form. To model the number of infections over time we need to specify a generation distribution g with density $g(\tau)$, (the time between when a person gets infected and when they subsequently infect another other people). The generation distribution is unknown, but we can approximate it by assuming it is the same as the serial interval distribution (time from onset to onset). For the serial interval/generation distribution we use estimates from Bi et al 2020 [cite] who estimate the generation distribution to be Gamma distributed:

$$\mathrm{g} \sim \text{Gamma}(6.5,0.62).$$

The generation distribution is shown below in Supplementary Fig. 2 and is assumed to be the same for all countries.



Supplementary Fig. 2. Generation/Serial interval distribution g with a mean of 6.5 days.

Given the generation distribution, the number of infections $c_{t,m}$ on a given day t, and country, m, is given by the following discrete convolution function:

$$c_{t,m} = \left(1 - \frac{\sum_{i=1}^{t-1} c_{i,m}}{N_m}\right) R_{t,m} \sum_{\tau=0}^{t-1} c_{\tau,m}\, g_{t-\tau},$$

where, similar to the probability of death function, the daily generation distribution is discretized by $g_s = \int_{s-0.5}^{s+0.5} g(\tau)\, d\tau$ for $\mathrm{s} = 2,3, \ldots$ and $g_1 = \int_0^{1.5} g(\tau)\, d\tau$. The population size of country m is denoted by N_m. We include the population adjustment $1 - \frac{\sum_{i=1}^{t-1} c_{i,m}}{N_m}$ to account for population saturation of susceptible: i.e. even in the absence of interventions, herd immunity will reduce the number of daily infected. We note here that we could include a factor in the serial interval accounting for individuals who die before they can infect others[10] but given the infection-to-death distribution this factor is negligible and we have chosen to exclude it.

The renewal equation states that infections today depend on the number of infections in the previous days, weighted by the discretized generation distribution. This weighting is then scaled by the country-specific time-varying reproduction number, $R_{t,m}$, that models the average number of secondary infections at a given time.

The functional form for the time-varying reproduction number was chosen to be as simple as possible to minimize the impact of strong prior assumptions: we use a piecewise constant function that scales $R_{t,m}$ from a baseline prior $R_{0,m}$ and is driven by known major non-pharmaceutical interventions occurring in different countries and times.

We included 6 interventions, one of which is constructed from the other 5 interventions, which are timings of school and university closures (k=1), self-isolating if ill (k=2), banning of public events (k=3), any government intervention in place (k=4), implementing a partial or complete lockdown (k=5) and encouraging social distancing and isolation (k=6). We denote the indicator variable for intervention $\mathrm{k} \in \{1,2,3,4,5,6\}$ by $I_{k,t,m}$, which is 1 if intervention k is in place in country m at time t and 0 otherwise. The covariate "any government intervention" (k=4) indicates if any of the other 5 interventions are in

effect, i.e. $I_{4,t,m}$ equals 1 at time t if any of the interventions $\mathrm{k} \in \{1,2,3,4,6\}$ are in effect in country m at time t and equals 0 otherwise. Covariate 4 has the interpretation of indicating the onset of major government intervention.

The effect of each intervention is assumed to be multiplicative. $R_{t,m}$ is therefore a function of the intervention indicators $I_{k,t,m}$ in place at time t in country m:

$$R_{t,m} = R_{0,m} \exp\left(-\sum_{k=1}^{6} \alpha_k I_{k,t,m} - \beta_{\mathrm{m}} \mathrm{I}^*_{\mathrm{t,m}}\right),$$

where $\mathrm{I}^*_{\mathrm{t,m}}$ is an indicator for the last intervention that was implemented in a country during the epidemic up to now. For all countries, with the exception of Sweden this is the lockdown, i.e. $\mathrm{I}^*_{\mathrm{t,m}} = \mathrm{I}_{5,\mathrm{t,m}}$. For Sweden this last intervention is banning of public events, i.e. $\mathrm{I}^*_{\mathrm{t,m}} = \mathrm{I}_{3,\mathrm{t,m}}$. The exponential form was used to ensure positivity of the reproduction number, with $R_{0,m}$ constrained to be positive as it appears outside the exponential. The impacts α_{k} are shared between all M countries and therefore they are informed by all available data. The country-specific random effect β_m on the last intervention is included to allow for variation between the countries in the effectiveness of the implementation of the interventions.

The prior distribution for $R_{0,m}$ was chosen to be

$R_{0,m} \sim \mathrm{N}^+(3.28, |\kappa|)$ with $\kappa \sim \mathrm{N}(0,0.5)$,

where κ is the same among all countries to share information about the variability of $R_{0,m}$. The value of 3.28 was chosen based on a previous meta analysis looking at the basic reproductive number[11].

The prior on the total reduction through an individual intervention (i.e. $\exp(-\alpha_{\mathrm{k}})$) which is not the last intervention and on the reduction once all interventions in place, i.e. on $\exp\left(-\sum_{\mathrm{k}=1}^{6} \alpha_{\mathrm{k}}\right)$ is displayed in the top row of Supplementary Fig. 3. The bottom row illustrates the prior on the effect of the last intervention in a country (i.e. $\exp(-\alpha_{\mathrm{k}} - \beta_{\mathrm{m}})$) and full effect of all interventions together ($\exp\left(-\sum_{\mathrm{k}=1}^{6} \alpha_{\mathrm{k}} - \beta_{\mathrm{m}}\right)$ bottom right). Details of the individual prior choices that result in this are below.

The impact of an intervention on $R_{t,m}$ is characterised by a set of parameters $\alpha_1, \ldots, \alpha_6$, with independent prior distributions chosen to be

$$\alpha_k \sim \mathrm{Gamma}(1/6,1) - \frac{\log(1.05)}{6},$$

i.e. the prior on each effect is Gamma distribution with shape parameter 1/6 and scale parameter 1, shifted to allow for negative values. This prior was chosen such that the probability that any individual intervention does not reduce $\mathrm{R}_{\mathrm{t,m}}$, i.e. $\mathrm{P}(\alpha_{\mathrm{k}} < 0)$, is about 48% and such that the joint effect of $\alpha_1, \ldots, \alpha_6$ on $\mathrm{R}_{\mathrm{t,m}}$ once all interventions are in-place (i.e. the distribution of $\exp\left(-\sum_{\mathrm{k}=1}^{6} \alpha_{\mathrm{k}}\right)$) is a uniform distribution on [0,1.05]. The intuition behind this prior is that it encodes our null belief that interventions could equally increase or decrease R_{t}, and the data should inform which.

The prior on the country-specific effects $\beta_1, \ldots, \beta_M$ of the last intervention is given by

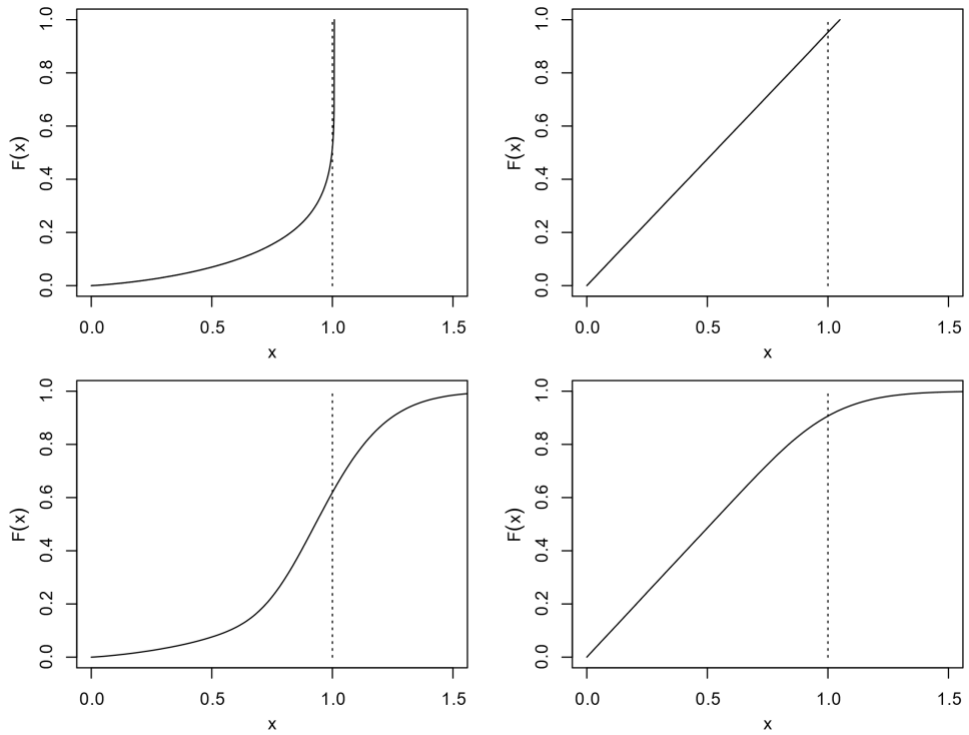
$$\beta_1, \ldots, \beta_M \sim N(0, \gamma) \text{ where } \gamma \sim N^+(0, .2).$$

We only included this country-specific random effect for the last intervention, as the last intervention is usually the effect of lockdown, which is the strongest in our analysis and as other interventions do not have identifiable effects for individual countries.

We assume that seeding of new infections begins 30 days before the day after a country has cumulatively observed 10 deaths. From this date, we seed our model with 6 sequential days of

infections drawn from $c_{1,m}, \ldots, c_{6,m} \sim \text{Exponential}(1/\tau)$, where $\tau \sim \text{Exponential}(0.03)$. These seed infections are inferred in our Bayesian posterior distribution. For more details and a sensitivity analysis see Section 0.

We estimated parameters jointly for all 11 countries in a single hierarchical model. Fitting was done in the probabilistic programming language Stan,[12] using an adaptive Hamiltonian Monte Carlo (HMC) sampler. We ran 8 chains for 8000 iterations with 2000 iterations of warmup and a thinning factor 4 to obtain 4000 posterior samples. Posterior convergence was assessed using the Rhat statistic and by diagnosing divergent transitions of the HMC sampler. Prior-posterior calibrations were also performed (see below).



Supplementary Fig. 3. Cumulative distribution function of prior on total reduction through one intervention through the fixed effect ($exp(-\alpha_k)$, top left), on the last intervention in a country ($exp(-\alpha_k - \beta_m)$, bottom left) fixed effect through all interventions together ($exp\left(-\sum_{k=1}^{6} \alpha_k\right)$, top right) and full effect of all interventions together ($exp\left(-\sum_{k=1}^{6} \alpha_k - \beta_m\right)$ bottom right).

Supplementary Discussion 1. Validation

We validate the accuracy of point estimates of our model using cross-validation. In our cross-validation scheme, we leave out 14 days of known death data (non-cumulative) and refit our model. We predict for these 14 days and evaluate the mean squared error. We also benchmark our current model against a latent nonparametric Gaussian process regression parametrisation for R_t (zero mean with squared exponential covariance function) – this is shown in Supplementary Table 1 below. Our predictions over the 14 day period are shown in Section 8.4.1 for each country on a logarithmic scale. Supplementary Table 1 shows we can forecast reasonably over short time scales but performance degrades rapidly over longer time scales. These results show that very long term forecasts (over months) are purely speculative and do not have empirical basis.

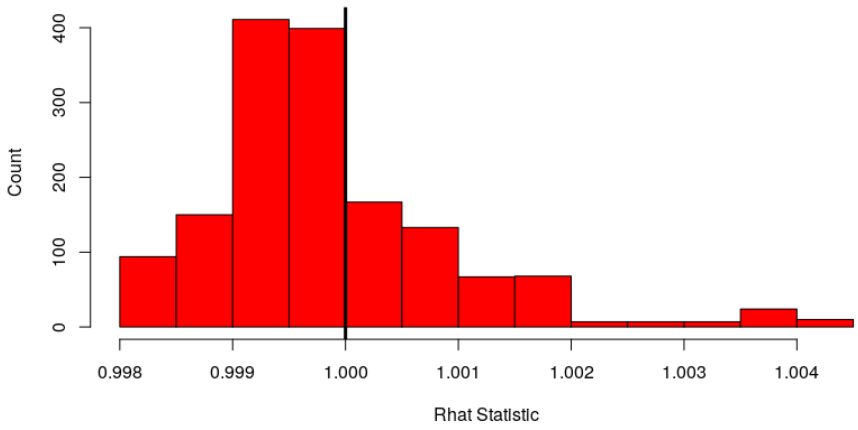
Supplementary Table 1 alongside our visual predictions in Section 8.4.1 provides strong empirical justification for our model specification and mechanism. Our predictions are reasonable over a 14 day period and, as expected, degrade with time horizon.

Along with from point estimates we all evaluate all our posterior credible intervals using the Rhat statistic. The Rhat statistic measures whether our Markov Chain Monte Carlo (MCMC) chains have converged to the equilibrium distribution (the correct posterior distribution). Supplementary Fig. 4 shows the Rhat statistics for all of our parameters.

Supplementary Fig. 4 indicates that our MCMC have converged. In fitting, we also ensured that the MCMC sampler experienced no divergent transitions - suggesting non-pathological posterior topologies.

Supplementary Table 1: Mean squared error between predictions and the actual number of deaths for our approach and Gaussian process regression. Our approach is far superior over 14 days even if the Gaussian process is sometimes better over 3 days.

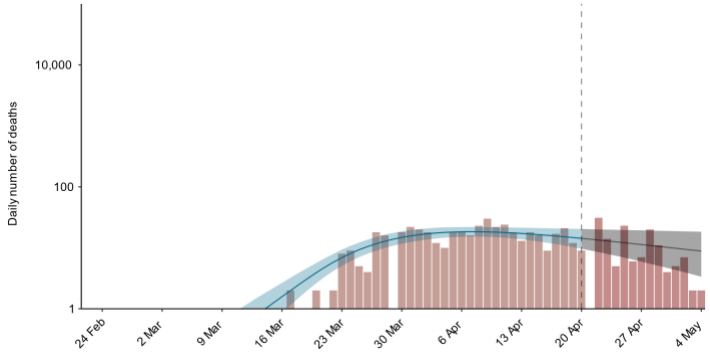
	Our approach (MSE)			Gaussian process regression (MSE)		
	3 Days	7 Days	14 Days	3 Days	7 Days	14 Days
Denmark	6.2	7.5	16	8.2	25	140
Italy	420	550	670	340	610	2,300
Germany	55	130	470	140	400	2,300
Spain	470	830	1,500	670	1,200	2,500
United Kingdom	200	350	1,000	490	1,600	6,100
France	880	670	810	800	820	2,600
Norway	3.8	4.8	9.4	4.9	13	93
Belgium	56	140	330	130	310	950
Austria	12	15	36	22	48	240
Sweden	35	88	350	57	170	680
Switzerland	16	37	80	32	82	290



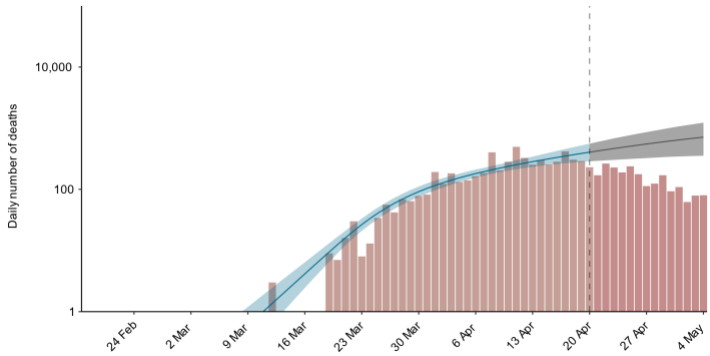
Supplementary Fig. 4. Rhat statistics - values close to 1 indicate MCMC convergence.

Supplementary Discussion 2. Retrospective prediction on a log-linear scale for model validation

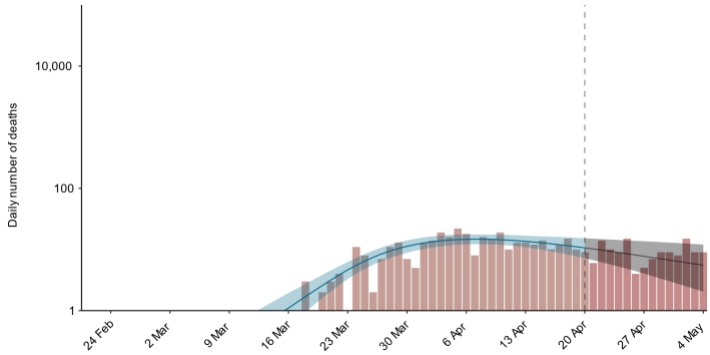
We show the performance of our hold our validation fits on a log-linear scale, where a model is fitted until the 2nd of April and then predictions made until 16th April (2 weeks/14 days). These model predictions are then compared to the real data to assess model performance. Supplementary Fig. 5 to Supplementary Fig. 15 show these predictions for all countries alongside the real data that the model was blind to.



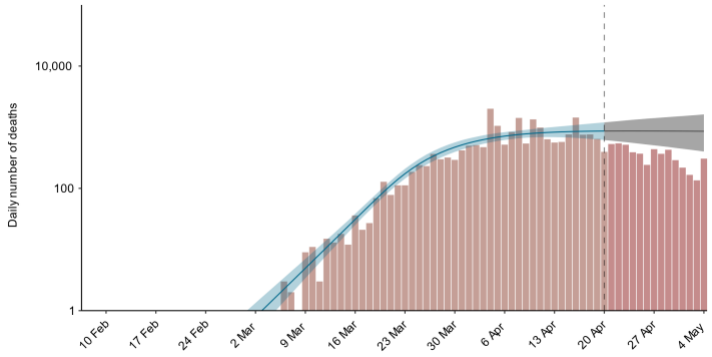
Supplementary Fig. 5: 14-day-ahead forecast for Austria.



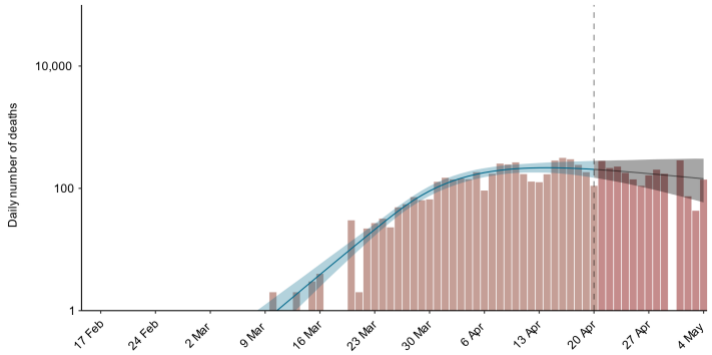
Supplementary Fig. 6: 14-day-ahead forecast for Belgium.



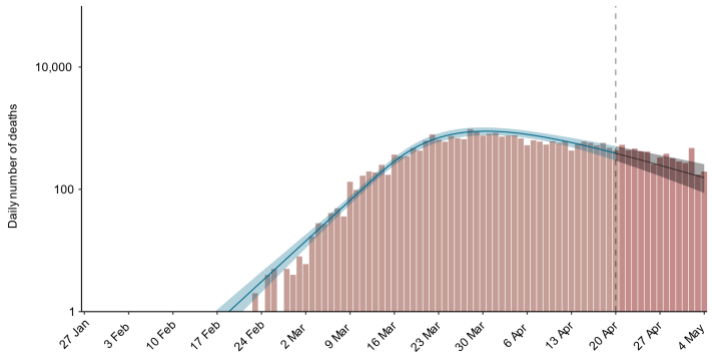
Supplementary Fig. 7: 14-day-ahead forecast for Denmark.



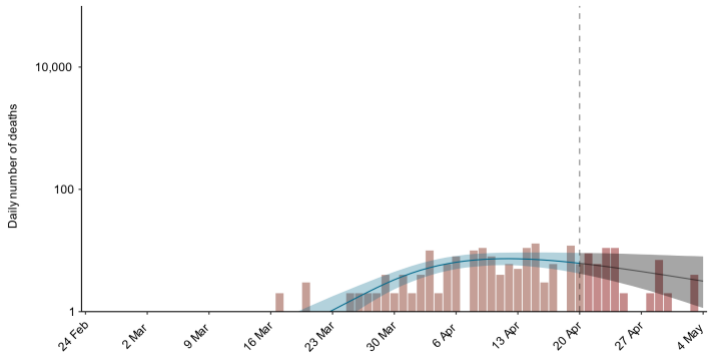
Supplementary Fig. 8: 14-day-ahead forecast for France.



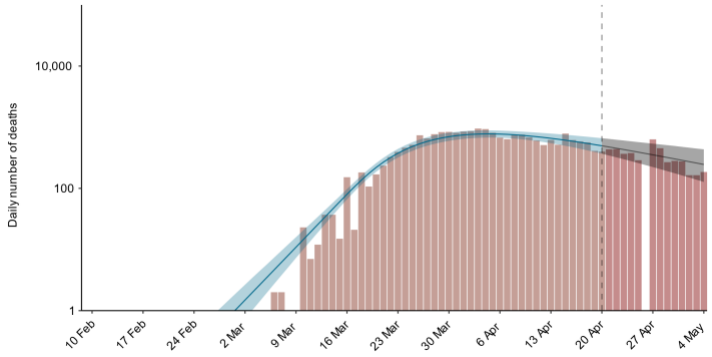
Supplementary Fig. 9: 14-day-ahead forecast for Germany.



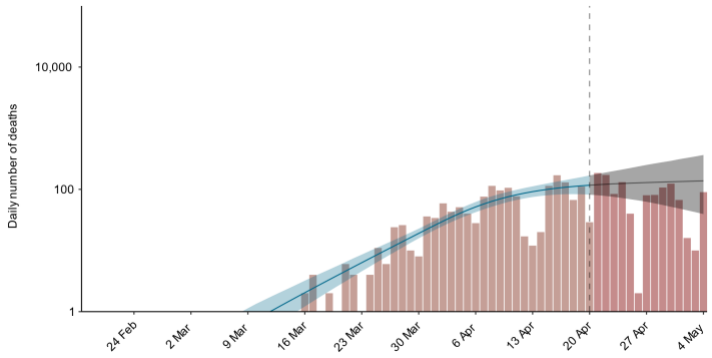
Supplementary Fig. 10: 14-day-ahead forecast for Italy.



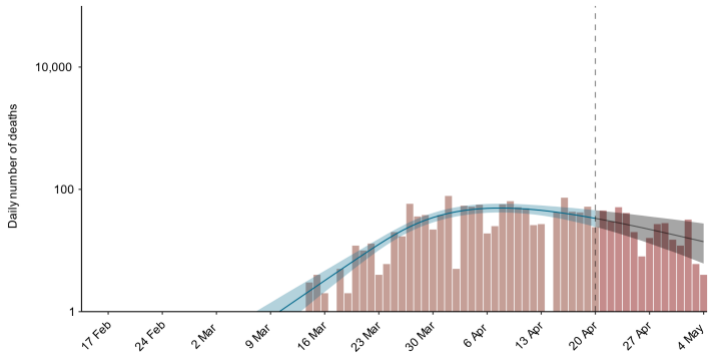
Supplementary Fig. 11: 14-day-ahead forecast for Norway.



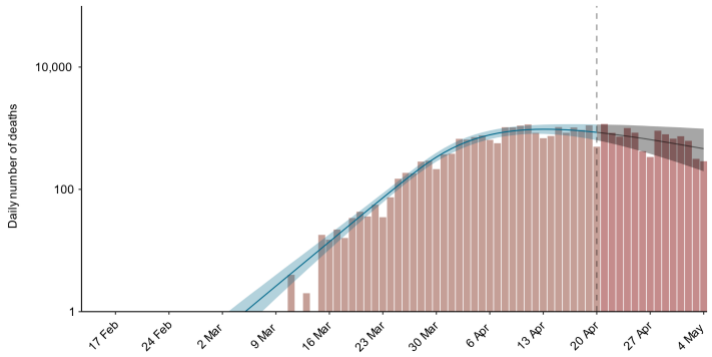
Supplementary Fig. 12. 14-day-ahead forecast for Spain.



Supplementary Fig. 13. 14-day-ahead forecast for Sweden.



Supplementary Fig. 14. 14-day-ahead forecast for Switzerland.

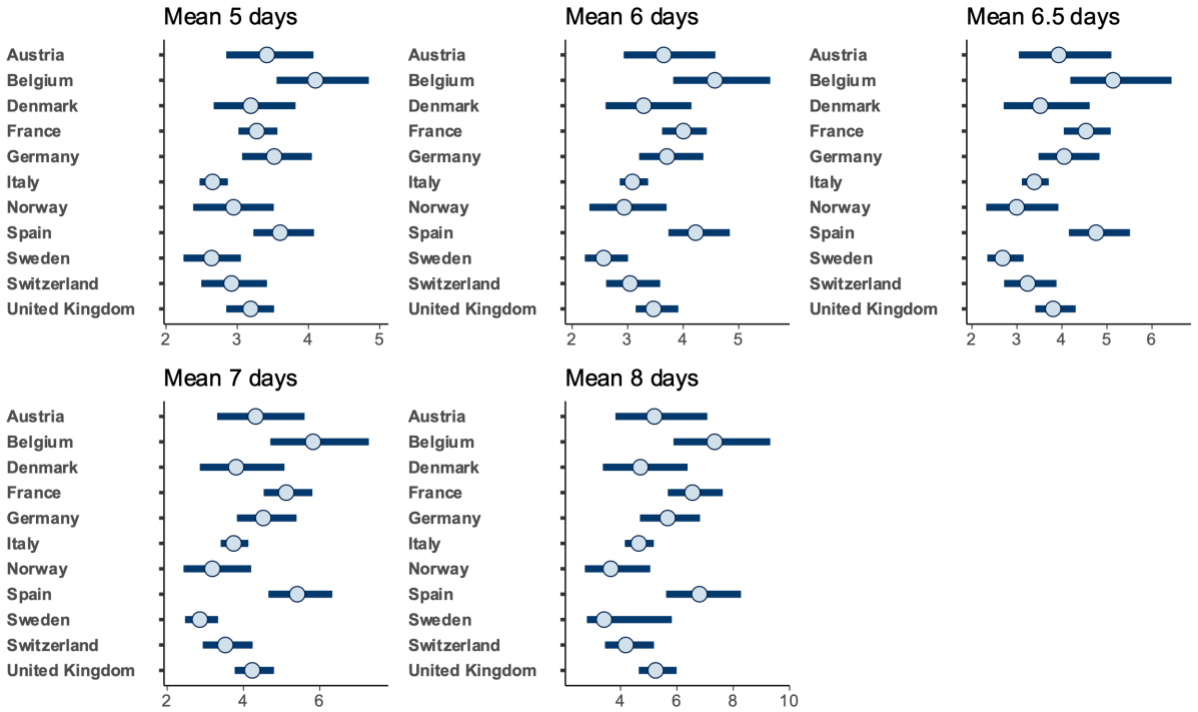


Supplementary Fig. 15. 14-day-ahead forecast for United Kingdom.

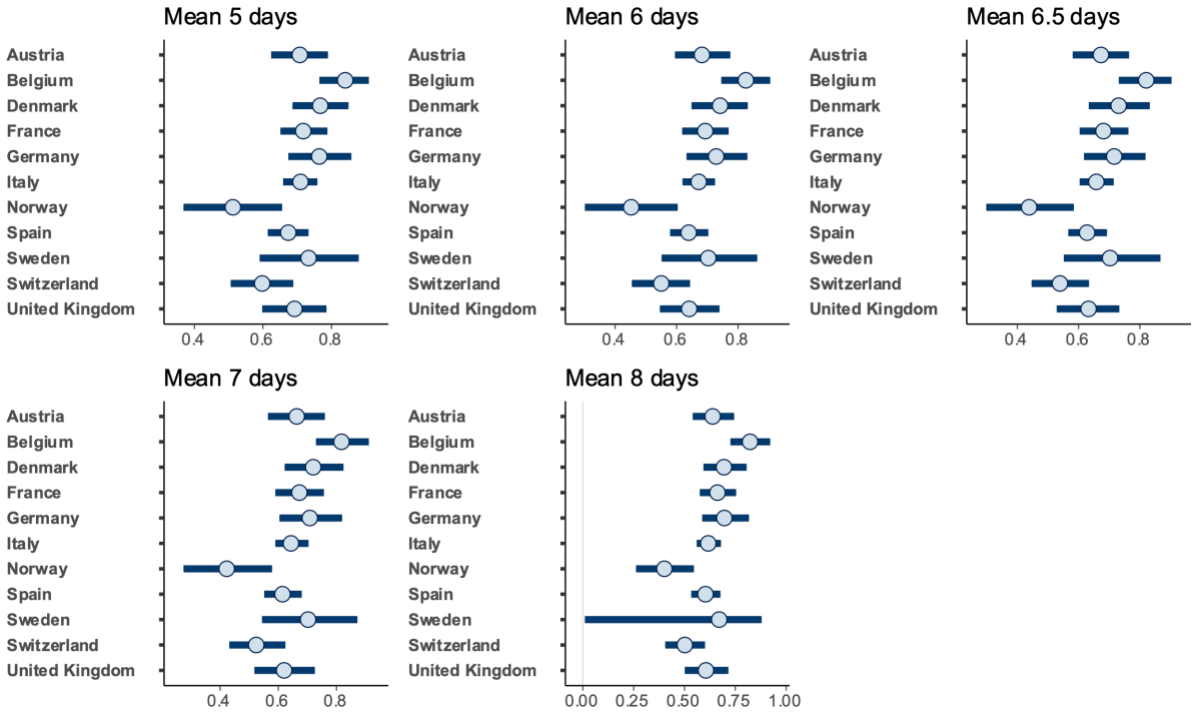
Supplementary Discussion 3. Sensitivity Analysis: Generation distribution

We investigated the sensitivity of our estimates of starting and final R_t to our assumed generation distribution. For this we considered several scenarios, in which we changed the generation distribution mean, from a value of 6.5 days, to have values of 5, 6, 7 and 8 days. These values were chosen as plausible serial intervals reported from Bi et al 2020[13].

In Supplementary Fig. 16, we show our estimates of R_0, the starting reproduction number before interventions, for each of these scenarios. The relative ordering of the R_0 in the countries is consistent in all settings. However, as expected, the scale of R_0 is considerably affected by this change – a longer generation results in a higher estimated R_0. This is because to reach the currently observed size of the epidemics, a longer assumed generation is compensated by a higher estimated R_0.



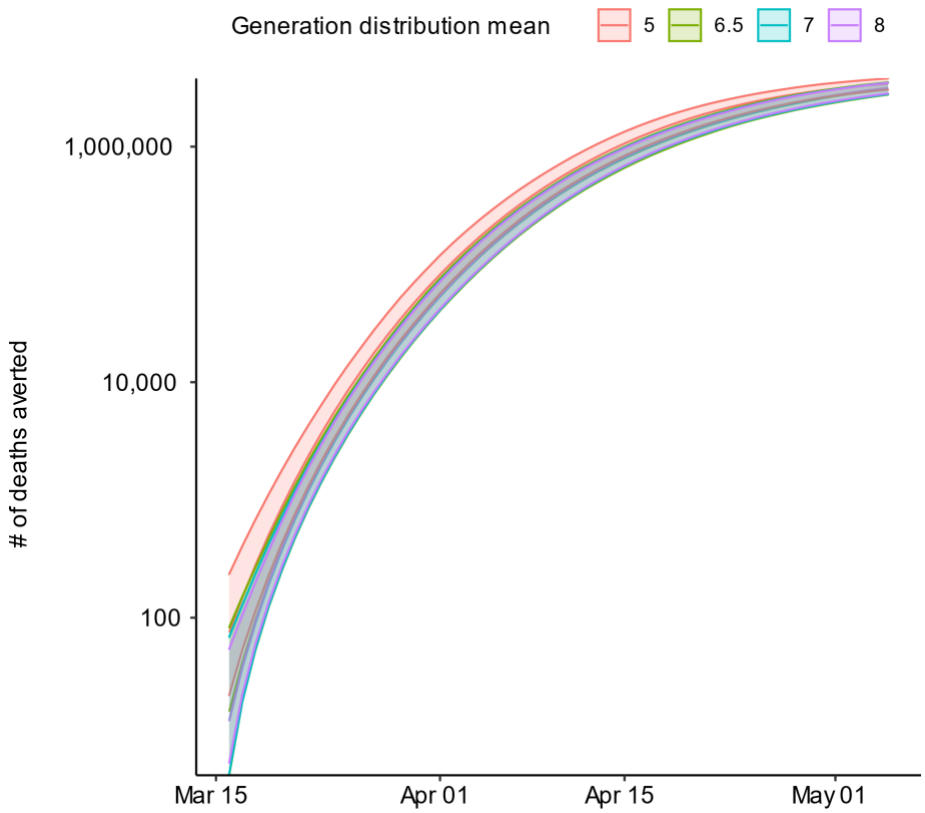
Supplementary Fig. 16. Initial reproduction number R_0 for different generation distributions (means between 5 and 8 days). We use 6.5 days in our main analysis.



Supplementary Fig. 17. R_t on 4th May 2020 estimated for all countries, with generation distribution means between 5 and 8 days. We use 6.5 days in our main analysis

Supplementary Fig. 17 shows t he final R_t estimated on 4th May 2020 for all countries, with generation distribution means again between 5 and 8 days. Following Bi et al 2020[13], we use 6.5 days in our main analysis., we show our estimates of R_t at the most recent model time point, again for each of these scenarios. The generation mean can influence R_t substantially, however, the posterior credible intervals of R_t are broadly overlapping and therefore do not change any of our conclusions regarding the impact of interventions.

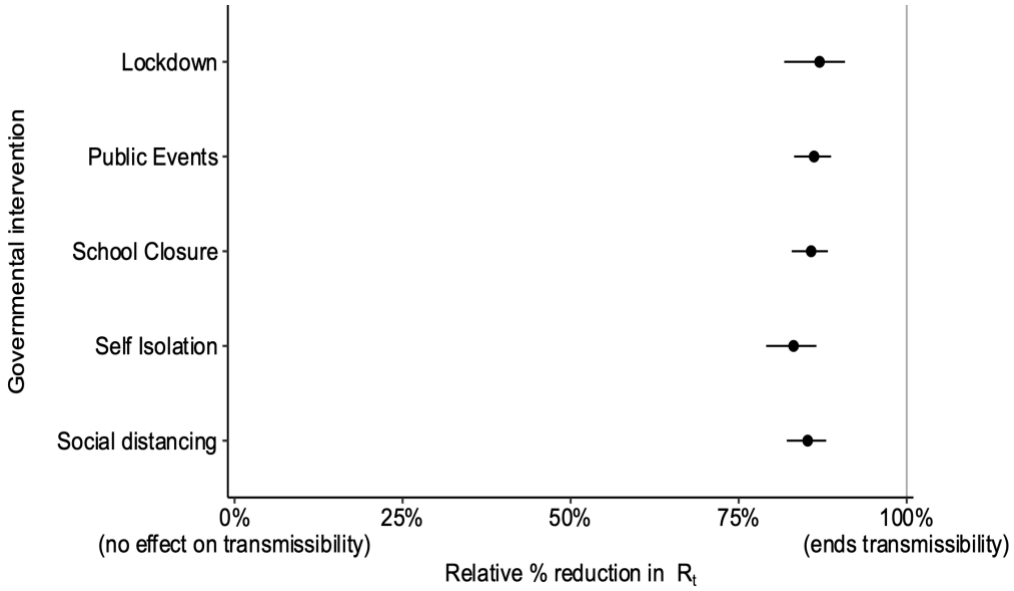
As we have shown in Supplementary Fig. 16 and Supplementary Fig. 17, the generation distribution changes R_0 and therefore can change our counterfactual estimates of the deaths averted. To ensure that the choice of generation distribution does not change our counterfactual conclusions, we calculate full counterfactual deaths averted for generation distributions 5, 6.5 (our choice in this paper), 7 and 8. As seen in Supplementary Fig. 18, while the choice of generation distribution does impact R_0, given our credible intervals there is no significant difference with intervals 5-8. With a lower generation mean the counterfactual R_0 starts lower, but the infection also spreads faster, the converse is true with a higher generation mean.



Supplementary Fig. 18. Counterfactual deaths averted with generation distribution means between 5 and 8 days. We use 6.5 days in our main analysis.

Supplementary Discussion 4. Uninformative prior sensitivity on α

We ran our model using an implausible uninformative prior distribution on the intervention effects, allowing the effect of an intervention to increase or decrease R_t. In addition, to avoid collinearity, we ran 6 separate models, with effects summarized below (compare with the main analysis in Figure 2). In this series of univariate analyses, we find (Supplementary Fig. 19) that all effects on their own serve to decrease R_t. This gives us confidence that our choice of prior distribution is not driving the effects we see in the main analysis. All covariates are similarly effective in reducing R_t.



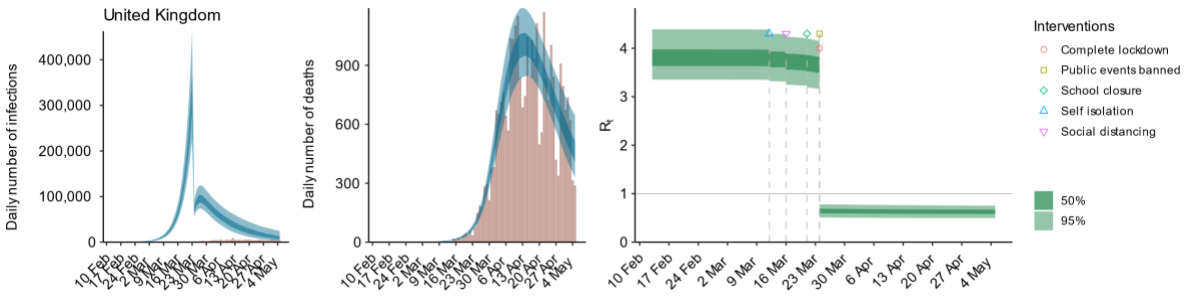
Supplementary Fig. 19. Effects of different interventions when used as the only covariate in the model.

Supplementary Discussion 5. Nonparametric fitting of R_t using a Gaussian process

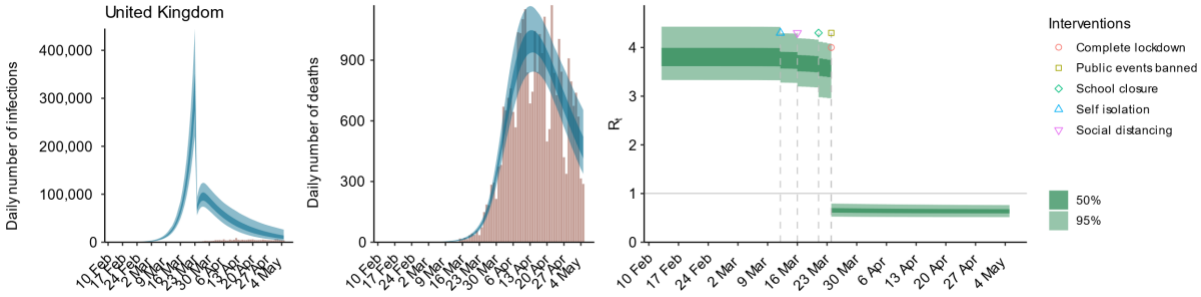
To assess prior assumptions on our piecewise constant functional form for R_t we test using a nonparametric function with a Gaussian process prior distribution. We fit a model with a Gaussian process prior distribution (with zero mean and squared exponential covariance function) to all countries. We find that the Gaussian process has a very similar trend to the piecewise constant model and reverts to the mean in regions of no data. The correspondence of a completely nonparametric function and our piecewise constant function suggests a suitable parametric specification of R_t. Supplementary Table 1 also shows that hold out validation performance from the Gaussian process was worse than our piecewise constant form.

Supplementary Discussion 6. Leave one country out analysis

Due to the different lengths of each European countries' epidemic, some countries, such as Italy have much more data than others (such as the UK). To ensure that we are not leveraging too much information from any one country we perform a "leave one country out" sensitivity analysis, where we rerun the model without a different country each time. Supplementary Fig. 20 and Supplementary Fig. 21 are examples for results for the UK, leaving out Italy and Spain. In general, for all countries, we observed no visually significant dependence on any one country.



Supplementary Fig. 20. Model results for the UK, when not using data from Italy for fitting the model. See the caption of Figure 1 for an explanation of the plots.

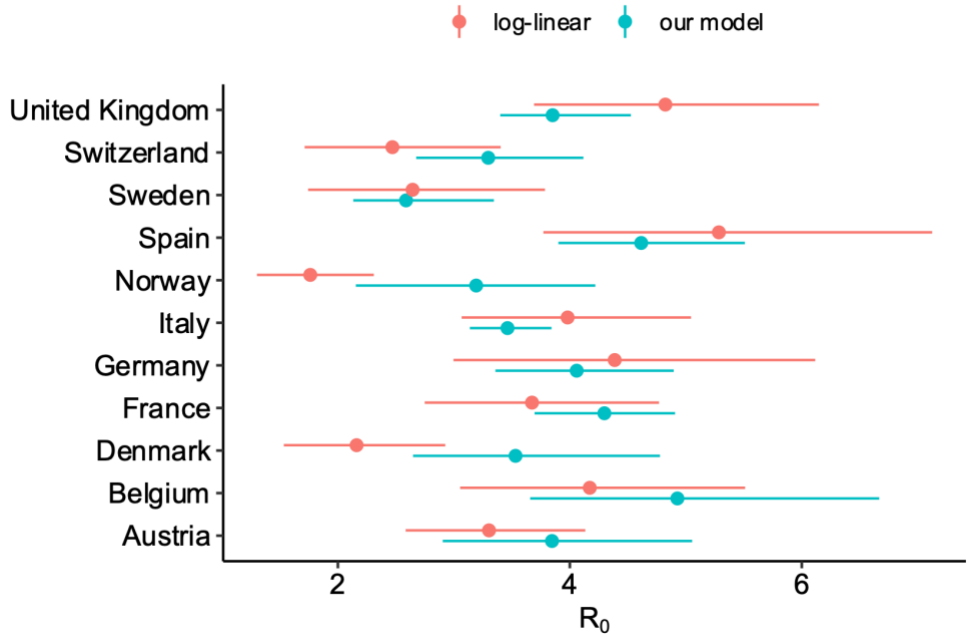


Supplementary Fig. 21. Model results for the UK, when not using data from Spain for fitting the model. See the caption of Figure 1 for an explanation of the plots.

Supplementary Discussion 7. Starting reproduction numbers vs theoretical predictions

To validate our starting reproduction numbers, we compare our fitted values to those theoretically expected from a simpler model assuming exponential growth rate, and a generation distribution mean. We fit a linear model with a Poisson likelihood and log link function and extracting the daily growth rate r. For well-known theoretical results[14] from the renewal equation, given a generation distribution $\mathrm{g}(\tau)$ with mean m and standard deviation s, given $\mathrm{a} = m^2/s^2$ and $\mathrm{b} = \mathrm{m}/s^2$, and subsequently $R_0 = \left(1 + \frac{r}{b}\right)^a$. Supplementary Fig. 22 shows theoretically derived R_0 along with our fitted estimates of $R_{t=0}$ from our Bayesian hierarchical model. As shown in Supplementary Fig. 22 there is large correspondence between our estimated starting reproduction number and the basic reproduction number implied by the growth rate r, with all confidence intervals overlapping.

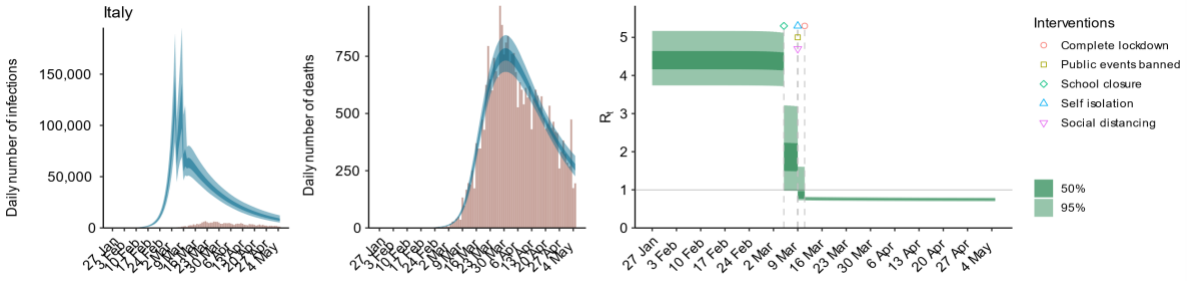
These theoretical fits are not to be taken as the true value but an estimate of R_0 from a different perspective. R_0 estimates from growth parameters are unreliable due to the difficulties in log linear fitting. In addition, this fitting implies a generative model where previous deaths cause future deaths, something that is not conceptually justified.



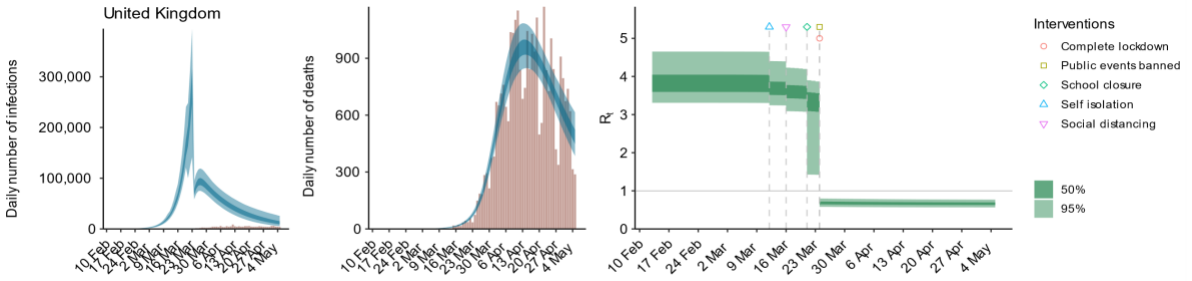
Supplementary Fig. 22. Our estimated R_0 (blue) versus theoretically derived R_0 from a log-linear regression fit.

Supplementary Discussion 8. Separate country analyses

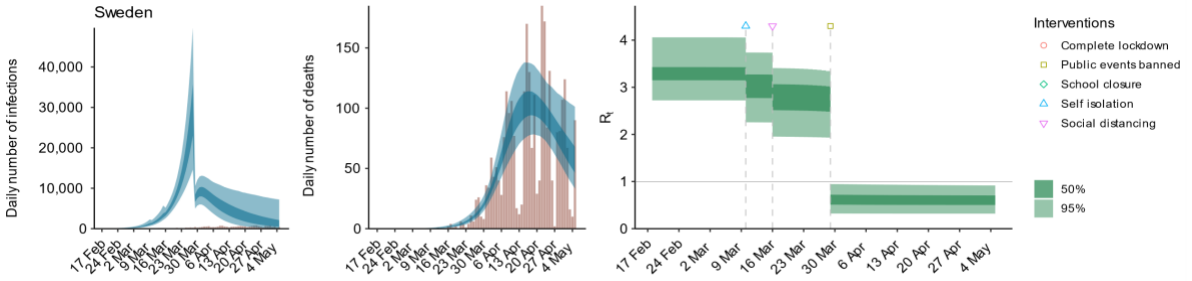
To justify the use of full and/or partial pooling we run an analysis where we fit our model to each country individually and perform no pooling of parameters. Figures Supplementary Fig. 23-Supplementary Fig. 26 show our results for Italy, Sweden the UK and France. These country represent a diverse range with early and late epidemics, as well as a diverse range of interventions.



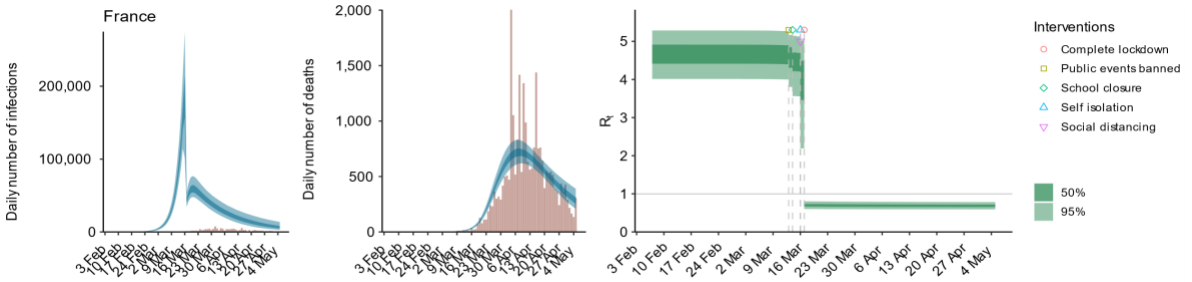
Supplementary Fig. 23. Model results for Italy with no pooling or joint fitting. See the caption of Figure 1 for an explanation of the plots.



Supplementary Fig. 24. Model results for the UK with no pooling or joint fitting. See the caption of Figure 1 for an explanation of the plots.



Supplementary Fig. 25. Model results for Sweden with no pooling or joint fitting. See the caption of Figure 1 for an explanation of the plots.

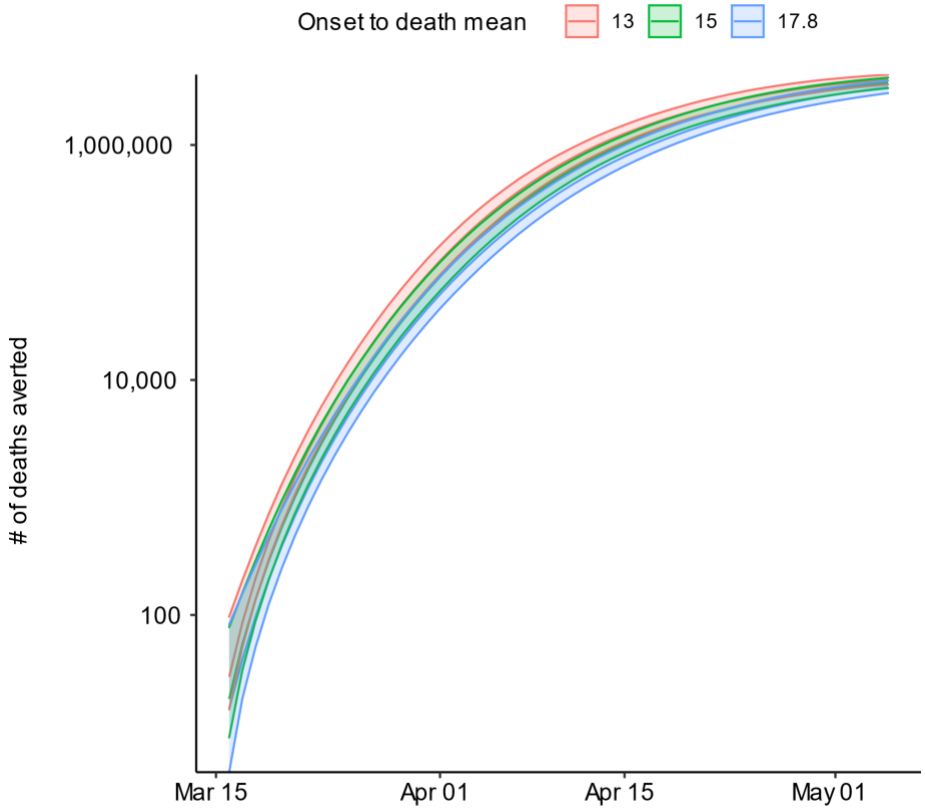


Supplementary Fig. 26. Model results for France with no pooling or joint fitting. See the caption of Figure 1 for an explanation of the plots.

These figures show considerable agreement with the (full and partial) pooled models but the uncertainty is greater in a model with no pooling providing scientific justification for a pooled model. The plots for France (which have considerable volatility) show that individual models are much more sensitive to idiosyncrasies in the data due to reporting. In general, these plots support other sensitivity analysis in this paper and show there is a signal of the impact of interventions even with individual models, but the uncertainty contracts considerably in pooled versions. We also note that the mean squared model fit on point estimates is also worse in from individual models on average, but this is better reflected via the Bayesian uncertainty.

Supplementary Discussion 9. Onset to death distribution

The choice of the mean onset to death distribution is another epidemiological parameter which has an effect on our counterfactual deaths averted. To ensure that the choice of onset to death distribution does not change our counterfactual conclusions, we calculate full counterfactual deaths averted for mean 13[15], 15[16] and 17.8[17] (our choice in this paper). As seen in Supplementary Fig. 27 there is little impact in changing the onset to death mean.



Supplementary Fig. 27. Counterfactual deaths averted with onset to death distribution means 13, 15 and 17.8. We use 17.8 days in our main analysis.

Supplementary Discussion 10. Sensitivity of probabilistic seeding scheme

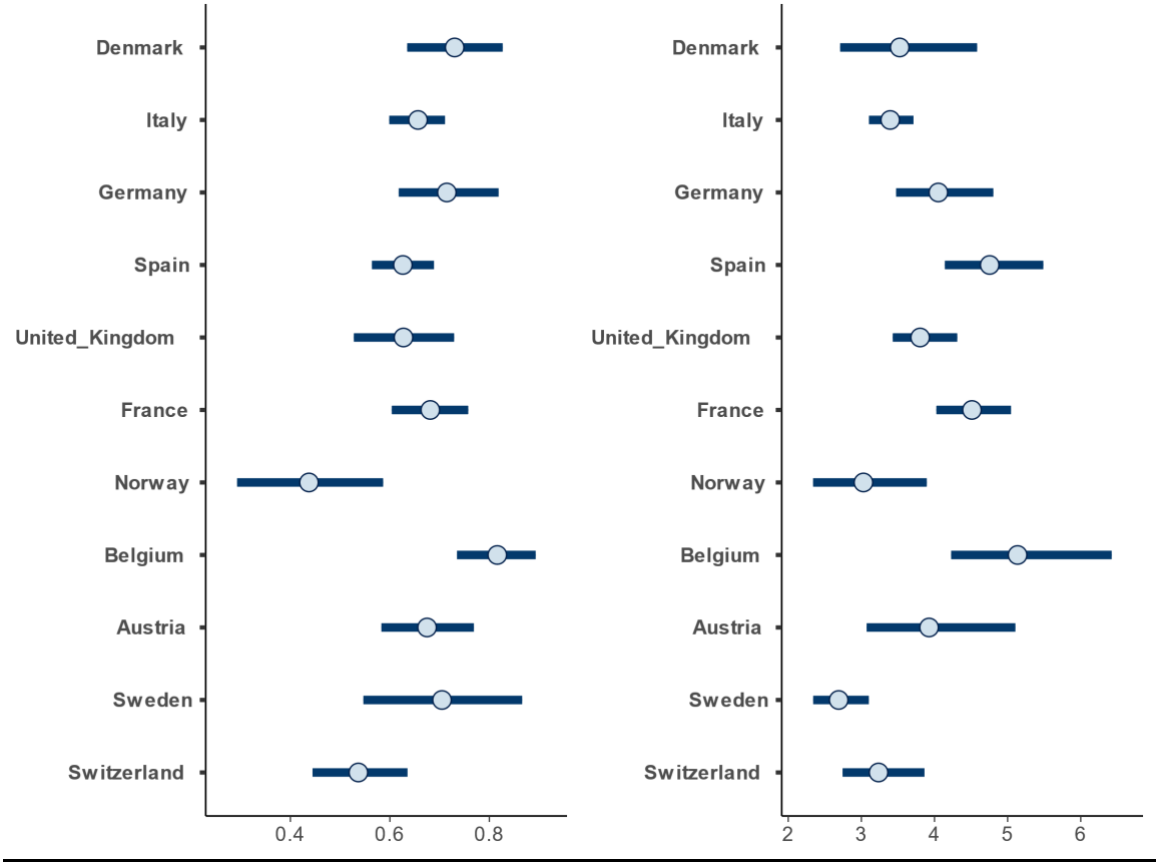
Our probabilistic seeding begins 30 days prior to this. We chose 10 deaths by visually examining the data and seeing that after 10 deaths, deaths became more or less continuous implying an epidemic sustained by local transmission. We chose seeding 30 days prior to this date due to our infection to death distribution.

To test the sensitivity of this choice statistically we used the Pareto smoothed importance-sampling leave-one-out cross-validation (PSIS-LOO)[18]. This approach has been shown to be robust in practice as well as theory[18]. Using these statistics for model selection we looked at pairwise comparisons varying the starting point of the epidemic (when a certain number of deaths is reached) and varying the seeding look back duration (number of days from the starting point). We looked at seeding from a cumulative 5, 10, 15, 20 cumulative deaths and looking back 25, 30, 35, 40 days.

To compare models we estimated the difference between the expected log pointwise predictive density scaled by the standard deviation around them following the PSIS-LOO methodology. There was no statistically significant difference between the model with 10/30 and the other seeding combinations. We therefore feel justified in our choice and do not think there is much sensitivity around this choice.

Supplementary Discussion 11. Under-reporting bias

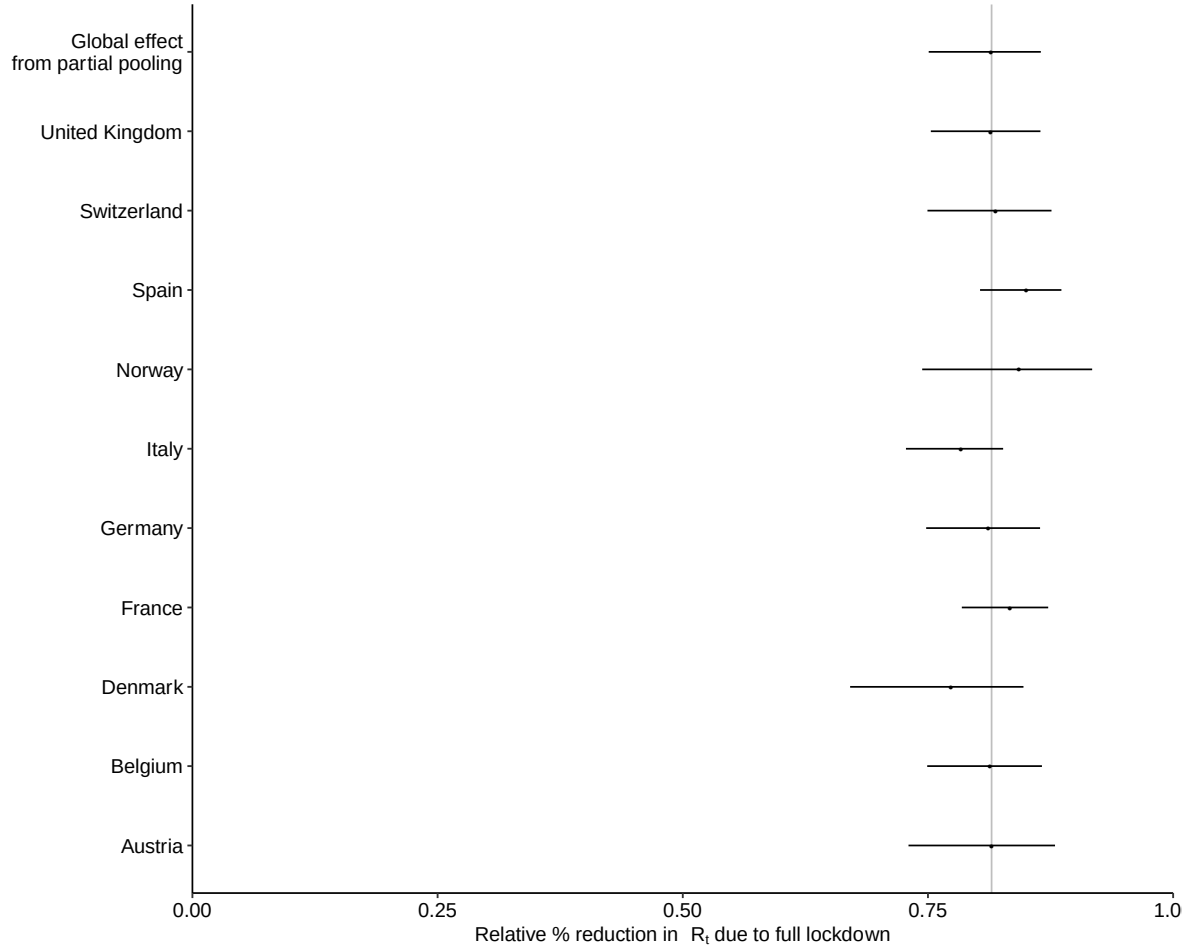
To understand the potential effect or underreporting and to determine whether signals of under-reporting can be estimated from heterogeneities in the data we conduct a sensitivity analysis. We assume a probabilistic multiplicative bias distributed as Beta(30,5). This prior says underreporting can range from none to 40% with a mean of around 15%. If we include this prior bias in our model we observe three things: First, as expected, our estimate of the numbers of infections and deaths increases. Second, we observe that there is no signal in the data to inform the underreporting parameter as the posterior is very close the prior. Third our substantive conclusions about R_t do not change. Supplementary Fig. 28 shows current R_t and R_0 and show these are not significantly different to what we estimate in a model with no under-reporting.



Supplementary Fig. 28. Current (left) and initial (right) reproduction numbers under a model fitted with an under-reporting bias prior.

Supplementary Discussion 12. Effect of partial pooling

This section shows the additional impact of partial pooling on the global effect of lockdown. Supplementary Fig. 29 shows the percentage reduction in R_t due to full lockdown as estimated in our partial pooling model (where, for each country, we report the combined global and country-level effect). The effect of partial pooling is modest in this case, but does have an impact. We considered partial pooling for other covariates but there is not enough signal in our data to warrant inclusion in our model at this time.



Supplementary Fig. 29. Effect of partial pooling on the reduction of R_t

Supplementary Notes. Data sources and Timeline of Interventions

Extended Data Figure 4 and Supplementary Table 2 display the interventions by the 11 countries in our study and the dates these interventions became effective. We categorized the interventions as follows:

School closure ordered: This intervention refers to nationwide extraordinary school closures which in most cases refer to both primary and secondary schools closing (for most countries this also includes the closure of other forms of higher education or the advice to teach remotely). In the case of Denmark and Sweden, we allowed partial school closures of only secondary schools. The date of the school closure is taken to be the effective date when the schools started to be closed (if this was on a Monday, the date used was the one of the previous Saturdays as pupils and students effectively stayed at home from that date onwards).

Case-based measures: This intervention comprises strong recommendations or laws to the general public and primary care about self-isolation when showing COVID-19-like symptoms. These also include nationwide testing programs where individuals can be tested and subsequently self-isolated. Our definition is restricted to nationwide government advice to all individuals (e.g. UK) or to all primary care and excludes regional only advice. These do not include containment phase interventions such as isolation if travelling back from an epidemic country such as China.

Public events banned: This refers to banning all public events of more than 100 participants such as sports events.

Social distancing encouraged: As one of the first interventions against the spread of the COVID-19 pandemic, many governments have published advice on social distancing including the recommendation to work from home wherever possible, reducing use of public transport and all other non-essential contact. The dates used are those when social distancing has officially been recommended by the government; the advice may include maintaining a recommended physical distance from others.

Lockdown decreed: There are several different scenarios that the media refers to as lockdown. As an overall definition, we consider regulations/legislations regarding strict face-to-face social interaction: including the banning of any non-essential public gatherings, closure of educational and public/cultural institutions, ordering people to stay home apart from exercise and essential tasks. We include special cases where these are not explicitly mentioned on government websites but are enforced by the police (e.g. France). The dates used are the effective dates when these legislations have been implemented. We note that lockdown encompasses other interventions previously implemented.

First intervention: As Extended Data Figure 4 shows, European governments have escalated interventions rapidly, and in some examples (Norway/Denmark) have implemented these interventions all on a single day. Therefore, given the temporal autocorrelation inherent in government intervention, we include a binary covariate for the first intervention, which can be interpreted as a government decision to take major action to control COVID-19.

Supplementary Table 2. Timeline of Interventions.

Country	Type	Event	Date effective
Austria	School closure ordered	Nationwide school closures. [19]	14/3/2020
	Public events banned	Banning of gatherings of more than 5 people.[20]	10/3/2020
	Lockdown ordered	Banning all access to public spaces and gatherings of more than 5 people. Advice to maintain 1m distance.[21]	16/3/2020
	Social distancing encouraged	Recommendation to maintain a distance of 1m.[21]	16/3/2020
	Case-based measures	Implemented at lockdown.[21]	16/3/2020
Belgium	School closure ordered	Nationwide school closures.[22]	14/3/2020
	Public events banned	All recreational activities cancelled regardless of size.[22]	12/3/2020
	Lockdown ordered	Citizens are required to stay at home except for work and essential journeys. Going outdoors only with household members or 1 friend.[23]	18/3/2020
	Social distancing encouraged	Public transport recommended only for essential journeys, work from home encouraged, all public places e.g. restaurants closed.[22]	14/3/2020
	Case-based measures	Everyone should stay at home if experiencing a cough or fever.[24]	10/3/2020
Denmark	School closure ordered	Secondary schools shut and universities (primary schools also shut on 16th).[25]	13/3/2020
	Public events banned	Bans of events >100 people, closed cultural institutions, leisure facilities etc.[26]	12/3/2020
	Lockdown ordered	Bans of gatherings of >10 people in public and all public places were shut.[26]	18/3/2020
	Social distancing encouraged	Limited use of public transport. All cultural institutions shut and recommend keeping appropriate distance.[27]	13/3/2020
	Case-based measures	Everyone should stay at home if experiencing a cough or fever.[28]	12/3/2020

France	School closure ordered	Nationwide school closures.[29]	14/3/2020
	Public events banned	Bans of events >100 people.[30]	13/3/2020
	Lockdown ordered	Everybody has to stay at home. Need a self-authorisation form to leave home.[31]	17/3/2020
	Social distancing encouraged	Advice at the time of lockdown.[31]	16/3/2020
	Case-based measures	Advice at the time of lockdown.[31]	16/03/2020
Germany	School closure ordered	Nationwide school closures.[32]	14/3/2020
	Public events banned	No gatherings of >1000 people. Otherwise regional restrictions only until lockdown.[33]	22/3/2020
	Lockdown ordered	Gatherings of > 2 people banned, 1.5 m distance.[34]	22/3/2020
	Social distancing encouraged	Avoid social interaction wherever possible recommended by Merkel.[35]	12/3/2020
	Case-based measures	Advice for everyone experiencing symptoms to contact a health care agency to get tested and then self-isolate.[36]	6/3/2020
Italy	School closure ordered	Nationwide school closures.[37]	5/3/2020
	Public events banned	The government bans all public events.[38]	9/3/2020
	Lockdown ordered	The government closes all public places. People have to stay at home except for essential travel.[39]	11/3/2020
	Social distancing encouraged	A distance of more than 1m has to be kept and any other form of alternative aggregation is to be excluded.[39]	9/3/2020
	Case-based measures	Advice to self-isolate if experiencing symptoms and quarantine if tested positive.[40]	9/3/2020
Norway	School closure ordered	Norwegian Directorate of Health closes all educational institutions. Including childcare facilities and all schools.[41]	13/3/2020
	Public events banned	The Directorate of Health bans all non-necessary social contact.[41]	12/3/2020
	Lockdown ordered	Only people living together are allowed outside together. Everyone has to keep a 2m distance.[42]	24/3/2020
	Social distancing encouraged	The Directorate of Health advises against all travelling and non-necessary social contacts.[41]	16/3/2020

	Case-based measures	Advice to self-isolate for 7 days if experiencing a cough or fever symptoms.[43]	15/3/2020
Spain	School closure ordered	Nationwide school closures.[44]	13/3/2020
	Public events banned	Banning of all public events by lockdown.[45]	14/3/2020
	Lockdown ordered	Nationwide lockdown.[42]	14/3/2020
	Social distancing encouraged	Advice on social distancing and working remotely from home.[46]	9/3/2020
	Case-based measures	Advice to self-isolate for 7 days if experiencing a cough or fever symptoms.[46]	17/3/2020
Sweden	School closure ordered	Colleges and upper secondary schools shut.[47]	18/3/2020
	Public events banned	The government bans events >500 people.[48]	12/3/2020
	Lockdown ordered	No lockdown occurred.	NA
	Social distancing encouraged	People even with mild symptoms are told to limit social contact, encouragement to work from home.[49]	16/3/2020
	Case-based measures	Advice to self-isolate if experiencing a cough or fever symptoms.[50]	10/3/2020
Switzerland	School closure ordered	No in person teaching until 4th of April.[51]	14/3/2020
	Public events banned	The government bans events >100 people.[51]	13/3/2020
	Lockdown ordered	Gatherings of more than 5 people are banned.[52]	2020-03-20
	Social distancing encouraged	Advice on keeping distance. All businesses where this cannot be realised have been closed in all states (kantons).[53]	16/3/2020
	Case-based measures	Advice to self-isolate if experiencing a cough or fever symptoms.[54]	2/3/2020
UK	School closure ordered	Nationwide school closure. Childminders, nurseries and sixth forms are told to follow the guidance.[55]	21/3/2020
	Public events banned	Implemented with lockdown.[56]	24/3/2020

	Lockdown ordered	Gatherings of more than 2 people not from the same household are banned and police enforceable.[56]	24/3/2020
	Social distancing encouraged	Advice to avoid pubs, clubs, theatres and other public institutions.[57]	16/3/2020
	Case-based measures	Advice to self-isolate for 7 days if experiencing a cough or fever symptoms.[58]	12/3/2020

Supplementary Table 3. Attack rate (AR) predicted during an unmitigated epidemic[59] and denominator population in thousands (POP) by country alongside the overall infection fatality rate.

Country		Age brackets																IFR
		0-5	5-10	10-15	15-20	20-25	25-30	30-35	35-40	40-45	45-50	50-55	55-60	60-65	65-70	70-75	75-80	80+	
Austria	AR	91%	99%	98%	97%	92%	87%	96%	97%	96%	93%	87%	83%	82%	67%	71%	58%	58%	1.04%
	POP	448	426	424	452	509	607	620	623	566	613	713	694	582	451	407	383	488	
Belgium	AR	86.4%	92.0%	96.6%	98.0%	97.6%	95.5%	97.4%	97.1%	96.1%	96.0%	93.3%	93.2%	88.3%	80.8%	83.8%	65.0%	65.0%	1.10%
	POP	634	669	671	641	658	728	746	758	752	767	795	803	736	634	556	384	658	
Denmark	AR	90%	99%	98%	96%	90%	86%	97%	98%	96%	93%	88%	84%	82%	66%	67%	59%	59%	1.02%
	POP	309	297	337	339	374	402	355	317	361	377	422	388	346	309	351	235	273	
France	AR	88%	94%	98%	98%	96%	96%	96%	97%	98%	97%	95%	95%	92%	85%	79%	79%	79%	1.26%
	POP	3620	3907	3996	3888	3697	3674	3942	4070	3943	4382	4363	4272	3973	3792	3524	2204	4027	
Germany	AR	92%	94%	97%	99%	97%	97%	96%	96%	98%	96%	93%	89%	87%	86%	79%	62%	62%	1.23%
	POP	4059	3822	3812	4119	4553	4824	5442	5430	5060	5184	6681	6807	5821	4823	3834	3638	5876	
Italy	AR	88%	95%	98%	99%	93%	94%	93%	94%	94%	90%	90%	86%	84%	75%	69%	57%	57%	1.24%
	POP	2325	2670	2857	2876	2943	3161	3366	3633	4189	4833	4908	4659	3954	3531	3392	2637	4529	
Norway	AR	90%	99%	98%	96%	90%	87%	96%	97%	96%	93%	89%	85%	83%	67%	70%	61%	61%	0.91%
	POP	302	313	321	322	353	373	377	362	347	378	377	335	311	275	267	180	229	
Spain	AR	93%	99%	98%	97%	94%	90%	97%	97%	94%	91%	87%	83%	82%	67%	70%	58%	58%	1.08%
	POP	1990	2244	2498	2238	2256	2362	2619	3283	4001	3938	3632	3414	2939	2401	2204	1811	2924	
Sweden	AR	89%	99%	98%	97%	92%	85%	96%	97%	97%	93%	89%	85%	83%	66%	68%	58%	58%	1.03%
	POP	601	593	586	541	544	733	693	627	609	655	679	617	567	527	564	430	532	
Switzerland	AR	91%	99%	98%	97%	92%	87%	96%	97%	96%	93%	87%	83%	82%	67%	70%	59%	59%	1.02%
	POP	452	433	410	425	484	556	598	622	571	596	677	644	536	442	422	330	459	
UK	AR	88%	98%	98%	99%	95%	95%	94%	96%	96%	95%	90%	88%	86%	82%	73%	65%	65%	1.04%
	POP	3924	4120	3956	3686	4075	4484	4707	4588	4308	4296	4635	4539	3905	3382	3388	2442	3451	

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