Large-scale frequent testing and tracing to supplement control of Covid-19 and vaccination rollout constrained by supply

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A B S T R A C T

Non-pharmaceutical interventions (NPI) were implemented all around the world in the fight against COVID-19: Social distancing, shelter-in-place, mask wearing, etc. to mitigate transmission, together with testing and contact-tracing to identify, isolate and treat the infected. The majority of countries have relied on the former measures, followed by a ramping up of their testing and tracing capabilities. We present here the cases of South Korea, Italy, Canada and the United States, as a look back to lessons that can be drawn for controlling the pandemic, specifically through the means of testing and tracing. By fitting a disease transmission model to daily case report data in each of the four countries, we first show that their combination of social-distancing and testing/tracing have had a significant impact on the evolution of their first wave of pandemic curves. We then consider the hypothetical scenario where the only NPI measures implemented past the first pandemic wave consisted of isolating individuals due to repeated, country-scale testing and contact tracing, as a mean of lifting social distancing measures without a resurgence of COVID-19.

We give estimates on the average isolation rates needed to occur in each country. We find that testing and tracing each individual of a country, on average, every 4.5 days (South Korea), 5.7 days (Canada), 6 days (Italy) and 3.5 days (US), would have been sufficient to mitigate their second pandemic waves. We also considered the situation in Canada to see how a frequent large-scale asymptomatic testing and contact tracing could have been used in combination with vaccination rollout to reduce the infection in the population. This could offer an alternative approach towards preventing and controlling an outbreak when vaccine supply is limited, while testing capacity has been increasingly enhanced.

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1. Introduction

In late 2019, a novel betacoronavirus called SARS-CoV-2 emerged from a live animal marketplace in Wuhan, Hubei Province, China, and has since inflicted a worldwide pandemic of a disease now referred to as COVID-19. The disease is highly contagious, with an estimated $R_0$ between 2.2 and 4.6 (Anastassopoulou, Russo, Tsakris, & Siettos, 2020; Guan et al., 2020) although it is important to consider that $R_0$ is not strictly biologically determined but rather heavily influenced by host behavioural and environmental factors (Neher, Dyrdak, Druelle, Emma, & Albert, 2020). The incubation period has been found to be 5.1–5.2 days, while 97.5% of patients display symptoms within 11.5 days (Guan et al., 2020; Lauer et al., 2020). The disease spreads primarily through the respiratory tract, through droplets and aerosols. Outbreaks continued throughout the world in 2020 and in 2021, with new cases reported daily. Most countries have passed a first wave in March—May of 2020 and a second wave in November 2020—January 2021, while many are in the midst of a new wave, under the presence of mutated, more infectious variants of concern (University of Manitoba, 2021). Countries have taken various degrees of social distancing measures: lockdown, shelter-in-place, banning gatherings and sport events, closing schools, mask-wearing etc. (e.g. (Ashleigh et al., 2020a; Ashleigh et al., 2020b; Centor & Fisman, 2020; Cereda et al., 2003, p. 2020; Ferguson et al., 2020; Tang et al., 2020)) in an effort to suppress disease transmission, or at least prevent it from reaching levels that would overwhelm a country’s critical care capacity. While proven effective to slow the spread, these measures have had a large effect on daily lives and economies throughout the world. Countries which managed to stave off their first waves have been implementing (in various degrees) relaxation measures during June—September of 2020, in an effort to restore, as much and as safe as possible, their socio-economic landscapes. The cycle of measures repeated itself during the second and third waves of the pandemic.

In this paper we are interested in examining the degree of success in staving off pandemic waves in four developed countries (Italy, Canada, South Korea and United States) when social distancing measures are paired with country-scale repeated testing and tracing strategies, which would have allowed more phasing out social distancing measures while preventing a resurgence of outbreaks (Kissler, Tedijanto, Goldstein, Grad, & Lipsitch, 2020; Laydon et al., 2020; Tindale et al., 2020). To start, fitting a disease transmission model to daily case reports in each country above allows the assessment of effectiveness of their COVID-19 countermeasures at two intermediate points in their pandemic history: passed their first wave - July 2020 and during their second wave - November 2020.

The analysis begins with Italy, Canada and the United States, three countries which have relied principally on social distancing and mask-wearing via universal shelter-in-place measures, while testing and contact tracing was implemented at an increased pace only after the first pandemic wave was more-or-less established in their populations. It continues on with South Korea, a country which has had a tighter control on COVID-19 through a combination of early aggressive testing and contact tracing, paired with social-distancing measures, but avoiding economic and social lockdown.

A policy scenario involving country-wide repeated asymptomatic testing and tracing could have avoided a second pandemic wave in Canada and Italy which can be seen by comparison with the past pandemic evolution data. On the other hand, relaxation of social-distancing combined with population’s fatigue and lower levels of compliance through the summer and fall have led directly to a second wave, and again to various degrees of lockdown measures. This could have been avoided through scaling up frequency of testing and tracing in the population at large, rather than lockdown measures, resulting in lower pandemic waves. Specifically, an average frequency of testing every individual every 4.5 days (and tracing contacts of discovered infected individuals) in Canada and Italy would have suffice in keeping incidence rates under control. A similar analysis for the United States and South Korea is presented together with frequencies of testing and tracing for their populations.

Last but not least, the work is brought into the present in the specific case of Canada, by implementing the proposed repeated large-scale asymptomatic testing and tracing policy with the current Canadian vaccination campaign (over January—April 2021), in the presence of variants of concern and their much more infectious nature, in line with current expert opinions (2021Cojocaru, Najafabadi, Wu, & Asgary; Liu, Arora, & Krajden, 2021; Polack et al., 2020; SchwartzAllison and Isaac, 2021). It is seen that, due to the vaccination impact, an average frequency of 30 days for every individual in Canada and Italy would have reduced the current incidence number by 12%, while a testing frequency of 20 days would have avoided the current third wave. This, once again, shows the power of large scale asymptomatic testing, as a middle ground between sever lockdown/social-distancing measures and controlled incidence while vaccination ramps up.

The structure of the paper is as follows: Section 2 introduces our model’s main ideas, notation, and assumptions. Section 3 presents the fitted infection curves for Italy, Canada, the U.S. and South Koreaand evaluates scenarios for countries to phase out social distancing while preventing a resurgence of COVID-19 outbreaks. Section 3 also presents the frequencies with which a tested (infected) individual and an exposed (traced) individual needed to be detected and isolated in order for each country to maintain an effective reproduction number of 1 (that is to say, each country maintains a “slow burn” of their pandemic), while assuming a major relaxation of social-distancing rules. Section 4 shows that repeated asymptomatic testing and tracing, together with vaccination campaigns could have avoided lockdown and would have reduced daily incidence considerably in Canada, over January to May 2021, for a frequency of 10, 14, 20, respectively 30 days. The paper closes with a thorough discussion of challenges and opportunities presented by the proposed policy in Section 5. Additional mathematical background is included in Appendix.
2. Materials and methods

2.1. The SEIRL model

The transmission of an infectious disease in a homogeneously mixed population is often described by a Susceptible-Infectious-Recovered (SIR) model (Ogilvy Kermack & McKendrick, 1927; van den Driessche, 2017), or its variants, most notably a Susceptible-Exposed-Infectious-Recovered (SEIR); see (Ma, 2020) for a recent review. A SEIR model normalized to a population of size $N$ is described by:

\[
\begin{align*}
\frac{ds}{dt} &= -\beta si, \\
\frac{de}{dt} &= \beta si - \sigma e, \\
\frac{di}{dt} &= \sigma e - \gamma i, \\
\frac{dr}{dt} &= \gamma i, \\
\end{align*}
\]  

(1)

with $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $r = \frac{R}{N}$, $s + e + i + r = 1$ and where $\beta$ is the rate of effective contacts, $1/\sigma = T_{lat}$ is the mean latent period (which may differ from the incubation period), and $1/\gamma = T_{inf}$ is the mean duration of infectiousness, with both times having exponential distributions. We also have the auxiliary equation for the cumulative number of cases,

\[
\frac{dc}{dt} = \sigma e.
\]

The daily incidence of cases on day $t$ is then

\[
inc_t = c_t - c_{t-1}.
\]

The spread of an infectious disease can be halted if its effective reproduction number $R_{eff} = R_0s$ can be decreased below 1. The effective reproduction number of the SEIR compartmental disease transmission models is

\[
R_{eff} = \frac{\beta}{\gamma}.
\]  

(2)

When $s = 1$ and we are near the disease-free equilibrium $(1, 0, 0, 0)$, the early growth of both $i$ and $inc$ is exponential (see e.g. (Ma, 2020)):

\[
i(t) = i_0e^{\sigma t}, \quad inc(t) = inc_0e^{\sigma t},
\]  

(3)

In the SEIR model we can estimate the growth factor near the DFE as in (Ma, 2020):

\[
\rho_{SEIR} = \frac{-(\sigma + \gamma) + \sqrt{(\sigma - \gamma)^2 + 4\sigma\beta}}{2},
\]  

(4)

and by solving for $\beta$ from Equation (4) we get:

\[
R_{0SEIR} = \frac{\rho_{SEIR}^2 + \sigma\rho_{SEIR}}{\sigma\gamma}.
\]  

(5)

For COVID-19, as for other pandemics (e.g. SARS, MERS, the 1918 Spanish flu), we can assume the entire population to be initially susceptible. Therefore, in the early stages of an outbreak, $R_{eff} = R_0$. We will also assume that infection with COVID-19 confers subsequent immunity, which does not wane significantly over the time horizon considered here. Thus, whether they die or recover, an infected person is considered removed from the pool of susceptibles. In the absence of a vaccine or other control measures, $s(t) = \frac{1}{c(t)}$, where $c(t)$ is the cumulative number of people infected at time $t$.

From Equation (2), assuming $\beta$ to be given, we see that $R_{eff}$ can be decreased in two ways: by decreasing $s$ at a rate higher than that due to infection alone (for instance by quarantine and lockdown; or by increasing $\gamma$. The former can be considered as an abstraction of social distancing measures, since these effectively take a part of the population “out of circulation” as far as disease transmission is concerned. The latter can be achieved by identifying and isolating infected individuals early, thus cutting short $T_{inf}$.
To explicitly depict the role of control measures, we adapt the SEIR model to a pandemic setting by adding an isolated (L) compartment. As before, we include the auxiliary equation for $C$, the cumulative number of infected. The resulting SEIRL model, is described by:

$$\frac{ds}{dt} = -\beta si,$$

$$\frac{de}{dt} = \beta si - \sigma e - \kappa_1 e,$$

$$\frac{di}{dt} = \sigma e - (\gamma + \kappa)i,$$

$$\frac{dr}{dt} = \gamma i,$$

$$\frac{dl}{dt} = \kappa i + \kappa_1 e,$$

$$\frac{dc}{dt} = \sigma e,$$

where, as in the standard SEIR model, $\beta$ is the mean rate of effective contacts, $1/\sigma = T_{lat}$ is the mean latent period, and $1/\gamma = T_{inf}$ is the mean infectious period. Finally, $1/\kappa_1 = T_{isol, lat}$ and $1/\kappa = T_{isol, inf}$ are the mean times for the latent and infectious, respectively, to be isolated as a consequence of asymptomatic testing and contact tracing, respectively.

Its effective reproduction number is then given by (see Appendix as adapted from [Ma, 2020]):

$$R_{eff, SEIRL} = \frac{\beta \sigma}{(\sigma + \kappa_1)(\gamma + \kappa)}.$$  \hspace{2cm} (6)

It can be shown (see Appendix) that the exponential growth rate (Equation (3)) of infected near the disease-free equilibrium is

$$\rho_{SEIRL} = \frac{-(\sigma + \kappa_1 + \gamma + \kappa)}{2} + \frac{\sqrt{((\sigma + \kappa_1) - (\gamma + \kappa))^2 + 4\sigma \beta \sigma}}{2},$$

and the rate of effective contacts is

$$\beta_{SEIRL} = \frac{(\sigma + \kappa_1 + \rho_{SEIRL})(\gamma + \kappa + \rho_{SEIRL})}{\sigma}.$$  \hspace{2cm} (7)

We can also express the effective reproduction number in terms of $\rho_{SEIRL}$:

$$R_{0, SEIRL} = \frac{(\sigma + \kappa_1 + \rho_{SEIRL})(\gamma + \kappa + \rho_{SEIRL})}{(\gamma + \kappa)\sigma}.$$  \hspace{2cm} (8)

2.2. Estimating $R_0$ from early exponential growth

While growth is still exponential, it follows from Equation (3) that

$$\log(inc(t)) \propto \rho t,$$

i.e. a log-linear plot of incidence versus time will have slope $\rho$. Indeed, early exponential growth can be seen to be a near-universal feature in COVID-19 daily case count data from around the world. Figs. 1 and 2 plot $\log(inc)$ versus time for South Korea, Italy, Canada and the U.S., using time series data of daily new cases compiled by the Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) ([Dong, Du, & Gardner, 2020], retrieved from [John's hopkins covid-19 d, 2021]).

\footnote{In the limit as $\sigma \to \infty$, the SEIR model reduces to the SIR model, and accordingly, as can readily be shown by L'Hospital’s rule.}

$$\lim_{\sigma \to \infty} \frac{(\rho_{SEIR} + \sigma)(\rho_{SEIR} + \gamma)}{\sigma} = \frac{\rho_{SEIR} + \gamma}{\gamma}.$$  \hspace{2cm} (9)
In all four countries the initial linear phase is clearly apparent, followed by a transition to sub-exponential growth. This transition is sharpest for South Korea, where growth switches abruptly to decay around 1 March. Regression fit results for $r$ and the corresponding doubling time, $T_{dbl}$, are given in Figs. 1 and 2 and Table 1. In all four cases, the transition to sub-exponential growth occurred at or after the time that widespread protective measures were first invoked.

$$T_{dbl} = \frac{\ln(2)}{r}$$  \hspace{1cm} (10)

together with dates for the onset of major national-level protective measures, are given in Figs. 1 and 2 and Table 1. In all four cases, the transition to sub-exponential growth occurred at or after the time that widespread protective measures were first invoked.

| Country     | $r$ initial growth | $R_0$   |
|-------------|--------------------|---------|
| S. Korea    | 0.22(0.15,0.29)    | 2.38(1.88,2.94) |
| Italy       | 0.18(0.16,0.2)     | 2.1(1.98,2.22)  |
| Canada      | 0.18(0.16,0.2)     | 2.11(1.97,2.26) |
| U.S.        | 0.3(0.27,0.33)     | 3.07(2.81,3.35) |

Estimates of initial exponential growth rate $r$ are obtained from regression fits to the early outbreak phases (Figs. 1 and 2). Corresponding values of $R_0$ assume $T_{lat} = T_{inf} = 2.5$ days. Estimates of the fraction of cases reported are taken from (Russell et al., 2020), see also (Russel et al., 2020).
Inferring $R_0$ from $\rho$ requires choosing values for the mean latent ($\frac{1}{\gamma}$) and infectious ($\frac{1}{\sigma}$) periods. The sum of these is the mean serial interval:

$$T_{ser} = T_{lat} + T_{inf} = \sigma^{-1} + \gamma^{-1}.$$  

(11)

Estimates of the serial interval of COVID-19 range from 3.95 to 6.6 days (Bi et al., 2020; Cereda et al., 2003, p. 2020; Ganyani et al., 2020; Tindale et al., 2020). We adopt a value of $T_{ser} = 5$ days. The latent period, $\frac{1}{\gamma}$ of the disease is not well constrained, but it can be shown (Appendix A) that for a given value of $T_{ser}$ and $\rho$, the maximum value of $R_0$ is obtained when $T_{lat} = T_{inf} = T_{ser}/2$. We assume this “worst-case” scenario and let $T_{lat} = T_{inf} = 2.5$ days.

2.3. Quantifying the effectiveness of COVID-19 countermeasures until November 2020

We begin with the remark that all 4 countries have enacted social distancing via school closures, nationwide shutdowns, shelter-in-place orders, mask wearing, etc., all in various combinations. South Korea was the first to impose measures (February 2020), followed by Italy, where the measures were ordered and coordinated eventually country-wide. In Canada most provinces enacted similar measures over the course of 1–2 weeks around March 20, 2020, while the United States has had the more heterogeneous spread of similar measures, depending on specific states.

The measures in these three countries were similar, in that schools and universities were closed, non-essential businesses were closed, anybody who could transition to working from home, with the exception of front-line workers, travel was restricted, both national and international, etc. However, each country implemented these in a different way. Italy has gradually worked up to the eventual lockdown phase (see (McNeil, 2020) throughout February and Ma, 2020) lockdown has been lifted through Ma, 2020. Italy reimposed some regional lockdown in November 2020. Canada has imposed a lockdown between March 11 and March 15, 2020 ((CBC News, 2020) then lifted it over the course of early summer 2020. Canada reimposed some regional lockdown in November 2020.) The United States had a heterogeneous approach (with states affected early, such as New York, Washington, California imposing shelter-in-place policies in March) followed by others after an emergency declaration nation-wide on March 13, 2020. The heterogeneity in social-distancing measures has continued in US, where the pandemic went through a subsequent second and a third wave. Finally, US was heterogeneous with respect to mask-wearing throughout 2020, while Canada and Europe have adopted mask-wearing in public, in retail and business places, in schools, etc. Schools re-opened in US, Canada and Europe in Fall 2020.

South Korea has followed a different model from the other three countries. Instead of lockdown and shelter-in-place, they increased production and implementation of testing and tracing to a large scale (using electronic tracing of contacts and enforced isolation (McNeil, 2020)), while having the added benefit that mask-wearing is a well-adopted and established social norm. Schools have continued to function in South Korea under social-distancing guidelines.

For each country, we fit the SEIR model solutions for daily incidence $\{inc_{\text{model},b}, \ldots, inc_{\text{model},n}\}$ to daily case reports. The model output is multiplied by a factor $kf$, where $k$ is an estimate of the fraction of symptomatic cases reported, obtained using delay-adjusted case fatality rates (Russellet al., 2020), and $f$ is the fraction of cases which are symptomatic, estimated to be $f = 0.5$, from a recent CDC report.  

We interpret the transition from exponential to sub-exponential growth (see Figs. 1 and 2) as the first signature of the effect of these restrictive measures in a given country, and use this as the starting point to infer the net effect that these measures have had up to the end of June 2020.

We compute $-\log L$, the normal negative log likelihood of the time series of observed daily incidences, $\{inc_{\text{obs},b}, \ldots, inc_{\text{obs},n}\}$, given the model output, as a function of model parameters

$$x = (i_0, q_1, q_2, \ldots, q_m)$$

where $i_0$ is the initial number of infected and the $q_i$ are reduction factors on the rate of disease transmission, varying over time, such that $\beta_i = q_i \beta$ (see Table 1). $R_0$ for each country is fixed at the respective values obtained via regression above. Parameters are drawn using uniform hypercube sampling. The best-fit solution is the one which minimizes $L$. We estimate the 95% confidence interval as comprising all solutions having $-\log L \leq (-\log L)_{\min} + 1.92$ (see e.g. (Cowan, 1998).

We present our best fits for Italy (in Fig. 14), Canada (in Fig. 3), the U.S. (in Fig. 16) and South Korea (in Fig. 15) below, including the following curves:

- Linear and semi-log plots of daily incidence data of confirmed cases per country, together with maximum-likelihood model fit (“with measures, confirmed”).
- Infected true number of infected, taking into account under-reporting and asymptomatic cases (“with measures, all”). Shown for comparison are the number of confirmed cases (“no measures, confirmed”) and all cases (“no measures, all”) expected to have occurred in the absence of countermeasures.

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2 COVID-19 Pandemic Planning Scenarios, https://www.cdc.gov/coronavirus/2019-ncov/hcp/planning-scenarios-h.pdf.
Cumulative incidence and inferred reduction in effective contact rates \((q_i \beta)\) due to social-distancing, mask wearing etc. These fits assume \(k = k_1 = 0\), in other words, the reduction in the effective contact rates \(q_i\)'s are a measure of each country's combination of measures to date, including social-distancing, testing and tracing.

To illustrate further that social-distancing and lockdown measures were not enough as a central focus to control the pandemic, we present here our model for all four countries through to November 2020, when the countries were in the second wave. We include here Canada and its pandemic profile below in Fig. 3, while Italy, South Korea and US are included in Figs. 14–16 in Appendix.

In Canada interventions managed the initial exponential rise in cases and brought the effective reproduction number below 1. Daily case numbers entered a second wave in the Fall of 2020. From Fig. 12, Canada maintained an average of 40%–50% reduction in the transmission rate \(\beta\) through social distancing measures (see Fig. 4).

3. Large-scale frequent testing and tracing as a way to relax social-distancing measures and control the spread beyond July 2020

3.1. Theoretical estimates after the first pandemic wave - the SEIRL model

As presented in Section 2, for a given set of values of \(\beta\), \(\sigma\) and \(\gamma\), Equation (6) gives us a closed form expression for \(R_{eff,SEIRL}\) as a function of \(k\) and \(k_1\). This relationship is depicted as a surface plot in Fig. 5 for \(\sigma = \gamma = \frac{1}{2}\) and \(\sigma = \gamma = \frac{1}{3}\). In the former case, \(R_{eff,SEIRL}\) is nearly twice as large as in the latter. It is interesting to note, though, that for both cases, the combinations of \(k\) and \(k_1\) that make \(R_{eff,SEIRL} = 1\) (i.e. the intersections of the respective surfaces with the \(R_0 = 1\) plane) are quite similar. This can be understood as follows: As \(\sigma\) and \(\gamma\) become small compared to \(k_1\) and \(k\), respectively, it is the value of \(k\) which becomes more important for determining the rate at which exposed/infected people are isolated.

From Equation (6), we obtain the relationship between \(k\) and \(k_1\) that makes \(R_{eff,SEIRL} = 1\):

\[
1 = \frac{s \hat{\beta} \sigma}{(\sigma + k_1)(\gamma + k)} \Rightarrow k = \frac{s \hat{\beta} \sigma}{\sigma + k_1} - \gamma.
\]

(12)

Extracting the current values of \(s\) from our simulations of the last section, we can now compute average isolation rates due to testing and tracing that would have ensured an effective reproduction number of 1, while assuming that the effective contact rates \(\beta\) would reverse to their values near the disease-free equilibrium, before any other social distancing measures were employed. We further assume that the isolation rate due to contact tracing \((k_1)\) is the same as the isolation rate due to testing \((k)\). We present our results compactly in Table 2 below.

In all cases, we chose \(\gamma = \sigma = \frac{1}{2s}\) for a \(T_{serv} = 5\) days and where \(s\) are the estimated values of susceptibles remaining in each country in mid July 2020.
At the end of June 2020, while the U.S. and South Korea did not seem to have an effective reproduction number under 1, Canada and Italy did have their effective reproduction number estimated to be $R_{eff} = 0.83$, as seen from Figs. 1 and 2. In their cases, we can redo our estimates for the 2 countries and compute the isolation rates due to testing and tracing so that they would have maintained their current value of $R_{eff} = 0.83$ (see Table 3):

In all cases, we chose $\gamma = \sigma = \frac{1}{T_{ser}}$ for a $T_{ser} = 5$ days and where $s$ are the estimated values of susceptibles remaining in each country in mid July 2020.

Figure 4. Canada - daily incidence and log-daily incidence fits to November 2020: Cumulative incidence (top) and inferred reduction of effective contacts ($\beta$), together with the corresponding effective reproduction numbers (vertical numbers) (bottom).

Figure 5. Effects of isolation rates due to testing and contact tracing on the initial value of $R_{0}$SEIRL model. We computed $\sigma = \gamma = \frac{1}{2.5}$ (upper most surface), $\sigma = \gamma = \frac{1}{5}$ (middle surface) and the reference surface $R_{0} = 1$.

Table 2
Model results for South Korea, Italy, Canada, and the U.S. for $R_{eff} = 1$.

| Country | $\beta$ | $s$ | $R_{eff}$ | $\kappa = \kappa_1$ | $\frac{1}{\kappa} \times \frac{1}{\kappa_1}$ |
|---------|---------|-----|-----------|---------------------|-----------------------------------|
| SK      | 0.961   | 0.999| 1         | 0.22                | (4.5, 4.5) days                   |
| Italy   | 0.841   | 0.937| 1         | 0.161               | (6.2, 6.2) days                   |
| Can     | 0.841   | 0.982| 1         | 0.175               | (5.7, 5.7) days                   |
| U.S.    | 1.225   | 0.96 | 1         | 0.288               | (3.5, 3.5) days                   |
3.2. Numerical estimates after the first pandemic wave

We present next pandemic mitigation scenarios under different testing and contact tracing rates, in the four countries under consideration in 2 cases: applied past the first wave (from July 2020 onward) and applied during the second wave (from November 2020 onward). We show how the theoretical estimates above arise in the context of the simulated pandemic evolution in each of the 4 countries up to July 1st, 2020, as a glimpse of what these policies could have accomplished. In subsection 3.3 below, we update our models and present the current situations, together with estimates on frequent testing and tracing that could have helped mitigate, at least in part, the second pandemic wave.

We depict first Canada and Italy (in Fig. 6 respectively), as they have similar estimates, in several respective testing and contact tracing scenarios. We clearly see that for values of $k/C_0 < k_1$, a second pandemic wave is averted in each respective country. This threshold is the least stringent in Italy, where about 6% of the population (accounting for asymptomatic and/or unreported cases) is inferred to have been infected in the first wave, as opposed to Canada.

The simulations for South Korea and the United States are presented in Fig. 7. We see that the isolation rates are the most stringent (lowest values in days) for the U.S., where the value of $R_0$ inferred from the initial exponential rise of cases was higher at the end of June 2020 than those of the other three countries ($\approx 1.2$). In the case of the United States, a large-scale testing and tracing operation alone would not have been able to curtail their summer epidemic curve, thus social-distancing measures would still have been needed.

### Table 3

Model results for Italy and Canada for $R_{eff} = 0.83$.

|       | $\beta$ | $s$    | $R_{eff}$ | $\kappa = k_1$ | $(\frac{1}{k_1}, \frac{1}{\kappa})$ |
|-------|---------|--------|-----------|----------------|----------------------------------|
| Italy | 0.841   | 0.937  | 0.83      | 0.216          | (4.62, 4.62) days                |
| Can   | 0.841   | 0.982  | 0.83      | 0.23           | (4.33, 4.33) days                |

3.3. Second waves and use of large-scale testing and tracing for control

Given the much higher infectious numbers in November 2020 vs. July 2020 as in Section 2.3, we see that testing and tracing at scale could have helped in the control of the pandemic (see Fig. 8), however they may have taken a while to curb down the incidence curve. In Italy’s case, a testing and tracing strategy of 4 days would result in a sharp curbing down of the infected curve in approximately 2–3 weeks.

In Canada (see Fig. 9), if testing and tracing every 4 days were implemented at the end of November 2020, then the growth in infected cases could have been curbed down sharply in 2–3 weeks. In fact, all testing-only strategies, as well as testing & tracing, would have resulted in a much lower peak and a dramatic arrest of the infected curve.

In South Korea, which also experienced a resurgence (but with an effective reproduction number lower than in the first wave), a testing and tracing frequency of 4 days replaced would have had a similar effect as in Canada (see Fig. 10 - upper panel).

In the case of US, a frequency of isolation due to testing and tracing every 3 days would have yielded the fastest results, with the most dramatic arrest of the infected curve (See Fig. 11). Even a frequency of 4 days would have curbed down the infections in approximately 6–8 weeks from November 2020 onward.

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Fig. 6. Predicted daily cases in Italy (left) and Canada (right) under different rates of isolation due to testing, or testing plus contact-tracing, accompanied by a cessation of distancing measures.
Fig. 7. Predicted daily cases in South Korea (left) and the US (right) under different rates of isolation due to testing, or testing plus contact-tracing, accompanied by a cessation of distancing measures.

Fig. 8. The effects of testing and tracing on the current transmission levels in Italy during the second wave.

Fig. 9. The effects of testing and tracing on the current transmission levels in Canada during the second wave.
4. Vaccination and large-scale asymptomatic testing and tracing - Canada in January–April 2021

To illustrate the potential power and use of our policy (in line with current expert opinions (SchwartzAllison and Isaac, 2021)), we quantify its use in the context of Canada in the first four months of 2021, specifically December 21, 2020 to April 30, 2021, with two underlying elements that are different (and new) to 2021: the increasing vaccination coverage in the country, and the presence of variants of concern (VOCs) (University of Manitoba, 2021). The vaccination campaign has started quite slow in Canada throughout January and February, but accelerated in March and April. By the end of April 2021, Canada had approximately 12 million vaccinated individuals with the 1st dose, among which approximately 1 million fully vaccinated (with both doses) (Public Health Agency of C, 2021).

We are thus presenting a simulated scenario in which the vaccination campaign is implemented at a rate meant to reach the target of 12 million people in 130 days (December 21, 2020—April 30, 2021), with an efficacy of approximately 70% (Polack et al., 2020) by modifying the SEIRL model of Section 2 to feature a vaccinated compartment as follows:

\[
\begin{align*}
\frac{ds}{dt} &= -\beta(t)s - ef\cdot p(t)\cdot s , \\
\frac{de}{dt} &= \beta(t)s - \sigma e - \kappa_1 e, \\
\frac{di}{dt} &= \sigma e - (\gamma + \kappa)i, \\
\frac{dr}{dt} &= \gamma i , \\
\frac{dl}{dt} &= \kappa i + \kappa_1 e, \\
\frac{dv}{dt} &= \delta(t)\cdot ef\cdot s,
\end{align*}
\]

where \( \delta(t) \) is a time-dependant vaccination rate (implemented as a piecewise continuous function), while \( ef \) denotes the efficacy of the vaccine, which is averaged to be \( ef = 70\% \).

Furthermore, we note the presence of the time dependant \( \beta(t) \) which is meant to represent the evolution in Canada of VOCs among the 2020 baseline corona virus effective contact rate (Li, et al., 2020). In fact, we implement the presence of the variant as a weighted average of the base (2020) effective contact rate and the VOCs, where the VOCs are generally thought of being 50% more infectious:

\[
\beta(t) := w_1(t)\beta + w_2(t)\beta_{VOC} = \begin{cases} 
\beta & t \in \{Dec.25,’20 – Jan.15,’21\} \\
0.9\beta + 0.1\beta_{VOC} & t \in \{Jan.15,’21 – Feb.10,’21\} \\
0.7\beta + 0.3\beta_{VOC} & t \in \{Feb.10,’21 – Mar.25,’21\} \\
0.6\beta + 0.4\beta_{VOC} & t \in \{Mar.25,’21 – Apr.30,’21\} \\
0.5\beta + 0.5\beta_{VOC} & t \in \{Apr.15,’21 – Apr.30,’21\}
\end{cases}
\]
where, according to (University of Manitoba, 2021) the VOCs account for 50% of all new cases in Canada by April 2021. We further recognize that Canada has been, on average, under some level of social-distancing measures throughout the Fall and into December 2020, thus the value of $\beta = \gamma R_{eff}$ for an estimated value of $R_{eff} = 1.2$, representing the reduction in the effective reproduction number at the beginning of January 2021, via collective NPI measures. Finally, we assume $\beta_{VOC} = 1.5\beta$. In a similar piecewise fashion, we assume values of vaccination rate:

$$
\rho(t) := \begin{cases} 
0.0005 & t \in \{Dec \ 25^{\prime}\20 \to \ Jan \ 15^{\prime}\21\} \\
0.0009 & t \in \{Jan \ 15^{\prime}\21 \to \ Feb \ 10^{\prime}\21\} \\
0.0022 & t \in \{Feb \ 10^{\prime}\21 \to \ Mar \ 25^{\prime}\21\} \\
0.0077 & t \in \{Mar \ 25^{\prime}\21 \to \ Apr \ 15^{\prime}\21\} \\
0.0083 & t \in \{Apr \ 15^{\prime}\21 \to \ Apr \ 30^{\prime}\21\} 
\end{cases}
$$

in such a way that the cumulative vaccination uptake over January to April of 2021 matches by and large the available data https://health-infobase.canada.ca/covid-19/vaccination-coverage/

We then simulated four scenarios assuming that instead of stringent lockdown measures in March/April, the policy would have been to rapid-test at scale the population, on a regular basis. Specifically, we simulated a frequency of testing and tracing of every individual every 30 days, then every 20 days, every 14 days and every 7 days. We show our results in Fig. 13 below:

It is clear that all levels of asymptomatic testing/tracing implemented would have helped keeping new cases under current level, while the vaccination campaign accelerated. To quantify directly our policy, we have computed the ration between the total number of new cases in each of the testing/tracing scenarios and the current total number of cases. We report our findings in Table 4 below:

Evidently, a frequent testing and tracing policy could help in controlling new infections, and in keeping the number of new cases within safe healthcare capacity. As the vaccinating campaign in Canada is likely to last through July or
end of August, depending on vaccine supply, the current policy can still be implemented while the campaign is in progress, in lieu of hard lockdown measures. Specifically, a frequency of an average of 20 days (red curve in Fig. 13) would have avoided the 3rd wave in Canada.

5. Discussion

In keeping with other published findings for these and other countries, our results suggest that the COVID-19 countermeasures taken in South Korea, Italy, Canada and the United States have had a substantial impact on the course of the disease during their pandemic waves. As illustrated in Figs. 8-11, if a change in control strategy causes $R_{0\text{eff}}$ to exceed 1, how quickly a second wave builds depends on the number of cases at the time the change has occurred.

In this work, we quantified the average level of repeated testing and tracing needed to allow a country to keep a near-normal functioning of society. Among the countries considered here, we estimate that a frequency of isolating individuals based on testing combined with contact-tracing ranging from once every 6.2 days (Italy) to once every 3.5 days (U.S.) could have worked to keep the pandemic under a “slow-burn” control, if implemented in Summer 2020 (specifically July onward). A higher frequency of 4.5 days would have helped the second pandemic waves in Canada, Italy and South Korea, while 3 days would help in the case of the US. Last but not least, a testing and tracing frequency of 20 days, on average, for Canada would have mitigated the 3rd wave, in the presence of vaccination.

Of the four countries, only South Korea has managed to not only ramp up and sustain large-scale testing, but also to convince its population to adopt tracing technology and adhere to strict isolation rules, certainly during the first wave. Testing capacity is up considerably in Italy, Canada and the US, however is only used as a reactive strategy for symptomatic individuals. A proactive testing and tracing strategy, such as voluntarily testing people in a repeated fashion in schools, manufacturing, airports, etc., (see for instance our work in (Cojocaru et al., 2021)) may have yielded better pandemic control.

Our policy scenarios here are subject to a number of limitations, of which we highlight two main ones. Our estimates assume testing with sensitivity at or near 100% and immediate isolation once a subject tests positive. Though reaching these targets would necessitate an undeniably large logistic effort, home-test kits availability combined with further advances in mobile device-based contact tracing can make these strategies possible. Canada started to test its electronic platform for voluntary participation in contact tracing in July 2020, with Ontario being the first province to test it on a larger scale (Covid-19 alert app starts, 2021). However, the adoption rate of the Covid-tracing app is approximately 10–15% for instance in Canada. Moreover, the lower than 100% accuracy of some of the rapid testing kits available, as well as their false positive or false negative rates may make the frequent implementation of large scale testing less attractive. Thus, one possible workaround is to employ pool testing (Zilinskas, Lancinskas, & Guarracino, 2021) or frequent random testing in smaller scale populations, such as schools (Cojocaru et al., 2021), manufacturing plants, etc., where pathogen transmission is known to be higher, and test less frequently parts of the population who are not as exposed.

The second limitation is that we are simulating large, heterogeneous, geographically widely-distributed populations with an unstratified disease transmission model. Although we have taken the proportion of asymptomatic COVID-19 cases to be 50%, informed by a recent CDC report, assuming asymptomatic infection confers immunity, this would mean a smaller remaining pool of susceptibles and thus a lower current effective reproduction number. Estimates of $R_0$ from time series data of cases depend, as always, on the assumed latent and infectious periods. As we have demonstrated through (Fig. 5), if these periods are longer than the isolation time, then it is the latter which principally drives the disease dynamics. Thus, our findings about threshold isolation times are relatively robust against the possibility of a substantially longer COVID-19 serial interval.

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Fig. 13. The evolution of the epidemic in Canada, under various frequencies of testing and tracing over January 2021–May 2021. The curve of highest peak represents a non-NPI-mitigated curve, but in the presence of vaccines.
Last but not least, testing and tracing policies are strongly dependent on public cooperation and compliance. As populations are becoming more anxious to resume normal work, school and social schedules, compliance with measures is harder to enforce. Populations must be relied on to comply with self-isolation if testing positive for the virus, as well as self-isolation upon being exposed to an infected person. Sustainable supply chains, accuracy and reliability of possible tests, as well as privacy issues around electronic contact tracing technology all present important issues countries must analyze. Finally, even with availability of effective vaccines and treatments, testing and tracing policies together with NPI measures could be policies to strive for in the immediate short-term, to avoid strong lockdown and shelter-in-place measures.

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Appendix

Local exponential growth around a disease free equilibrium with \( s(0) \leq 1 \) in an SEIRL model

We want to find a relation between the exponential growth of the infected compartment in an SEIRL model (13) and the reproductive number \( R_0 \) around a disease-free equilibrium of the type \( (\tilde{s}, 0, 0, 0) \) which arises as a possibility in a first wave (\( \tilde{s} = 1 \)) or a second wave of a pandemic such as COVID-19 (\( \tilde{s} < 1 \)).

In this case, we conduct a similar computation as in (Ma, 2020), but considering the 4 dimensional system of equations for \( s, e, i, l \) leads us to the Jacobian of the SEIRL:

\[
J = \begin{pmatrix}
-\beta_i & 0 & -\beta s & 0 \\
\beta i & -(\sigma + \kappa_1) & \beta s & 0 \\
0 & \sigma & -(\gamma + \kappa) & 0 \\
0 & 0 & \kappa & 0
\end{pmatrix}
\]

If computed at the disease free equilibrium \( (\tilde{s}, 0, 0, 0) \) we further obtain:

\[
J = \begin{pmatrix}
0 & 0 & -\beta s & 0 \\
0 & -(\sigma + \kappa_1) & \beta s & 0 \\
0 & \sigma & -(\gamma + \kappa) & 0 \\
0 & 0 & \kappa + \kappa_1 & 0
\end{pmatrix}
\]

Again we note that the linearized equations for \( s \) and \( l \) are decoupled from the equations of \( e \) and \( i \), thus, to get information on the growth rate of the infected compartment, let us try to solve the linearized reduced system in \( (e, i) \) based on the reduced Jacobian:

\[
J_{\text{reduced}} = \begin{pmatrix}
-(\sigma + \kappa_1) & \beta s \\
\sigma & -(\gamma + \kappa)
\end{pmatrix}
\]

Solve: \( \det(\rho I_2 - J_{\text{reduced}}) = 0 \)

Its characteristic equation is:

\[
\rho^2 - \rho((\sigma + \kappa_1) + (\gamma + \kappa)) + (\sigma + \kappa_1)(\gamma + \kappa) - \sigma \beta s = 0
\]

The eigenvalues of this matrix can be computed to be
Continuing as in (Ma, 2020), we express

\[
\rho_{1.2} = \frac{-(\sigma + k_1 + \gamma + k)}{2} \pm \frac{\sqrt{(\sigma + k_1 + \gamma + k)^2 - 4((\sigma + k_1)(\gamma + k) - \sigma \beta \bar{s})}}{2}
\]

\[
\rho_{1.2} = \frac{-(\sigma + k_1 + \gamma + k) \pm \sqrt{((\sigma + k_1) - (\gamma + k))^2 + 4\sigma \beta \bar{s}}}{2}
\]

We first note that \((\sigma + k_1) - (\gamma + k))^2 + 4\sigma \beta \bar{s} > 0\), given all parameters are positive. This implies that \(\rho_1 \neq \rho_2 \in \mathbb{R}\) and clearly \(\rho_2 < 0\). We check whether \(\rho_1 > 0\) by looking at

\[
\sqrt{((\sigma + k_1) - (\gamma + k))^2 + 4\sigma \beta \bar{s}} > \sigma + k_1 + \gamma + k \iff
\]

\[
(\sigma + k_1) - (\gamma + k) + 4\lambda \beta \bar{s} > ((\sigma + k_1) + (\gamma + k))^2 \iff
\]

\[-2(\sigma + k_1)(\gamma + k) + 4\sigma \beta \bar{s} > 2(\sigma + k_1)(\gamma + k) \Rightarrow
\]

\[
\sigma \beta \bar{s} > (\sigma + k_1)(\gamma + k) \Rightarrow \bar{s} > \frac{\sigma + k_1)(\gamma + k)}{\sigma \beta}
\]

Therefore, as before, we have that

\[
\rho_1 > 0 \text{ as long as } \bar{s} > \frac{(\sigma + k_1)(\gamma + k)}{\sigma \beta}
\]

Inequality (14) simply shows that in order to not have an exponential growth from our disease free equilibrium (in other words the infection dies out), we need to allow that the initial fraction of susceptibles is lower than

\[
\bar{s} \leq \frac{(\sigma + k_1)(\gamma + k)}{\sigma \beta}
\]

We note that \(\beta\) and \(\gamma\) are disease-dependent values on which we cannot exert control. However, \(k\) and \(k_1\) are parameters on which we can exert an exogenous control (specifically to increase them, thus raising the upper bound on fractions \(\bar{s}\) with no exponential growth in infected) which will be outlined in detail in the next section.

Continuing as in (Ma, 2020), we express \(\beta\) as a function of \(\bar{s}, \sigma, \gamma, k, k_1\) from (13) and we get:

\[
2\rho_1 + (\sigma + k_1) + (\gamma + k) = \sqrt{((\sigma + k_1) - (\gamma + k))^2 + 4\sigma \beta \bar{s}} \Rightarrow
\]

\[
4\rho_1^2 + (\sigma + k_1)^2 + 2(\sigma + k_1)(\gamma + k) + (\gamma + k)^2 + 4\rho_1(\sigma + k_1) + 4\rho_1(\gamma + k) + (\sigma + k_1)^2 - 2(\sigma + k_1)(\gamma + k) + (\gamma + k)^2 + 4\sigma \beta \bar{s}
\]

\[
4\rho_1^2 + 4(\sigma + k_1)(\gamma + k) + 4\rho_1(\sigma + k_1) + 4\rho_1(\gamma + k) = 4\sigma \beta \bar{s} \Rightarrow
\]

\[
\rho_1^2 + (\sigma + k_1)(\gamma + k) + \rho_1(\sigma + k_1) + \rho_1(\gamma + k) = \beta
\]

\[
\frac{(\sigma + k_1 + \rho_1)(\gamma + k + \rho_1)}{\sigma \bar{s}} = \beta
\]

Following (van den Driessche, 2017), we can use the next generation matrix to deduce \(R_0\) as the dominant eigenvalue of the next generation matrix:
\[ FV^{-1} = \left( \frac{\beta\sigma \tilde{s}}{(\sigma + k_1)(\gamma + \kappa)} \right) \Rightarrow R_0 = \frac{\beta\sigma \tilde{s}}{(\sigma + k_1)(\gamma + \kappa)} \]

Now using the expression of \( \beta \) in that of \( R_0 \) we are able to express the effective reproductive number as a function of the exponential growth and of \( \gamma, \sigma, \kappa, k_1 \):

\[ R_0 = \frac{\sigma \tilde{s}}{(\sigma + k_1)(\gamma + \kappa + \rho_1)} \frac{(\sigma + k_1 + \rho_1)(\gamma + \kappa + \rho_1)}{(\sigma + k_1)(\gamma + \kappa)} \Rightarrow R_0 = \frac{(\sigma + k_1 + \rho_1)(\gamma + \kappa + \rho_1)}{(\sigma + k_1)(\gamma + \kappa)} \quad \text{and} \quad R_{\text{eff}} = s(t)R_0, \quad \forall t > 0 \]

Similar to (5) we denote by \( R_{0\text{SEIRL}} \):

\[ R_{0\text{SEIRL}} = \frac{(\sigma + k_1 + \rho_1)(\gamma + \kappa + \rho_1)}{(\gamma + \kappa)} \]

Clearly, if \( \kappa = k_1 = 0 \) then \( R_{0\text{SEIRL}} \) reduces to \( R_{0\text{SEIR}} \) in (5) of Section 2.

Let us now note that we have shown that the exponential growth factor (13), as well as the \( R_{0\text{SEIRL}} \), are dependent on the rates \( k \) and \( k_1 \), that is to say, we denote by

\[ \rho(k, k_1) = \frac{-((\sigma + k_1 + \gamma + \kappa) + \sqrt{(\sigma + k_1 - (\gamma + \kappa))^2 + 4\sigma\beta\tilde{s}}}}{2} \]

and by \( R_0(k, k_1) = \frac{(\sigma + k_1 + \rho_1)(\gamma + \kappa + \rho_1)}{(\gamma + \kappa)} \)

The reproductive number as a function of \( T_{\text{lat}} \)

Let us express the reproductive number, in general, as a function of \( T_{\text{lat}} = \frac{1}{\sigma} \) and \( T_{\text{ser}} = T_{\text{inf}} + T_{\text{lat}} = \frac{1}{\gamma} = T_{\text{ser}} - T_{\text{lat}} \Rightarrow \gamma = \frac{1}{T_{\text{ser}} - T_{\text{lat}}} \)

From 5 we have that

\[ R_0 = \frac{(\rho + \gamma)(\rho + \sigma)}{\gamma \sigma} = \frac{\left(\rho + \frac{1}{T_{\text{lat}}}\right)}{\frac{1}{T_{\text{ser}} - T_{\text{lat}}}} \left(\rho + \frac{1}{T_{\text{ser}} - T_{\text{lat}}}\right) = (\rho T_{\text{lat}} + 1)(\rho(T_{\text{ser}} - T_{\text{lat}}) + 1). \]

Then

\[ R_0 = -(T_{\text{lat}} \rho - T_{\text{ser}} \rho - 1)(T_{\text{lat}} \rho + 1) \Rightarrow \]

\[ \frac{dR}{dT_{\text{lat}}} = -\rho(T_{\text{lat}} \rho + 1) - (T_{\text{lat}} \rho - T_{\text{ser}} \rho - 1)\rho \]

where we can solve for a \( T_{\text{lat}} \) value which maximizes \( R_0 \), namely

\[ \frac{dR}{dT_{\text{lat}}} = 0 - 2T_{\text{lat}} \rho + T_{\text{ser}} \rho \Rightarrow T_{\text{lat}} = \frac{T_{\text{ser}}}{2}. \]
Fig. 14. Italy - daily incidence and log-daily incidence fits to November 2020. (A) Upper panels: Linear and semi-log plots of daily incidence data of confirmed cases in Italy, together with maximum-likelihood model fit ("with measures, confirmed") Also shown is the inferred true number of infected, taking into account under-reporting and asymptomatic cases ("with measures, all"). Shown for comparison are the number of confirmed cases ("no measures, confirmed") and all cases ("no measures, all") expected to have occurred in the absence of countermeasures. (B) Lower panels: Cumulative incidence (top) and inferred reduction of effective contacts ($\beta$), together with the corresponding effective reproduction numbers (vertical numbers) (bottom).
Last but not least, the US has never staved off their first pandemic wave, moving into a second wave in Summer 2020 and then a dramatic 3rd wave (Fig. 16). In all four countries, interventions arrested the initial exponential rise in cases and brought the effective reproduction number below 1. In Italy, South Korea and Canada, daily case numbers have since been brought far below their peak values through the summer of 2020, but entered a second wave in the fall. The US has never staved off their first pandemic wave, moving into a second wave in Summer 2020 and then a 3rd wave (Fig. 16).

If we quantify the average $\beta$ in the four countries we see that, for instance, Canada, Italy and US have managed to maintain an average of 40%—50% reduction factors through social distancing measures, however the US has implemented the measures with a larger initial delay (so at much higher initial daily incidence) and larger heterogeneity than Canada, thus their pandemic curves have evolved differently. In South Korea, the average $\beta$ reduction is higher, at around 70%.

South Korea (see Fig. 15) experienced a very similar early exponential growth in cases, and hence has a similar inferred $R_0$ as the other three countries. However, its mitigation and control measures stood out from the beginning in the fact that the country employed a rapid scale-up of testing, concurrent with contact tracing and isolating of infected individuals. In fact its

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**Fig. 15.** South Korea - daily incidence and log-daily incidence fits to November 2020. (A) **Upper panels:** Linear and semi-log plots of daily incidence data of confirmed cases in Italy, together with maximum-likelihood model fit (“with measures, confirmed”). Also shown is the inferred true number of infected, taking into account under-reporting and asymptomatic cases (“with measures, all”). Shown for comparison are the number of confirmed cases (“no measures, confirmed”) and all cases (“no measures, all”) expected to have occurred in the absence of countermeasures. (B) **Lower panels:** Cumulative incidence (top) and inferred reduction of effective contacts ($\beta$), together with the corresponding effective reproduction numbers (vertical numbers) (bottom).
higher reduction in $\beta$ is clearly seen. There were also social distancing measures imposed, but notably no shelter-in-place (McNeil, 2020). Last but not least, mask wearing is a regular policy that the population adopts widely (not only for this pandemic, but also for flu).

Fig. 16. United States - daily incidence and log-daily incidence fits to November 2020. (A) Upper panels: Linear and semi-log plots of daily incidence data of confirmed cases in Italy, together with maximum-likelihood model fit (“with measures, confirmed”) Also shown is the inferred true number of infected, taking into account under-reporting and asymptomatic cases (“with measures, all”). Shown for comparison are the number of confirmed cases (“no measures, confirmed”) and all cases (“no measures, all”) expected to have occurred in the absence of countermeasures. (B) Lower panels: Cumulative incidence (top) and inferred reduction of effective contacts ($\beta$), together with the corresponding effective reproduction numbers (vertical numbers) (bottom).

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