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An SEIR Infectious Disease Model with Testing and Conditional Quarantine

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An SEIR Infectious Disease Model with Testing and Conditional Quarantine*

David Berger Kyle Herkenhoff Simon Mongey

March 29, 2020

Disclaimer: We are not epidemiologists, and view this paper as proof of concept.

Abstract

We extend the baseline Susceptible-Exposed-Infectious-Recovered (SEIR) infectious disease epidemiology model to understand the role of testing and case-dependent quarantine. Our model nests the SEIR model. During a period of asymptomatic infection, testing can reveal infection that otherwise would only be revealed later when symptoms develop. Along with those displaying symptoms, such individuals are deemed *known positive* cases. Quarantine policy is case-dependent in that it can depend on whether a case is *unknown*, *known positive*, *known negative*, or *recovered*. Testing therefore makes possible the identification and quarantine of infected individuals and release of non-infected individuals. We fix a quarantine technology—a parameter determining the differential rate of transmission in quarantine—and compare simple testing and quarantine policies. We start with a baseline quarantine-only policy that replicates the rate at which individuals are entering quarantine in the US in March, 2020. We show that the total deaths that occur under this policy can occur under looser quarantine measures and a substantial increase in random testing of asymptomatic individuals. Testing at a higher rate in conjunction with targeted quarantine policies can (i) dampen the economic impact of the coronavirus and (ii) reduce peak symptomatic infections—relevant for hospital capacity constraints. Our model can be plugged into richer quantitative extensions of the SEIR model of the kind currently being used to forecast the effects of public health and economic policies.

Clean code for the model is available on our websites.

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"Once again, our key message is: test, test, test." — @WHO, March 16, 2020

"We suggest a strategy of massive testing that goes far beyond the group currently being tested — those most likely infected. Instead, we need to test as many people as possible. If we know who is infected, who is not and who has recovered, we could greatly relax social isolation requirements and send both the uninfected and the recovered back to work."

— Searchinger (Princeton), LaManita (Virginia Tech Med.), Douglas (Cornell Med.), March 23, 2020, Washington Post

Introduction

We are interested in understanding the role of testing asymptomatic cases and targeted quarantine in the trajectory of the coronavirus pandemic. Our working hypothesis is that in combination with a quarantine policy that isolates individuals conditional on being known positive cases, increased testing may lead to shorter-lived quarantine measures. To study this we incorporate incomplete information in the textbook SEIR model (Susceptible-Exposed-Infectious-Recovered) (Kermack and McKendrick, 1927). Unknown, asymptomatic cases may be resolved by testing.[1] This enables policies that vary depending on whether an individual case is an unknown, known positive, known negative, or recovered. Figure 1 describes these possibilities. In a calibrated version of the model, we show that increasing random testing and relaxing targeted quarantine measures can deliver the same amount of deaths with a lower impact on the economy and lower peak symptomatic case load.

This paper comes with four very serious disclaimers. First, we are not epidemiologists. However, after reading a number of papers we concluded that there was not a framework for discussing some of the pressing public health policy questions, in particular the potential role of broad testing in ameliorating quarantine measures. Should countries *quarantine everyone* at large social cost, or *test everyone* and apply quarantine in a more directed fashion. Some models feature testing conditional on developing symptoms which allows for better care and reduced mortality, but to the best of our knowledge no models considered testing asymptomatic individuals so that positive cases can be recognized and isolated. We would be very happy to learn from medical professionals and epidemiologists that we have misread the literature and that this has been studied before.

Second, our model does not feature the full set of features that one would desire in order to make quantitative statements and predictions. These would include transmission across geography, an age distribution of individuals with systematically different probabilities of infection conditional on contact with a positive case. Our model is, however, a simple extension of and nests a textbook SEIR model which forms the backbone of more sophisticated quantitative models. We also do not model the *medical care* block in detail. Like the SEIR model we abstract from issues such as congestion of medical services. To that extent, we hope that this paper demonstrates that incomplete information, testing and conditional policies can be simply and intuitively integrated into richer models. We view the technical and computational costs low relative to the payoffs.[2]

[1] Recent empirical evidence from random samples drawn in an Italian town suggest that around 50 to 75 percent of infected cases are asymptomatic: Link to La Repubblica article, March 16, 2020.

[2] Specifically, while the SIER model augmented for quarantine would have 8 states—the 4 S-E-I-R states each augmented for quarantine

Third, for most of this paper we fix an *effectiveness* of quarantine in reducing meeting rates of individuals. We assume that complete isolation is off the table, however note here that improving quarantine would have large effects. Therefore our exercise should be interpreted as follows: given access to a quarantine technology of some fixed effectiveness, how does testing allow that technology be applied differently across individuals, potentially mitigating costs of the pandemic. A different paper could be written on the quantitative effects of increasing the effectiveness of quarantine. In Section 7 we repeat our main counterfactual under a more effective quarantine and show how testing allows quarantine measures to be relaxed even further.

Finally, our model is *not* a behavioural economic model that integrates an epidemiological model as in Kremer (1996) or the equilibrium model of Greenwood, Kircher, Santos, and Tertilt (2019). We think understanding the role of testing in information acquisition should be key to any such integration. A simple S(E)IR model integrated into an economic model with only common (non-targeted) quarantine policies available will *unavoidably* lead to a trade-off between mortality and economic activity. More quarantine, less mortality, and vice versa. By increasing testing of asymptomatic cases and conditional quarantine, we show that the model can deliver constant mortality rates and higher economic activity, as measured by the fraction of individuals out of quarantine. Theories of quarantine vs. mortality trade-offs are therefore discussions of second best policies, while testing presents a potentially better option.

Contribution. We include the minimal necessary modifications of the SEIR model in order to be able to address the public health effects of testing asymptomatic cases. We augment the SEIR model, which we nest, as follows. In the SEIR model an individual may be characterized as being in one of four health states: susceptible (S), exposed (E), infected (I) and recovered (R). Our aim is to try to understand the role of asymptomatic transmission and how testing and / or quarantine of asymptomatic cases can effect the prorogation of infection and mortality. Our modifications therefore makes policies contingent on what is known about an individual. The policy we consider is quarantine which lowers the rate of transmission. With incomplete information, an individual that has contracted the corona virus, but is yet to present symptoms, will be infectious and subject to the quarantine rule for unknown cases. If tested, however, the true health state of the individual is revealed and they are subject to the same quarantine rules as known positive cases. Similarly such an individual, if untested, cannot be subject to quarantine policies that apply to known positive cases.

Results. We calibrate the model to data on the spread of the coronavirus and medical outcomes. This calibration is 'standard' with respect to the SEIR models published over the last month. As a baseline we simulate the model without policy interventions, which delivers the same trajectory for the pandemic as the SEIR model. We then consider a benchmark counterfactual with common quarantine measures and no testing. We then ask the question, *If we increase testing, how much can we relax quarantine measures while making sure that deaths do not increase?* We show that increasing testing can accommodate extensive relaxation of quarantine measures. If we assume that economic output, and social well-being are inversely proportional to the number of individuals quarantined, this implies

and non-quarantine—our model requires 12 states, with the additional 4 states reflecting the information structure of the model.

A. Information – No testing

	Asymptomatic	Symptomatic
Not infected	Unknown	-
Infected		Positive

B. Information - Testing

	Asymptomatic	Symptomatic
Not infected	Negative	-
Infected	Positive	Positive

C. Example of targeted policies – No testing

	Asymptomatic	Symptomatic
Not infected	Partial	-
Infected	quarantine	Full quarantine

D. Example of targeted policies – Testing

	Asymptomatic	Symptomatic
Not infected	Release	-
Infected	Full quarantine	

Figure 1: Incomplete information, testing, and an example of targeted quarantine policies

that testing can result in a pandemic with smaller economic losses and social costs while keeping the human cost constant. That is, the common sense result prevails.

Overview. This paper has seven sections. Section 1 reviews the related SEIR literature and recent papers using this model to quantify the effects of the corona virus pandemic. Section 2 reviews some of the data regarding infection and mortality, as well as policy responses in the form of testing and quarantine measures. Section 3 describes the model. Section 4 provides details of how we calibrate the model and provides baseline simulations of the pandemic under no policy response. This replicates the familiar trajectories of infection and mortality of SEIR models that have been used to model the evolution of the pandemic. Section 5 provides our main counterfactuals, where we compare the consequences of *common quarantine and no testing* with *targeted quarantine and testing* policies. Section 7 repeats these counterfactuals under a more effective quarantine technology. Section 8 concludes.

1 Literature review

Brauer and Castillo-Chavez (2012) provide a summary of recent SEIR models. SEIR stands for Susceptible, Exposed (people not yet infectious), Infectious, and Removed (quarantined or immune). In particular, they discuss frameworks of quarantine (setting aside individuals who are exposed) and isolation (setting aside individuals who are infected, often called hospitalization).

A recent policy paper by Imperial College COVID-19 Response Team (2020) incorporates several policy parameters into an SEIR model that is enriched to accommodate geographical transmission and age dependency of transmission and mortality rates.[3] In particular, they consider a model with quarantine, asymptomatic patients, and testing of *hospitalized* patients, with policy thresholds that depend on positive test rates. Their predictions have been reported widely in the press. Our contribution is to model (i) the matching process between different subgroups, thus endogenizing R_0, and (ii) highlighting the importance of *testing asymptomatic patients* and, (iii)

[3] At the time of writing the codes for Imperial College COVID-19 Response Team (2020) were not publicly available, and the paper does not feature any equations that would allow a researcher to replicate their model.

quarantine policies that are contingent on the testing outcomes. Lastly, we use our measure of the fraction of individuals quarantined as a measure of loss of economic activity. This allows us to evaluate the role of widespread testing which, as a policy, may have a similar mortality rates but lower quarantine rates.

Recent examples of testing and diagnosis in an SEIR model include Chowell, Fenimore, Castillo-Garsow, and Castillo-Chavez (2003) who model the Severe acute respiratory syndrome (SARS) epidemic in 2002. The purpose of testing and diagnosis in Chowell, Fenimore, Castillo-Garsow, and Castillo-Chavez (2003) is an improvement in healthcare, which reduces the rate of recovery from nearly one half.[4] In our model, the role for testing and diagnosis is being able to efficiently target quarantine measures.

Recent examples of quarantine in an SEIR model include Feng (2007) who derive closed form expressions for the maximum and final rates of infection. Feng (2007) has two notions of quarantine: one in which exposed individuals (who may not be infectious) are set aside, and another in which infectious individuals are set aside (often discussed as hospitalization). In our model, quarantine is similarly case dependent, but can only depend on observed health status. Exposed individuals that do not display symptoms cannot be quarantined without being identified in a random testing of asymptomatic individuals.

Empirically, the literature has begun to document the rate of transmission and incubation periods. Wu, Leung, and Leung (2020) compile a summary of $\mathcal{R}_0$ across various viruses (SARS-CoV, MERS-CoV, Commonly circulating human CoVs (229E, NL63, OC43, HKU1)), and estimate an SEIR model with international outflows. Using data from Wuhan, they report an $\mathcal{R}_0$ of 2.68, and an incubation period of 6.1 days. The World Health Organization (2020) report that the time from symptom recovery to detection fell from 12 days in early January to 3 days in early February 2020. After symptom onset, it typically takes 2 weeks for a mild case to recover, or 3 to 6 weeks for severe cases.

Empirically, the literature has also begun to document the role of quarantine in reducing transmission, and the rate of asymptomatic transmission. Kucharski, Russell, Diamond, Liu, Edmunds, Funk, Eggo, Sun, Jit, Munday, et al. (2020) estimate that in China, the basic reproductive rate $\mathcal{R}_0$ fell from 2.35 one week before travel restrictions on Jan 23, 2020, to 1.05 one week after travel restrictions. They use an SEIR model and estimated on this data to forecast the epidemic in China, extending the model to explicitly account for infections arriving and departing via flights. Using data from Wuhan, Wang et al (2020) report a baseline reproductive rate of 3.86, that fell to 0.32 after the vast lock-down intervention. They also find a high rate of asymptomatic transmission, leading us to consider the asymptomatic state to be infectious as opposed to the baseline SEIR model which assumes that the 'exposed' state is non-infectious.[5] A high rate of asymptomatic carry of the virus has been identified in Iceland, one of the few countries to adopt random testing of asymptomatic individuals.[6]

In the economics literature Atkeson (2020) considers the effectiveness of temporary quarantine measures in a baseline SEIR model similar to Feng (2007). Eichenbaum, Rebelo, and Trabandt (2020) nest a similar SIR model

[4] They report a SARs incubation period of 2 to 7 days, with most infected individuals either recovering after 7 to 10 days, or dying. The SARS mortality rate is 4 percent or more. They estimate a basic reproductive number $R_0 = 1.2$. They model a diagnosis rate and diagnosed state. Individuals recover at a fast rate if diagnosed (8 days without diagnosis, 5 days with diagnosis).

[5] https://www.medrxiv.org/content/10.1101/2020.03.03.20030593v1

[6] https://www.buzzfeed.com/albertonardelli/coronavirus-testing-iceland. "Early results from deCode Genetics indicate that a low proportion of the general population has contracted the virus and that about half of those who tested positive are non-symptomatic".

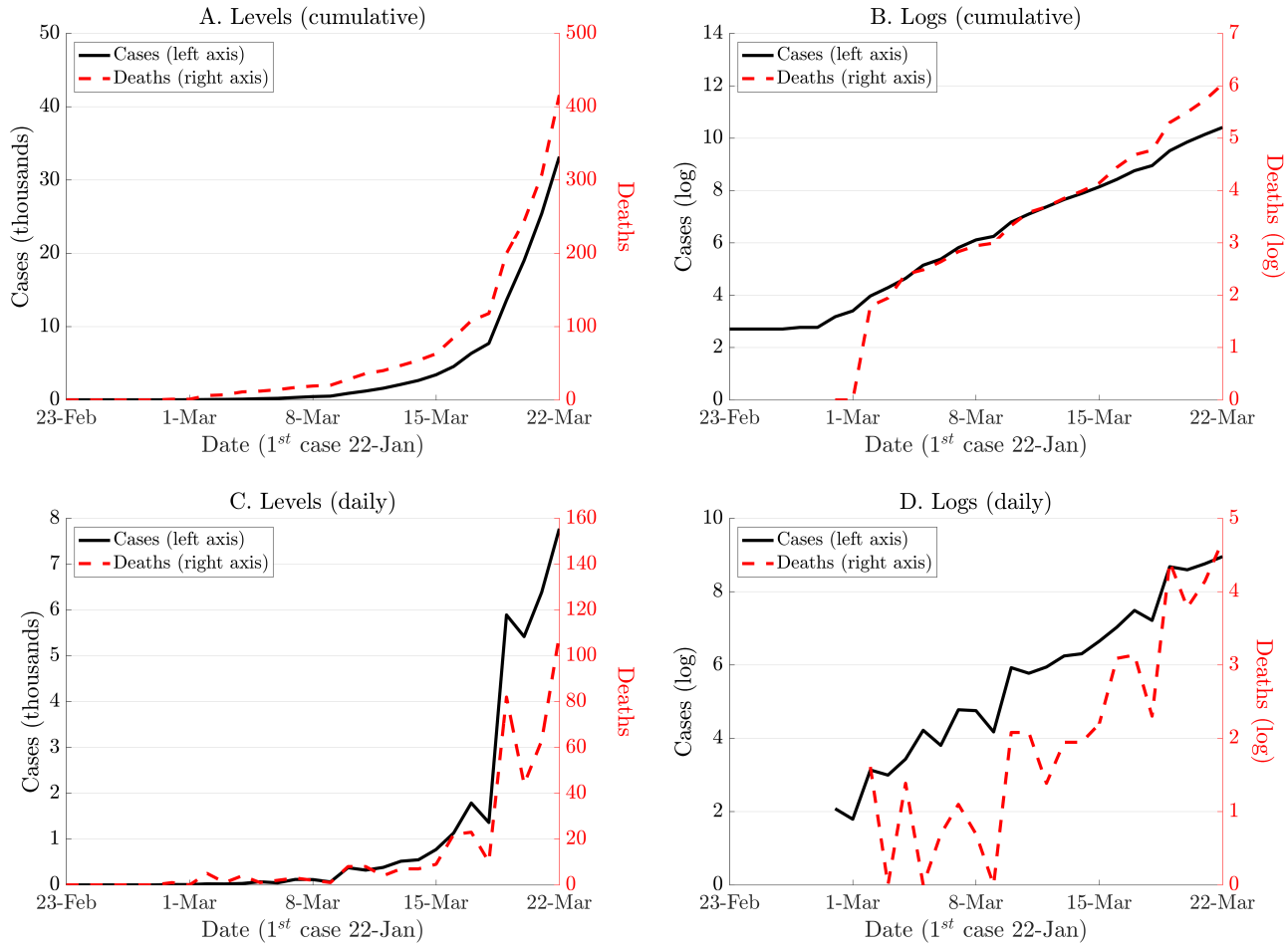

Figure 2: US cumulative cases and deaths - 4 weeks up to March 22

Notes: Source: John Hopkins CSSE, https://github.com/CSSEGISandData/COVID-19. Data reflect non-repatriated cases, and so exclude the cases from the Diamond Princess and Grand Princess cruise ships.

in a canonical general equilibrium macroeconomic model of consumption, savings and labor supply. Individuals catch and transmit the virus when consuming and working. They measure the effect of quarantine policies on output and mortality. Our contribution to this strand of the economics literature is to enrich the underlying SEIR by introducing scope for testing policies which may mitigate the output costs of quarantine policies while not exacerbating the decline in output. It would be relatively straight-forward to integrate the information structure of our model into Eichenbaum, Rebelo, and Trabandt (2020) in order to evaluate the economic benefits of broad based testing.

2 Data on cases, deaths, quarantine and testing

This section provides a short overview of the evolution of the coronavirus pandemic in the United States.

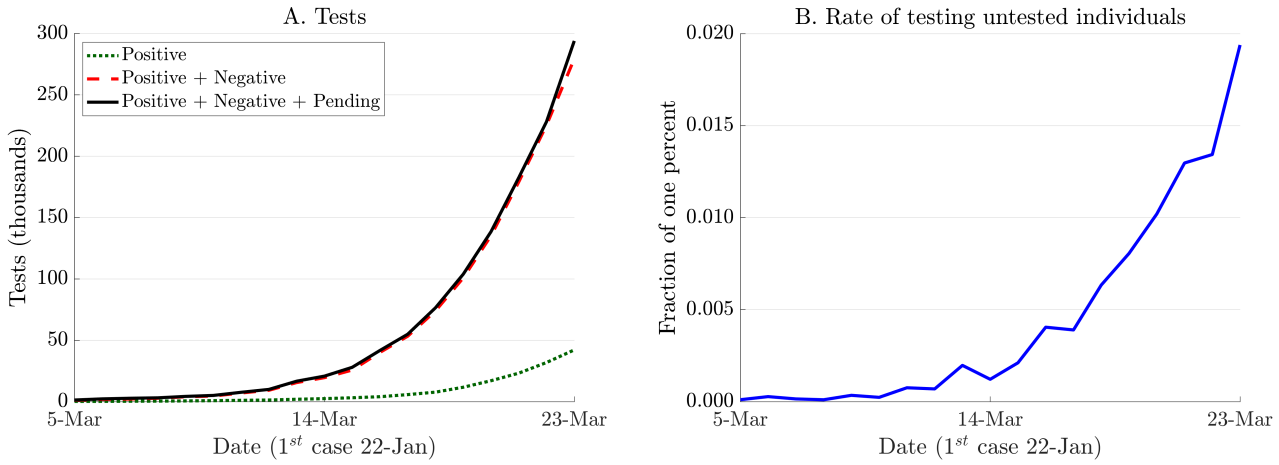

Figure 3: US testing

Notes: Source: John Hopkins CSSE, https://github.com/CSSEGISandData/COVID-19. Panel B plots the fraction of the untested population that is tested each day. Let T_t be total cumulative tests—the black line in Panel A—, then Panel B plots $(T_t - T_{t-1})/(340m - T_t)$. The y-axis of Panel B is in fractions of one percent, i.e. 0.01 on the y-axis corresponds to a daily testing rate of 0.01 percent.

Cases. The first case was reported in the U.S. on January 22, 2020. Figure 2 plots the evolution of confirmed cases and deaths resulting from COVID-19.[7] Table 1 reports the growth rate of cases (new cases divided by cumulative cases) using different measurements. There are several dates with outlier growth rates due to testing rollouts. The growth rate of cases is roughly 40 percent with these outliers included, and closer to 30 percent when we exclude the outliers. Due to the lack of testing, the growth rate of cases in January and February is zero, thus lowering the overall growth rate of cases significantly.

Deaths. Figure 2 also plots the number of deaths and the cumulative number of deaths. Similar to the number of cases, the number of deaths is stagnant prior to March. It then grows at a high rate with pronounced spikes. The average growth rate in deaths is 48 percent per day, but also includes significant outliers due to sudden changes in reporting.

Testing. Figure 3 reports cumulative tests and the testing rate per day. At its peak to date, the US tested just short of 0.02 percent of its untested population in a single day. We will use this rate to benchmark the rates of testing considered in counterfactuals. In particular we will consider testing rates that are significantly higher than what we currently observe in the United States.

Quarantine. Table 2 reports the fraction of individuals who are quarantined in the United States. There are large discrete jumps in the quarantine rate when California, New York, and Illinois announced state-wide shelter in place orders.[8] This is another important policy parameter. We must convert this series into a daily quarantine rate. Roughly 24% of the population was quarantined over the course of 19 days since March 4, 2020. We approximate

[7] We include our tabulations of the source data on our websites. At the moment data on recoveries is not particularly accurate, however we can add this later.

[8] We will refer to New York's policy as shelter-in-place, despite alternative language used by the government of New York.

Table 1: US average daily growth rate of cases

Since first case on 1/22	21.2%
March - From 1st to 19th	40.8%
March - From 1st to 19th - Exclusing outliers with rates $\geq$ 50%	31.1%

Source: Derived from data available from John Hopkins CSSE, https://github.com/CSSEGISandData/COVID-19.

Table 2: US quarantine

Date	Event	Quarantined	Frac. of US Pop.
3/4/2020		0	0.00%
3/10/2020	New Rochelle	79,946	0.02%
3/16/2020	Bay Area	6,747,000	1.98%
3/19/2020	California	39,639,946	11.66%
3/21/2020	Illinois, New Jersey	61,193,957	17.99%
3/22/2020	New York	80,647,518	23.72%

Source: Dates of enactment taken from various news outlets

this with a quarantine rate of roughly 1% per day. More quarantines have followed rapidly *during* the writing of this article.

3 Model

Throughout this section Figure 4 and Figure 5 may be useful to the reader. Figure 4 maps our model of *transmission* into the SEIR model. Figure 5 overlays this with our model of *information* and testing.

3.1 Overview

We make five modifications to the standard SEIR model.

1. **Health states.** As shown in Figure 4 we relabel these states in order to make a later distinction in terms of testing and quarantine. These we call *health states*. We also allow for the possibility that the *exposed* state is infectious, that is that there is possibly asymptomatic transmission.

   i. Non-infected, Asymptomatic (NA) - Individuals that have not been exposed to the virus, and are by definition asymptomatic. This corresponds to **S** in the SEIR model: *Susceptible.*

   ii. Infected, Asymptomatic (IA) - Individuals that have met an infected individual but are as yet asymptomatic. This corresponds to **E** in the SEIR model: *Exposed.* Relative to the SEIR model we allow that these individuals may also transmit the virus albeit at a lower frequency.

   iii. Infected, Symptomatic (IS) - Individuals that have met an infected individual and are now showing symptoms. This corresponds to **I** in the SEIR model: *Infectious.*

iv. Recovered, Asymptomatic (RA) - Infected individuals that have entered the recovery phase and are no longer infected. As in the textbook SEIR model we assume these individuals are immune.[9] This corresponds to **R** in the SEIR model: *Recovered.*

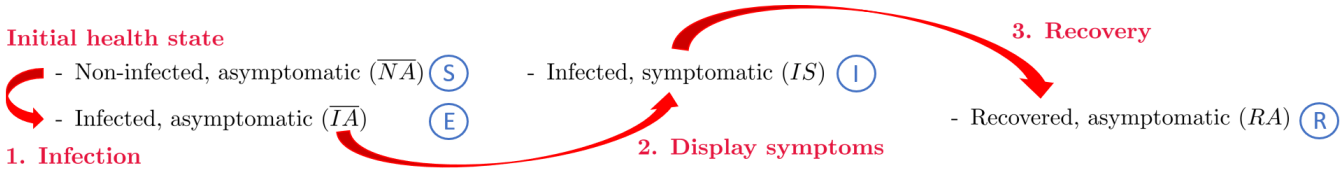

Figure 4: Transmission and the relationship between our model and the SEIR model

Notes: This figure shows how our states map into the SEIR model. To understand the role of testing we group the *asymptomatic* states S, E and label these *Non-infected,Asymptomatic* (NA) and *Infected, Asymptomatic* (IA). Without testing, authorities nor individuals are able to differentiate between these states. To denote this lack of information, we put a bar over them: $\overline{NA}$, $\overline{IA}$. Exposed individuals show symptoms, which is the I state of the SEIR model. We label this *Infected, Symptomatic* (IS). Individuals may then recover, which is the R state of the SEIR model. We label this *Recovered, Asymptomatic* (IA).

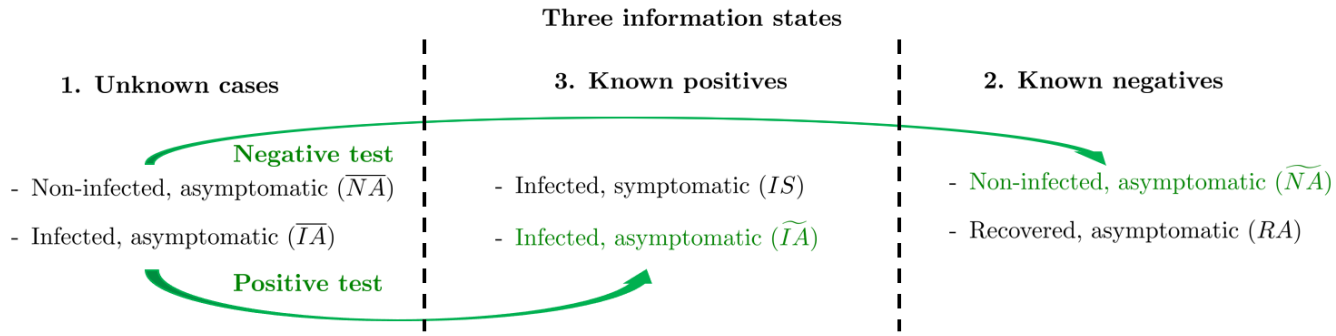

Figure 5: SEIR model with incomplete information and testing of asymptomatic individuals

Notes: This figure augments Figure 4 to show how we extend the SEIR model to accommodate testing and incomplete information. We add two additional states that can be revealed by testing, which differentiate asymptomatic individuals $\{\overline{NA}, \overline{IA}\}$. We denote these with a tilde: $\widetilde{IA}$ for identified infected, asymptomatic cases, and $\widetilde{NA}$ for identified non-infected, asymptomatic cases. We assume that symptomatic cases IS are instantly identifiable so are *known positives*, and that recovered cases have been tracked such that RA cases are *known negatives*.

Figure 4 tracks an individual case through these states. In terms of *medical transmission*, we assume that *infected* individuals are contagious, although with different rates of transmission. The different rates of transmission nest the case that only IS individuals can transmit the disease, which is the case in the SEIR model. *Non-infected* individuals cannot transmit the disease $\{NA, RA\}$.

The medical block of the model is very simple and could be enriched in many ways.[10] Following the standard SEIR model: (i) infected asymptomatic individuals show symptoms at rate δ, (ii) infected, symptomatic

[9] To the best of our knowledge there is no empirical evidence regarding immunity following COVID-19. A quantitative version of this model would want to take this into account. This is not the point of departure studied in this paper.

[10] See http://gabgoh.github.io/COVID/index.html by Gabriel Goh for an example of an SEIR model of *Transmission Dynamics* that appends a rich model of *Clinical Dynamics* which models hospitalization, length of hospital stay, and more. These states would intercede between IS, RA and D, which is not the focus of this paper.

individuals recover at rate ω^R and die at rate ω^D. Note that all individuals that become infected show symptoms at some point, this could be relaxed.

2. **Incomplete information.** We allow for incomplete information, as described in Figure 5. In terms of policy, we assume that unless tested, individuals without symptoms are indistinguishable and so must be treated in the same way by quarantine policy. To achieve this we distinguish between two types of NA and IA individuals. Adding these new cases in green to Figure 4 gives Figure 5. In the first case the diagnosis regarding infection is unknown. These are *unknown cases* which we denote $\overline{NA}$ and $\overline{IA}$. In the second case the diagnosis regarding infection is known, which we denote $\widetilde{NA}$ and $\widetilde{IA}$. This information structure implies that testing and quarantine policies can not distinguish between the following pairs of cases: unknown cases $\{\overline{NA}, \overline{IA}\}$, known positives $\{\widetilde{IA}, IS\}$, and known negatives $\{\widetilde{NA}, RA\}$. Our assumption that $\{\widetilde{NA}, RA\}$ are not distinguishable is a simplifying assumption in order to maintain a finite set of states, which we discuss below.

3. **Meeting and transmission rates.** We assume that the underlying parameters consist of an explicit interaction of *social meeting rates*, which are mutable to quarantine / social distancing policies, and *medical transmission rates*, which are the medical rates of transmission between two individuals that meet.

   We denote quarantine and non-quarantine states by Q and NQ, respectively. Interacted with our 4 health states, plus two additional information states, this gives 12 total states that individuals can be in. The *meeting rates* of non-quarantined individuals is given by λ, and for quarantined individuals by λ^Q. We interpret the ratio factor by which quarantine reduces the rate of social interaction (λ/λ^Q) as the *quarantine technology* and treat it as a parameter.

   We denote the *transmission rates* by $\rho^A(\rho^S)$ for asymptomatic (symptomatic) cases to accommodate evidence that transmission rates are higher in symptomatic cases. These give the probability that, conditional on meeting an infected case $(\overline{IA}, \widetilde{IA}, IS)$, a non-infected individual $(\overline{NA}, \widetilde{NA})$ becomes infected. Crucially, individuals do not know who is infected, and do not know that they have met an infected person.[11]

4. **Testing.** We introduce a role for testing. Our information structure has assumed that when symptoms present, the individual and society know that the individual is infected. In this paper we do not cover testing of symptomatic individuals, although this is obviously a hugely important area.[12] We assume that testing of asymptomatic individuals takes place at a rate τ. Testing fully reveals an individual's health state. Tests do not produce false negatives or false positives.

   An issue arises in that individuals who have previously tested negative can become infected. This would require them to transition to either $\widetilde{IA}$ or $\overline{IA}$. If we assume either, then they move into a different group for

[11] This seems like a reasonable assumption to us despite one of the requisites for testing in many countries being that individuals can identify an infected individual that they interacted with.

[12] Note that in our model if we were to test symptomatic individuals then all tests would yield positives. In the data a small fraction of tests yield positives. In the US our interpretation of this is not that the US is testing asymptomatic people, but rather that individuals with similar symptoms due to common colds and the flu are being tested. To introduce testing of symptomatic individuals one would really want to extend the model to introduce an additional disease that presents observationally identical symptoms that can then be separated by testing.

the purpose of policy. However the transition would not be observed since the individual remains asymptomatic. Addressing this completely would require significantly enriching the model.[13] To avoid this, and in the spirit of this paper being a first step, we assume that testing has a 'tagging' property, such that the transition from $\widetilde{NA}$ to $\widetilde{IA}$ is observed. We highlight this in the notes to Table 3.

5. **Conditional quarantine.** We allow for quarantine policy and restrict this to depend on the *observable* health state of the individual. To keep the Markovian structure of the SEIR model, we quarantine individuals at constant rates. When there is no testing, individuals are moved from non-quarantine (NQ) to quarantine (Q) at rates ξ^u, ξ^+, ξ^r, for unknown, known positive and recovered cases. When there is testing, individuals are moved from non-quarantine (NQ) to quarantine (Q) at rates ξ^u, ξ^-, ξ^+, ξ^r, for unknown, known negative, known positive, and recovered cases, where now the known positive cases include $\widetilde{IA}$ individuals. We assume a set of corresponding rates at which individuals are *released* from quarantine: r^u, r^-, r^+, r^r.

3.2 Transmission

Given the above description of the model, we now describe transition rates of individuals between states. We work in continuous time and when simulating the model we consider a discrete time approximation in which a period is one hour and days are 14 hours long.

States. Individuals in the model are in one of 13 states:

- {Non-infected & Asymptomatic}×{Quarantine, Non-quarantine}×{Unknown, Known negative} → 4 states
- {Infected & Asymptomatic}×{Quarantine, Non-quarantine}×{Unknown, Known positive} → 4 states
- {Infected & Symptomatic} ×{Quarantine, Non-quarantine} → 2 states
- {Recovered & Aymptomatic} ×{Quarantine, Non-quarantine} → 2 states
- Deceased → 1 state

There is initially a distribution of a unit mass of individuals. When we simulate the model, we will assume that these individuals are non-quarantined, asymptomatic and unknown cases, with a small number being infected: $\overline{NA}, NQ$ and $\overline{IA}, NQ$. We denote the mass of individuals in a state X in period t by M_t^X.

Social interaction. In order to transmit the disease, individuals must first meet. We assume random matching. Non-quarantined individuals meet other individuals at rate λ, while quarantined individuals meet others at rate λ^Q. To save on notation we use, for example, NA to denote both $\overline{NA}$ and $\widetilde{NA}$ when distinguishing between the two is not relevant.

[13] A richer model would include something like the following. Individuals tests are viewed as 'good' for some number of days. Policies may therefore apply to individuals who were tested in, say, the 'last 60 days'. It is understood that some of these individuals would become infected and this would not be observed unless re-tested or symptoms develop. Given the law of large numbers, one could write down the law of motion for the fraction of 'tested negatives' that have since become positive. In this model individuals would require re-testing to keep track of the pandemic, a clear necessary extension of this model in order to use it quantitatively.

The conditional probabilities of meetings are as follows. The mass of individuals that are out in the world to bump into is given by M_t, and depends on the mass of individuals that are quarantined and non-quarantined:

$$M_t = \lambda M_t^{NQ} + \lambda^Q M_t^Q.$$

The masses of non-quarantined and quarantined individuals are given by:

$$\begin{aligned} M_t^{NQ} &= M_t^{NA,NQ} + M_t^{IA,NQ} + M_t^{IS,NQ} + M_t^{RA,NQ} \quad , \\ M_t^{Q} &= M_t^{NA,Q} \ + M_t^{IA,Q} \ + M_t^{IS,Q} \ + M_t^{RA,Q}. \end{aligned}$$

Conditional on meeting an individual, the probability that the individual is infected (non-infected) is given by π_t^I $\left(\pi_t^N\right)$:

$$\begin{aligned} \pi_t^I &= \frac{M_t^I}{M_t} = \frac{\lambda M_t^{I,NQ} + \lambda^Q M_t^{I,Q}}{M_t} = \frac{\lambda \left[M_t^{IA,NQ} + M_t^{IS,NQ}\right] + \lambda^Q \left[M_t^{IA,Q} + M_t^{IS,Q}\right]}{M_t} \quad , \\ \pi_t^N &= \frac{M_t^N}{M_t} = \frac{\lambda M_t^{A,NQ} + \lambda^Q M_t^{A,Q}}{M_t} = \frac{\lambda \left[M_t^{NA,NQ} + M_t^{RA,NQ}\right] + \lambda^Q \left[M_t^{NA,Q} + M_t^{RA,Q}\right]}{M_t}. \end{aligned}$$

Conditional on meeting an infected individual, the probability that the infected individual is symptomatic (asymptomatic) is given by π_t^{IA} $\left(\pi_t^{IS}\right)$:

$$\pi_t^{IA} = \frac{\lambda M_t^{IA,NQ} + \lambda^Q M_t^{IA,Q}}{M_t^I} \quad , \quad \pi_t^{IS} = \frac{\lambda M_t^{IS,NQ} + \lambda^Q M_t^{IS,Q}}{M_t^I}.$$

Infection. When individuals meet an infected individual, they become infected with probability ρ^A $\left(\rho^S\right)$ if the individual they meet is asymptomatic (symptomatic). Once infected, an individual does not know that they are infected as they are initially asymptomatic. A test, which occurs at rate τ, would reveal that they are infected, and the subject to quarantine policies of infected individuals. We assume that infected individuals all show symptoms and do not transition straight to a recovery.[14] Infected, asymptomatic, individuals show symptoms at a rate δ. Infected symptomatic individuals then recover at rate ω^R and die at rate ω^D. Recovered individuals gain complete immunity in our experiments.

Transmission rate. Combining the above, the rate of infection of a quarantined (non-quarantined) person is given by $\lambda^Q \alpha_t$, $(\lambda \alpha_t)$, where α_t is the probability of infection conditional on a random meeting:

$$\alpha_t = \pi_t^I \left[\pi_t^{IS} \rho^S + \pi_t^{IA} \rho^A\right].$$

[14] This is to avoid the issue of having *recovered* individuals that do not know that they were ever infected. We plan to extend this later on. The issue with this possibility is that we proliferate the state-space, adding a new state of Recovered, Uninformed, Asymptomatic. This will be *different* to Non-infected, Uninformed, Aysmptomatic, due to the different immunity properties of the Recovered individual. Such a recovered individual can then become infected, and so on and so forth, creating infinitely many states. Our assumption that all infected individuals eventually know that they are infected by showing symptoms, and then know that they have recovered keeps the state-space finite while still allowing for the key addition of asymptomatic transmission and incomplete information.

Note that the infection rate can be written

$$\lambda\alpha_t = \left(\rho^S\lambda\right) \times \pi_t^I \left[\pi_t^{IS} + \pi_t^{IA}\left(\frac{\rho^A}{\rho^S}\right)\right].$$

Data on the rate of transmission alone will be insufficient to separately identify ρ^S and λ, although below we discuss how variation in quarantine policy may be able to estimate these separately in future research.

3.3 Transition rates

As an example of the mechanics of the model, we describe the full set of transition rates for non-infected asymptomatic individuals, and infected asymptomatic individuals. These are the two cases that can be distinguished by testing asymptomatic individuals. Table 3 provides transition rates between all 13 states. Along with initial conditions for the distribution of individuals across health and information states is sufficient to simulate the model.

3.3.1 Non-infected, asymptomatic individuals

We consider this state as all non-infected individuals in the model are assumed to begin in one of these states. There are four possible states for non-infected, asymptomatic individuals. They can be an *unknown* or *known negative* case, and they can be *non-quarantined* or *quarantined*.

1. Consider an individual that is an unknown case and non-quarantined: $\overline{NA}, NQ$.
   - **Quarantine -** At rate ξ^u they take up quarantine and transition to $\overline{NA}, Q$
   - **Infection -** At rate λ they meet a random individual. With probability $\pi_t^I\pi_t^{IS}$ $\left(\pi_t^I\pi_t^{IA}\right)$ that individual is infected and symptomatic (asymptomatic). The individual then becomes $\overline{IA}, NQ$ with probability $\rho^S\left(\rho^A\right)$ depending on who the meeting is with. The total transition rate to $\overline{IA}, NQ$ is therefore $\lambda\alpha_t$.
   - **Testing -** At rate τ, they are tested and since tests are perfect, learn they are not infected, so transition to being a known negative case: $\widetilde{NA}, NQ$.
2. Consider an individual that is an unknown case and quarantined: $\overline{NA}, Q$.
   - **Quarantine -** At rate r^u they are released from quarantine and transition to $\overline{NA}, NQ$.
   - **Infection -** The rate of infection is lower in quarantine: $\lambda^Q\alpha_t \leq \lambda\alpha_t$.
   - **Testing -** At rate τ, they are tested, learn they are not infected, and transition to being a known negative case: $\widetilde{NA}, Q$.
3. Consider an individual that is a known negative case and non-quarantined: $\widetilde{NA}, NQ$
   - **Quarantine -** Since they are recognized as a negative case they may be quarantined at a lower rate $\xi^- \leq \xi^u$. A policy of indiscriminate quarantine would have $\xi^- = \xi^u$. A policy that allows negative cases to circulate would have $\xi^- = 0$.

- **Infection -** The individual still becomes infected at rate $\lambda\alpha_t$ and in this case becomes an known infected, asymptomatic case: $\widetilde{IA}, NQ$.

4. Consider an individual that is a known negative case and quarantined: $\widetilde{NA}, Q$
   - **Quarantine -** Since they are recognized as a negative case they may be released from quarantined at a higher rate $r^- \geq r^u$. A policy of indiscriminate quarantine would have $r^- = r^u$. A policy that allows negative cases to circulate would have $r^- = 1$.
   - **Infection -** The rate of infection is now reduced to $\lambda^Q\alpha_t$

3.3.2 Infected, asymptomatic individuals

For brevity we consider the case only for non-quarantined individuals.

1. Consider an individual that is a unknown case: $\overline{IA}, NQ$
   - **Quarantine -** Since they are also unknown cases, the rate of quarantine is the same that which must face $\overline{NA}, NQ$ individuals. At rate ξ^u they transition to quarantine: $\overline{IA}, Q$.
   - **Infection -** Since they are already infected there is no transition to infection.
   - **Testing -** At rate τ, they are tested and since tests are perfect, learn they are not infected, so transition to being a known positive case: $\overline{IA}, NQ$.
2. Consider an individual that is a known positive case: $\widetilde{IA}, NQ$
   - **Quarantine -** Since this is a known case then it can be subjected to the same rate of quarantine as infected, symptomatic cases. At rate ξ^+ they transition to quarantine: $\widetilde{IA}, Q$.
   - **Infection -** Since they are already infected there is no transition to infection.
   - **Testing -** Since they are already tested there is no further testing.

3.3.3 Transition rates between all states

Using the above logic and the structure of the model we can construct the matrix of flows between all 12 active states and into the deceased state. Table 3 describes all such transition rates.

3.3.4 Nesting the SEIR and SIR models

The SEIR model is nested in our model under the following parameter restrictions.

- No quarantine: $\lambda/\lambda^Q = 1$
- No asymptomatic transmission: $\rho_A/\rho_S = 0$
- No testing: $\tau = 0$

In this case individuals move from $\overline{NA} \to \overline{IA} \to IS \to RA$, which correspond to the $SEIR$ states. To obtain the SIR model, additionally set $\delta = 1$, such that infectiousness is immediate.

A. Initial state		B. Next instant states												
		Non-infected, Asymptomatic				Infected, Asymptomatic				Infected, Symptomatic		Recovered		Dead
		$\overline{NA}, NQ$	$\overline{NA}, Q$	$\widetilde{NA}, NQ$	$\widetilde{NA}, Q$	$\overline{IA}, NQ$	$\overline{IA}, Q$	$\widetilde{IA}, NQ$	$\widetilde{IA}, Q$	IS, NQ	IS, Q	RA, NQ	RA, Q	D
NA	$\overline{NA}, NQ$		ξ^u	τ		$\lambda\alpha_t$								
	$\overline{NA}, Q$	r^u			τ		$\lambda^Q\alpha_t$							
	$\widetilde{NA}, NQ$				ξ^-			$\lambda\alpha_t$						
	$\widetilde{NA}, Q$			r^-					$\lambda^Q\alpha_t$					
IA	$\overline{IA}, NQ$						ξ^u	τ		δ				
	$\overline{IA}, Q$					r^u			τ		δ			
	$\widetilde{IA}, NQ$								ξ^+	δ				
	$\widetilde{IA}, Q$							r^+			δ			
IS	IS, NQ										ξ^+	ω^R		ω^D
	IS, Q									r^+			ω^R	ω^D
R	RA, NQ												ξ^r	
	RA, Q											r^r		

Table 3: Transition rates between health and information states

Notes: This table gives the transition rates between states. Note that in any instant only one transition can occur. For example, an individual that is infected and asymptomatic and not quarantined may transition to symptomatic and quarantined, but *not* to symptomatic and not-quarantined. The individual then may transition from symptomatic and non-quarantined into quarantine. **Blue** terms refer to policies applied to *unknown cases*. **Red** terms refer to policies applied to *known positive cases*. **Green** terms refer to policies applied to *known negative cases*. The **Pink** terms are the result of the testing-as-tagging assumption: once tested and *known negative*, the transition to infection is observed so the individual becomes a *known positive*.

3.4 Measurement

3.4.1 Basic reproduction number

Consider a hypothetical 'date-zero' case. An individual is in the state $\overline{IA}, NQ$, while the rest of the population is in $\overline{NA}, NQ$ and there are no quarantine procedures in place. A summary statistic of the transmission rate is the expected number of infections caused by this single infected person: $\mathcal{R}_0^{IA,NQ}$. We can state this recursively as follows. At rate δ the individual becomes symptomatic, which will change their medical transmission rate to $\rho^S \geq \rho^A$:[15]

$$\mathcal{R}_0^{IA,NQ} = \lambda\rho^A + (1-\delta)\,\mathcal{R}_0^{IA,NQ} + \delta\mathcal{R}_0^{IS,NQ}$$
$$\mathcal{R}_0^{IS,NQ} = \lambda\rho^S + \left(1-\omega^R-\omega^D\right)\mathcal{R}_0^{IS,NQ}.$$

This implies that

$$\mathcal{R}_0^{IS,NQ} = \lambda\frac{\rho^S}{\omega^R+\omega^D} \quad , \quad \mathcal{R}_0^{IA,NQ} = \frac{\rho^S\lambda}{\delta}\left[\frac{\rho^A}{\rho^S} + \frac{\delta}{\omega^R+\omega^D}\right] \tag{1}$$

The nested case of the *SIR* model, which removes the *exposed* state, is obtained by setting $\delta = 1$ and has a *transmission rate* $\mathcal{R}_0 = \rho\lambda/\left(\omega^D+\omega^R\right)$.

We can try to use data on transmission rates from Wuhan to bound the effectiveness of quarantine. We view the Wuhan response as a *quarantine everyone* policy. If everyone is quarantined then

$$\mathcal{R}_0^{IA,Q} = \frac{\rho^S\lambda^Q}{\delta}\left[\frac{\rho^A}{\rho^S} + \frac{\delta}{\omega^R+\omega^D}\right]$$

therefore the relative rates of transmission pre- and post-quarantine policy are informative of λ/λ^Q which is our measure of the *quarantine technology*: $\lambda^Q\big/\lambda = \mathcal{R}_0^{IA,Q}\big/\mathcal{R}_0^{IA,NQ}$. In Wuhan, $\mathcal{R}_0^{IA,NQ} = 3.86$, while post qurantine measures leads to$\mathcal{R}_0^{IA,Q} = 0.32$. The Wuhan *quarantine technology* delivers $\lambda^Q/\lambda \approx 0.10$. We therefore view this as an *upper bound* on the quarantine technology in the United States: $(\lambda^Q/\lambda)_{US} \in [0.10, 1.00]$.

3.4.2 Measures of activity

To summarize some of our results we construct five metrics: Output, symptomatic infection, reported cases, mortality and social well-being.

Output. A reasonable approximation of economic activity is that it scales with the number of non-quarantined workers. We further assume that quarantined workers are $A_{rel} \in [0,1)$ less productive than non-quarantined workers, and that symptomatic workers do not produce. We therefore define output Y_t as

$$Y_t = M_t^{NA,NQ} + M_t^{IA,NQ} + M_t^{RA,NQ} + A_{rel}\left(M_t^{NA,Q} + M_t^{IA,Q} + M_t^{RA,Q}\right).$$

[15] In the case where $\rho^I = \rho^A$ and the transition from asymptomatic to symptomatic is instantaneous—i.e. as in the SIR model—then we have the recursion $\mathcal{R}_0 = \lambda\rho + \left(1-\omega^D-\omega^R\right)\mathcal{R}_0$ which gives $\mathcal{R}_0 = \lambda\rho/\left(\omega^D+\omega^R\right)$.

In the initial period all individuals are non-quarantined, so $Y_0 = 1$. Therefore Y_t is in units of the percent change in output from the initial period.

Symptomatic infection. A reasonable approximation of the load on the hospital system is that it scales with the number of infected, symptomatic individuals. We therefore define hospital load H_t as

$$H_t = \eta_H M_t^{IS}.$$

We do not consider a richer model of the rate of hospitalization of symptomatic cases, or the incidence of intensive care. Empirical evidence suggests around 20 (5) percent of symptomatic cases require hospitalization (intensive care). One could enrich the model such that mortality rates depend on H_t due to congestion and lack of resources, but this is not the focus of this paper. We therefore present results as the percentage change in H_t period-on-period, which subsumes linear scaling.

Testing and reported cases. Cases are reported when an asymptomatic infection case is tested, which occurs at rate τ, or the instant an asymptomatic infection becomes symptomatic, which occurs at rate δ. Give $R_t = 0$, then

$$\Delta R_t = (\tau + \delta)\, M_t^{\overline{IA}}.$$

We also track the number of tests. Initial tests are zero $\mathcal{T}_t = 0$ and then

$$\Delta \mathcal{T}_t = \tau \left(M_t^{\overline{NA}} + M_t^{\overline{IA}} \right).$$

Mortality. Since the death state is absorbing total mortality is simply $X_t = M_t^D$. In our counterfactuals we consider combinations of testing and quarantine policies that keep this number at the end of the pandemic constant, and compare the implications for symptomatic infections and output.

Social well-being. We consider a measure of social interaction. Non-quarantined individuals interact and we add up these meetings each period to get a measure of social interaction. There are M_t^{NQ} individuals that are non-quarantined, in various health states. The rate at which these individuals meet non-quarantined individuals is $\lambda \pi_t^{NQ}$, where $\pi_t^{NQ} = \lambda M_t^{NQ} / (\lambda M_t^{NQ} + \lambda^Q M_t^Q)$. Therefore our period t measure of social well-being is

$$S_t = \lambda M_t^{NQ} \times \left(\frac{\lambda M_t^{NQ}}{\lambda M_t^{NQ} + \lambda^Q M_t^Q} \right).$$

The upper bound for S_t is given by a virus-free society in which all individuals are non-quarantined, so $S_0 = \lambda$. The lower bound for S_t is zero, which occurs when all individuals are quarantined.

Parameter		Source / Target	Value
A. Known medical			
Rate at which infected become symptomatic	δ	6 days incubation period	$1/6$
Relative rate of asymptomatic transmission	ρ^A/ρ^S	No current evidence	1
Recovery	ω^R	14 day recovery period	$1/14$
Mortality	ω^D	Mortality rate of 1 percent	$\left(0.01/0.99\right) \times \omega^R$
B. Calibrated			
Rate of meeting	λ	Normalized contact rate	1
Rate of transmission	ρ^S	Given λ, gives $\mathcal{R}_0^{IA,NQ} = 2.5$	0.0091
C. Policy parameters			
Effectiveness of quarantine technology	λ^Q/λ	Half of that implied by Wuhan $\Delta\mathcal{R}_0$	0.5
Testing of unidentified and asymptomatic cases	τ	25 to 50 times peak US testing rate	0.5% per day
Quarantine rates for observable cases	$\left\{\xi^u, \xi^-, \xi^+, \xi^r\right\}$	See Section 5	
Release rates from quarantine for observable cases	$\left\{r^u, r^-, r^+, r^r\right\}$	See Section 5	

Table 4: Model parameters and values

4 Calibration

4.1 Parameters

Parameter values are given in Table 4. The parameters of the model can be classified intro three groups. The first relate to *'known' medical* parameters, which would be the equivalent of technological parameters in an economic model, and that we can take from the literature that has formed so far. Obviously the extent to which these parameters are well understood will evolve over time and we may use this information later on. The second relate to parameters that are similarly technological in that we think that they represent immutable features of the model, but that we do not have values for and require calibration. The third are policy parameters and relate to (i) testing rates, (ii) effectiveness of quarantine, (iii) rules for quarantine. We describe these in the next section when describing our counterfactuals.

Known medical. We assume that the rate at which infected individuals transition from asymptomatic to symptomatic cases, δ, is such that the average incubation period is 6 days (Wu, Leung, and Leung, 2020). World Health Organization (2020) report that the average recovery period is 14 days for mild infections, we therefore set $\omega^R = 1/14$. There is little data on the relative rates of infection of symptomatic and asymptomatic individuals.[16] We assume a common infection rate: $\rho^A/\rho^S = 1$.

From surveying estimates we target a mortality rate of 1 percent. In the model we denote this by π^D, which is

[16] https://www.buzzfeed.com/albertonardelli/coronavirus-testing-iceland. "Early results from deCode Genetics indicate that a low proportion of the general population has contracted the virus and that about half of those who tested positive are non-symptomatic".

the fraction of individuals experiencing symptoms (IS) that die. Then

$$\pi^D = \frac{\omega^D}{\omega^R + \omega^D}.$$

We use this to determine ω^D given ω^R and $\pi^D = 0.01$.

Unknown and calibrated. We use empirical estimates of the *rate of basic transmission* and equation (1) to calibrate λ and ρ^S. We treat $\mathcal{R}_0^{IA,NQ}$ as data, taking the value of 2.5, which is in the middle of the range of empirical estimates. Using equation (1) provides an equation in two unknowns $\{\lambda, \rho^S\}$.

Without further data these parameters cannot be separately identified. We therefore set $\lambda = 1$ and back out the implied ρ^S that is consistent with (1). To match the same basic rate of transmission requires

$$\rho^S = \frac{\mathcal{R}_0^{IA,NQ}}{\frac{\lambda}{\delta}\left[\left(\frac{\rho^A}{\rho^S}\right) + \frac{\delta}{\omega^R + \omega^D}\right]}.$$

In the future, within-region across-time variation in quarantine measures may allow us to separately identify $\{\lambda, \rho^S\}$. We set the quarantine technology $\lambda^Q/\lambda = 0.50$.

5 Counterfactuals

Our aim is to provide a small handful of counterfactuals with a minimal set of parameters. The configuration of these parameters is given in Table 5, and their values are given in Table 6. Section 5 and Section 6 refer to Case 1 in these tables, we consider Case 2—in which we repeat the exercise under more effective quarantine—in Section 7

Initial conditions. We seed the economy by choosing initial conditions that replicate the U.S. COVID-19 experience. We assume an initial infected population of 300 individuals and 1 detected case. We measure all model and data counterparts as of the 100th detected case.

Vaccine. We abstract from the long-run, and instead focus on testing and quarantine in the current phase of the pandemic. Consistent with this, we assume that in each case a vaccine is introduced to the economy after 500 days. The vaccine moves individuals in any of the NA states through to RA, NQ state, which makes them immune. The vaccine rolls out slowly, at a rate of 0.10 percent per day.

Counterfactuals. We then consider three different cases for the policy parameters: $\left\{\xi^u, \xi^-, \xi^+, \xi^r\right\}$, $\left\{r^u, r^-, r^+, r^r\right\}$, τ. We express these parameters as daily rates, despite the model being hourly. With so many parameters we have many degrees of freedom. We constrain these parameters in a simple way across counterfactuals so that we can be precise, but others may wish to consider many alternatives. We consider one at the end. Given that we have

assumed immunity, in all cases we set the quarantine rate of recovered individuals ξ^r to zero and their release rate r^r to 1.

Baseline. Our baseline model features no quarantine and no testing. With no testing ξ^- and r^- are off the table, since no unknown cases are tested and identified as negative. We then set $\xi^+ = \xi^u = 0$ and $r^+ = r^u = 1$.[17] This is the worst-case scenario in which the government does nothing to stop the spread of the virus.

Policy interventions. We consider two policy interventions that capture broad quarantine and targeted quarantine with testing. These policies begin on March 18th, which is two weeks after the first 100 cases are reported in the data and in the model. Aiming to cut down on parameters, we assume that in both cases known positive cases are quarantined and not released: $\xi^+ = 1$, $r^+ = 0$. We therefore have 6 parameters remaining: ξ^u and r^u in the quarantine case, and ξ^u, ξ^-, r^u and r^- in the testing case.

1. No testing - Common Quarantine. Our first policy is an approximation of what we have observed in the United States in March, 2020. In this counterfactual there is no testing of asymptomatic individuals and so no *known negative* cases. There is therefore a common quarantine rate for all asymptomatic individuals. We set this rate in counterfactual number 2 to $\xi_2^u = 0.010$, implying a 1 percent per day quarantine rate. This is in line with the data in Table 2, in which roughly 24 percent of the US population was quarantined within 19 days. We assume that the rate of release from quarantine is zero.

2. Testing - Targeted quarantine. Our second policy assumes that the government tests asymptomatic individuals at a rate τ. While the US is testing at a rate of roughly 0.01 percent of the population per day.[18] We assume that the US increases its testing capacity by roughly 50 fold to $\tau = 0.5\%$ per day. In levels, this would require testing 1,700,000 *asymptomatic* people per day, while the US is currently testing around 50,000 *symptomatic* people per day.

In the spirit of our paper being a proof of concept, we choose for comparison a very simple policy. We maintain the rate of quarantine of unknown cases and assume that known negatives are not released ($r_3^- - = 0$). These stack the decks *against* the testing policy having large effects. The only targeted quarantine measure that we take is to assume that non-quarantined known negative cases are quarantined at rate $\xi_3^- = \Delta \times \xi_2^-$, with $\Delta < 1$. We then choose a value for Δ such that the policy delivers the same number of total deaths as the common quarantine policy. This procedure delivers a value of $\Delta = 0.20$. When testing asymptomatic cases, the rate of quarantine of known negative cases can be cut by a factor of five without increasing the total number of deaths caused by the pandemic.

[17] For technical reasons, when we set a parameter to 1 we set it to a number $> .98$ percent per day (effectively 1).

[18] Countries like South Korea are testing at a rate of approximately 0.05 percent per day. This comes from reports of South Korean testing capacity of 20,000 per day (https://www.wired.co.uk/article/south-korea-coronavirus) and a population in South Korea of 51.47 million.

A. Counterfactuals	B. Parameters								
	Quarantine rates				Release rates				Testing
	ξ^+	ξ^u	ξ^-	ξ^r	r^+	r^u	r^-	r^r	τ
Baseline - Do nothing	0	0	—	0	1	1	—	1	0
Case 1 - Quarantine technology - $\lambda^Q/\lambda = 0.50$ **- Section 5 & 6**									
1. No testing - Common quarantine	1	ξ^u	—	0	0	0	—	1	0
2. Testing - Targeted quarantine	1	ξ^u	$\left(\Delta \times \xi^u\right)$	0	0	0	0	1	τ
Case 2 - Strong quarantine technology - $\lambda^Q/\lambda = 0.30$ **- Section 7**									
1. No testing - Common quarantine	1	ξ^u	—	0	0	0	—	1	0
2. Testing - Targeted quarantine	1	$\left(\psi \times \xi^u\right)$	0	0	0	0	0	1	τ

Table 5: Configuration of policy parameters for each counterfactual

Notes: This table gives the configurations of the policy parameters of the model under our three counterfactuals. Recovered individuals are immune and so never quarantined and always released. In the **Baseline case** there is no quarantine and no testing. Under the **1. No testing - Common quarantine** policy there is no testing, so uninfected and infected asymptomatic cases cannot be distinguished. Symptomatic cases are the only known positives, and these are completely quarantined and not released. Unknown cases are quarantined at rate ξ_2^u and not released. Under the **2. Testing - Targeted quarantine** policy there is testing of asymptomatic individuals at rate $\tau > 0$. Negative, asymptomatic cases are distinguished, quarantined at a lower rate, but released at the same rate as unknown cases. Given a value of τ we choose Δ such that overall deaths from Cases 1 and 2 are equivalent.

Description	Policy parameter	Daily rate
1. No testing - Common quarantine		
Common quarantine rate	ξ^u	1.0 %
2. Testing - Targeted quarantine		
Testing rate	τ	0.50 %
Case 1 - Quarantine technology $\lambda^Q/\lambda = 0.50$		
Differential quarantine rate: Known negatives	Δ	0.20
Case 2 - Strong quarantine technology $\lambda^Q/\lambda = 0.30$		
Differential quarantine rate: Unknown cases	ψ	0.30

Table 6: Counterfactual parameters

Notes: The parameter Δ is chosen so that both counterfactuals incur the same total deaths.

6 Results

Figure 6 plots our main results where we compare counterfactuals one and two. Statistics for these are given in Tables 7, 8, 9, which include the Baseline simulation. Panel A plots the cumulative number of reported cases. Panel B plots the number of infected, symptomatic cases. Given a constant rate of symptoms requiring medical

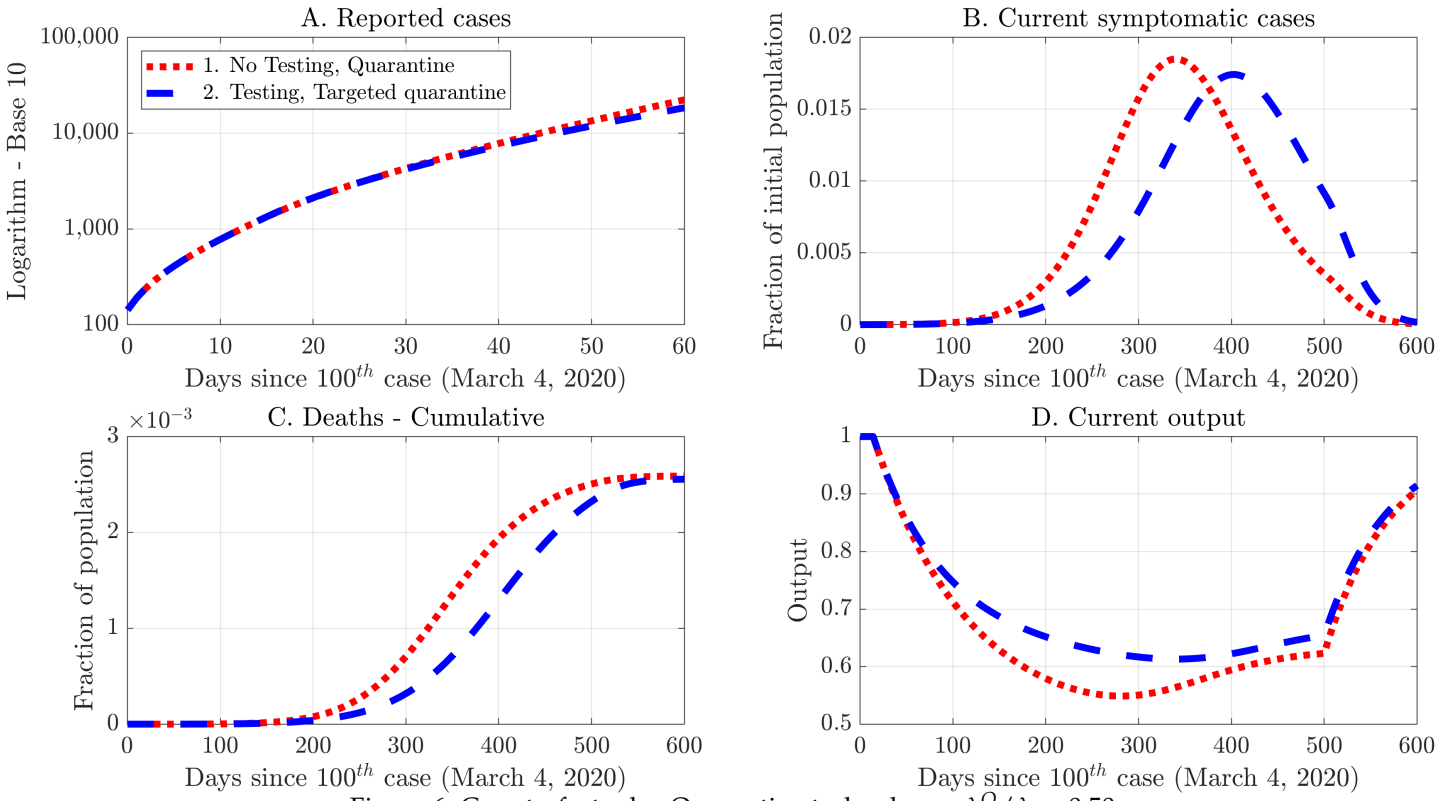

Figure 6: Counterfactuals - Quarantine technology - $\lambda^Q/\lambda = 0.50$

Notes: The red dotted line corresponds to the counterfactual **1. No testing - Common quarantine**. The blue dashed line corresponds to the counterfactual **2. Testing - Targeted quarantine**. Output is total non-quarantined, asymptomatic workers. Output in period zeros is equal to one since all workers are non-quarantined and asymptomatic.

attention, we can think of Panel B as capturing the number of individuals entering the hospital system. Panel C plots the cumulative fraction of the population that dies. Panel D plots measured output under the assumption that non-quarantined individuals produce 50 percent as much as quarantined individuals ($A_{rel} = .5$).

Cases. Common quarantine is effective at slowing the cumulative number of reported cases. Testing and targeted quarantine are slightly more effective.

Case load. Panel B plots the fraction of infected symptomatic individuals in the economy. Both counterfactual policies 'flatten the curve' relative to the baseline. The reduction in peak infection load is lower under the testing policy. If we interpret case load as the stress put on hospital capacity, targeted quarantine with testing generates the smallest peak load of cases. Common quarantine pushes the peak infection back by about 170 days, whereas the targeted quarantine with testing tends to put the peak case load back by 250 days, buying an additional quarter to prepare the medical system. Table 9 reports these statistics.

Deaths. Quarantine is an effective tool at reducing the number of deaths. The current US common quarantine policy, if continued to be enacted at the same rate (1% of the U.S. population entering quarantine per day), would

more than halve the fraction of the population that dies from the disease. Table 7 reports the deaths in levels in each of the scenarios. We deliberately set the parameters of the targeted quarantine policy to deliver the same cumulative deaths as the common quarantine policy, as can be seen clearly in Figure 6C. The testing policy backloads these deaths. In the short run, there are fewer deaths, but in the long run, as known negative cases are quarantined at a lower rate, total deaths converge.

Output. Table 7 shows that the baseline economy features very little output loss, driven entirely by the massive loss of life. This is the only tradeoff of quarantine in the textbook SEIR model: if a government quarantines individuals to reduce deaths, the lower output. The testing model and policy provide a third way, where output losses are less, due to relaxed quarantine but the *same* number of deaths is achieved.

In other words, targeted quarantine and testing alters the output-death tradeoff. With extra degrees of freedom in terms of policy, the government can do better than common quarantine both in terms of *deaths and output*. Figure 6D shows this clearly. Under targeted quarantine and testing, fewer individuals needs to be quarantined, output is significantly higher in the first 100 days of the pandemic and recovers more quickly. Accumulating output produced each period over the first year of the pandemic, output is 10 percent higher under the testing policy. in the long run the change in output only reflects the loss of life over the pandemic, and both policies deliver the same loss of life, long run output is the same.

We also report these results relative to pre-COVID-19 levels in Table 8. With targeted quarantine, the level of output is 10 percent higher in the first 200 days than with common quarantine, and then the two economies recover at a similar rate.

Caution. While we do not want readers to interpret our numbers literally since we are not epidemiologists and this is a not a rich quantitative SEIR model, we view Figure 6, panels C and D as illustrating our main point: targeted quarantine allows governments that can implement significant testing to produce more output than under the common quarantine policy. If the medical system produces fewer deaths under a more distant and lower peak case load, then the testing policy would also deliver fewer deaths. The policy can produce fewer deaths and higher output.

6.1 Robustness

For brevity we make one note regarding the robustness of our results to enriching the *medical block* of the model. We use this to highlight the usefulness of benchmarking counterfactuals.

Quantitative models being used to forecast the trajectory of the pandemic have richer medical blocks that incorporate congestion and capacity constraints in the health care system. From our understanding of these models we think that the following is true. Take an SEIR model and append an arbitrarily rich medical block. Now consider two policies A and B that deliver the same *total number of infections* over the pandemic—that is, the area underneath the curve in Figure 6B. If policy A has a lower peak than policy B then policy A will result in fewer deaths than policy B.

Experiment	Deaths			
	After 100 days	After 200 days	After 300 days	After 600 days
A. Deaths in Levels				
Baseline - Do nothing	10,013	2,572,026	3,037,155	3,040,479
1. No testing - Common quarantine	731	23,989	228,605	879,634
2. Testing - Targeted quarantine	603	12,306	102,605	868,471
B. Deaths Relative to Baseline				
1. No testing - Common quarantine	-9,282	-2,548,036	-2,808,550	-2,160,845
2. Testing - Targeted quarantine	-9,410	-2,559,719	-2,934,550	-2,172,008

Table 7: Counterfactual Deaths

Experiment	Output			
	After 100 days	After 200 days	After 300 days	After 600 days
1. Baseline - Do nothing	1.00	0.91	0.99	0.99
2. No testing - Common quarantine	0.72	0.58	0.55	0.90
3. Testing - Targeted quarantine	0.75	0.65	0.62	0.91

Table 8: Counterfactual Output: $\left(Output_t = M_t^{A,NQ} + 0.50 \times M_t^{A,Q}\right)$

Experiment	Peak infection	Days to peak
A. Levels		
Baseline - Do nothing	68,368,137	166
1. No testing - Common quarantine	6,288,619	341
2. Testing - Targeted quarantine	5,921,942	403
B. Percent relative to Baseline		
1. No testing - Common quarantine	-90.80 %	105.42 %
2. Testing - Targeted quarantine	-91.34 %	143.77 %

Table 9: Counterfactual Peak Infections

We have constructed our counterfactuals such that the area under the epidemiology curves are the same. To see this recall that there is a constant rate of transition from symptomatic states to death. Therefore, under the law of large numbers, fixing the total number of deaths across counterfactuals by construction fixes the total number of infections across counterfactuals as well. That is, we know that by construction we have *flattened the curve* in moving from the common quarantine to the test and targeted quarantine policy. Under a richer medical block, the testing and quarantine policy will result in fewer deaths.

7 More effective quarantine

Before concluding we consider how our counterfactual and available policies change under a more effective quarantine, that is a lower λ^Q/λ. Recall that we considered a value of 0.10 for this statistic for Wuhan, and in out main counterfactual exercise considered a half as effective quarantine technology in the US, such that $\lambda^Q/\lambda = 0.50$. We

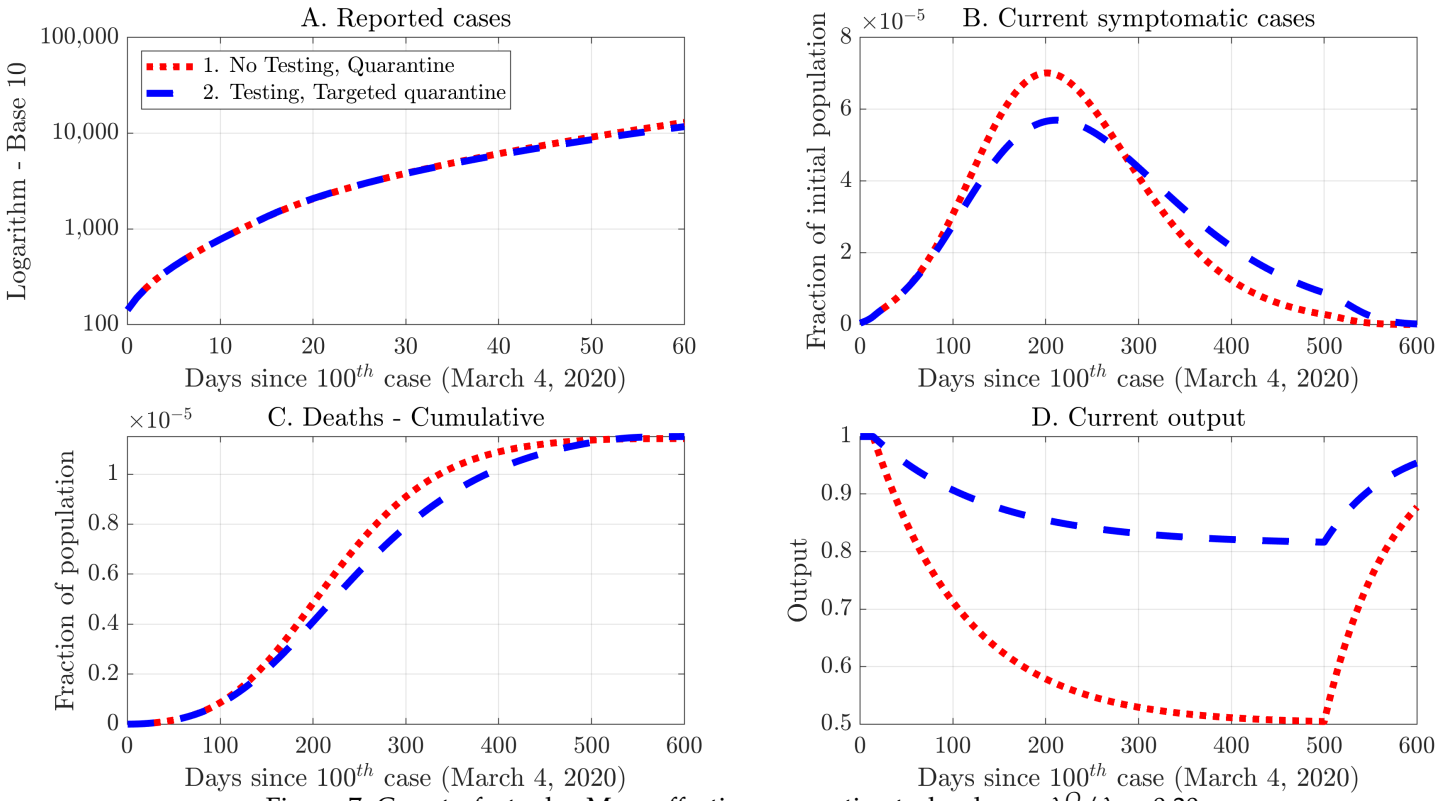

Figure 7: Counterfactuals - More effective quarantine technology - $\lambda^Q/\lambda = 0.30$

Notes: The red dotted line corresponds to the counterfactual **1. No testing - Common quarantine**. The blue dashed line corresponds to the counterfactual **2. Testing - Targeted quarantine**. Output is total non-quarantined, asymptomatic workers. Output in period zeros is equal to one since all workers are non-quarantined and asymptomatic.

now consider a more effective quarantine, halfway between these with $\lambda^Q/\lambda = 0.30$. Now with a more effective quarantine, even if we set $\Delta = 0$ and quarantine no individuals that have tested negative, then the policy generates fewer deaths than the no testing, common quarantine policy. This gives extra space for policy to reduce quarantining other individuals. We again model this simply, reducing the rate of quarantine of *unknown cases* to $\psi \times \xi^u$, with $\psi \leq 1$. Table 5 and Table 6 describe this additional counterfactual, and show that we can set $\psi = 0.30$ and still incur the casualties from the epidemic as the baseline quarantine policy. Figure 7 shows that this substantially reduces the decline in our measure of output, and again 'flattens the curve' in terms of projected symptomatic infections.

8 Conclusion

This short paper conceptualizes a minor and easily implemented change to the standard SEIR model of infectious disease transmission. We assume that quarantine policies can only depend on observed health states, which creates a role for testing in distinguishing between infected and non-infected asymptomatic individuals. We demonstrate via a simple calibration of the model, that testing asymptomatic individuals can stand-in for costly quarantine

measures. We make this notion precise by simultaneously reducing quarantine measures and increasing testing such that the overall mortality rate of the pandemic remains constant at *'Quarantine Everyone'* levels. With fewer individuals quarantined, we infer that output of the economy would decline substantially less. Thus, targeted quarantine and testing alters the output-death tradeoff. The government can do better than common quarantine both in terms of *deaths and output*.

The model here is not immediately applicable for serious quantitative work. However, we think that our exercises show that adding incomplete information and a role for testing through targeted quarantine does not overly complicate the baseline model and allows discussion of testing policies that cannot be discussed in the baseline complete information model. These additional features could be integrated into more quantitative epidemiology models that append to the SEIR model demographics, geography, imperfect immunity, and so on.

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APPENDIX

A Additional tables and figures

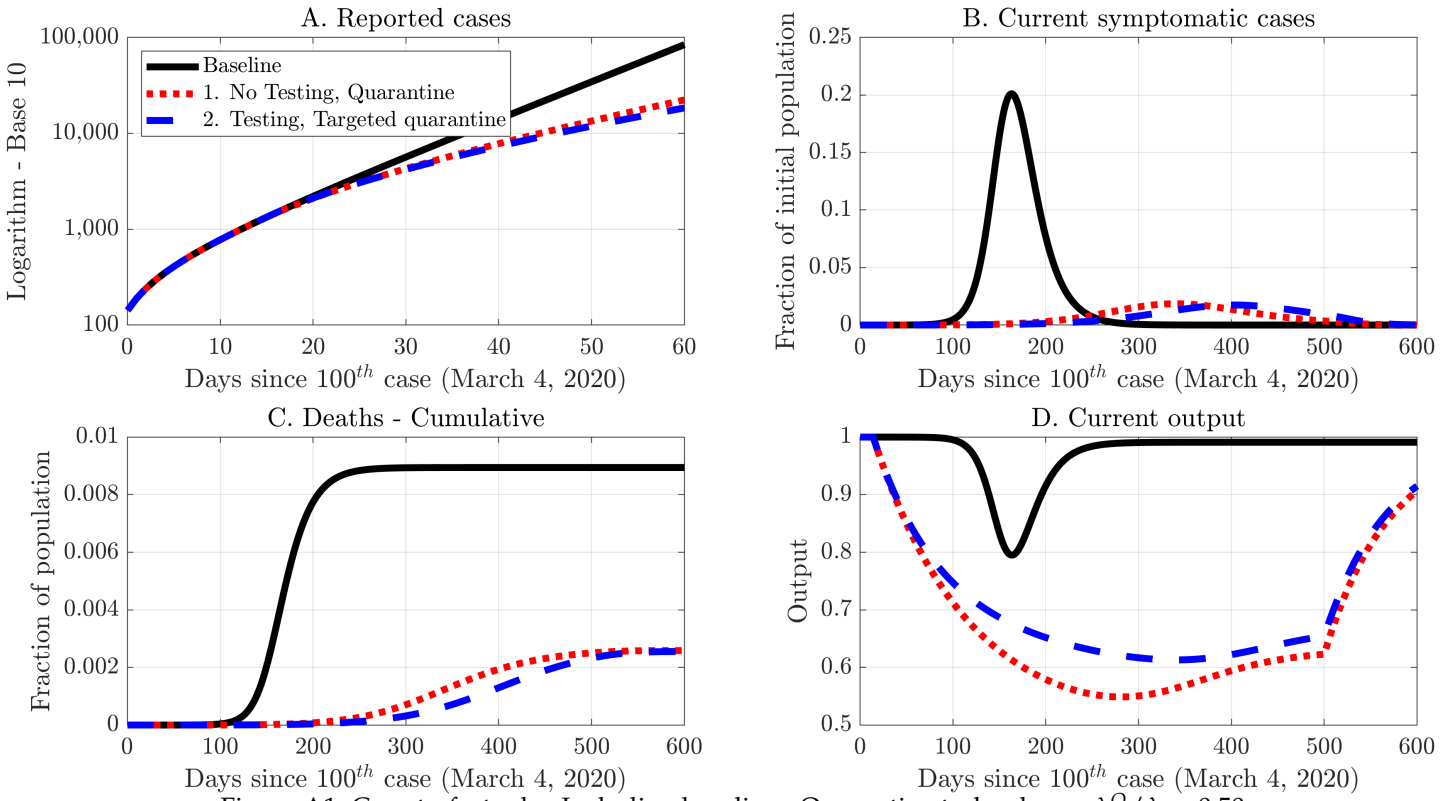

Figure A1: Counterfactuals - Including baseline - Quarantine technology - $\lambda^Q/\lambda = 0.50$

Notes: In each panel the black solid line corresponds to counterfactual **Baseline - Do nothing**. The red dotted line corresponds to the counterfactual **1. No testing - Common quarantine**. The blue dashed line corresponds to the counterfactual **2. Testing - Targeted quarantine**. Output is total non-quarantined, asymptomatic workers. Output in period zero is equal to one since all workers are non-quarantined and asymptomatic.

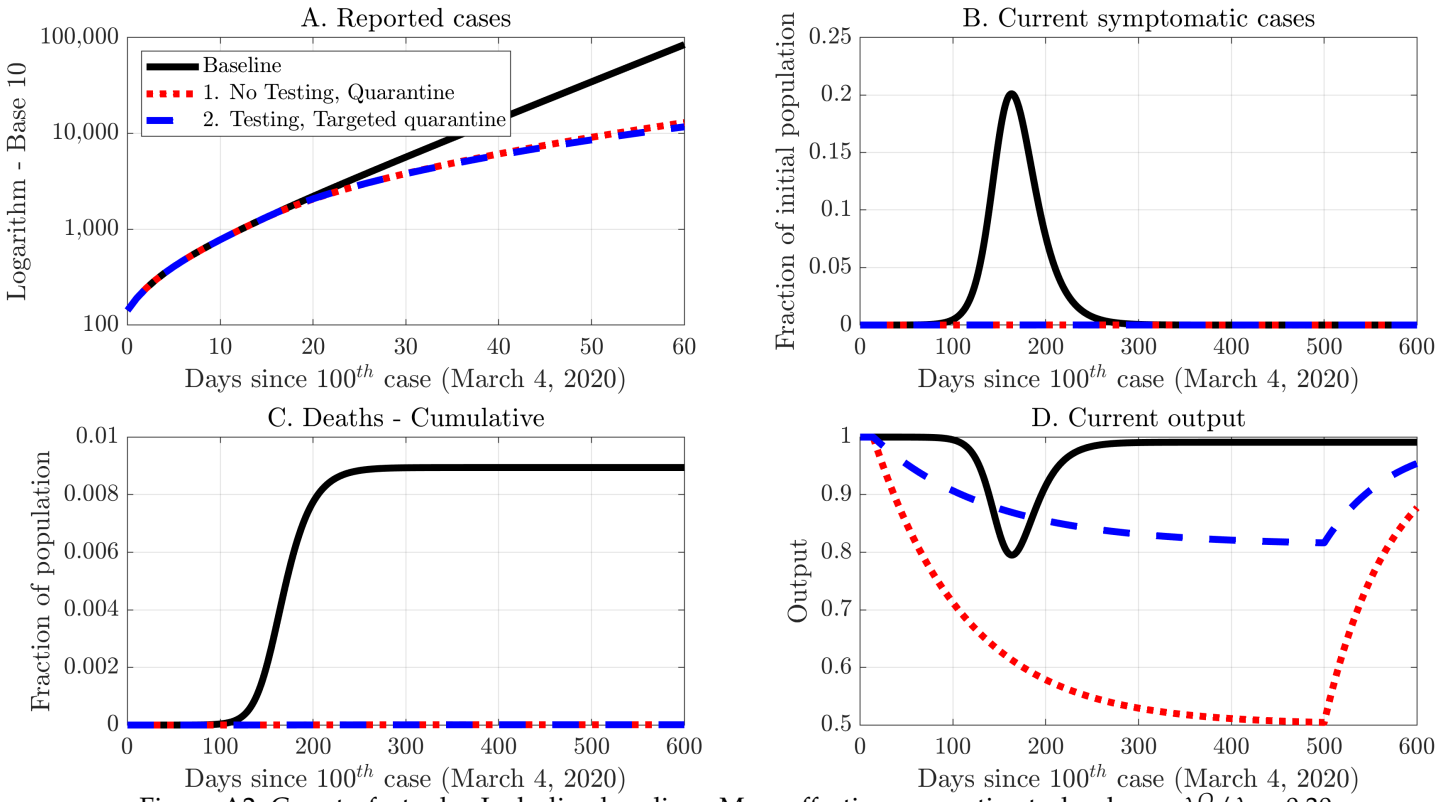

Figure A2: Counterfactuals - Including baseline - More effective quarantine technology - $\lambda^Q/\lambda = 0.30$

Notes: In each panel the black solid line corresponds to counterfactual **Baseline - Do nothing**. The red dotted line corresponds to the counterfactual **1. No testing - Common quarantine**. The blue dashed line corresponds to the counterfactual **2. Testing - Targeted quarantine**. Output is total non-quarantined, asymptomatic workers. Output in period zero is equal to one since all workers are non-quarantined and asymptomatic.