PANDEMIC RECESSIONS AND CONTACT TRACING

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Abstract
We study contact tracing in a new macro-epidemiological model with asymptomatic transmission and limited testing capacity. Contact tracing is a testing strategy that aims to reconstruct the infection chain of newly symptomatic agents. This strategy may be unsuccessful because of an externality leading agents to expand their interactions at rates exceeding policymakers' ability to test all the traced contacts. Complementing contact tracing with timely deployed containment measures (e.g., social distancing or a tighter quarantine policy) corrects this externality and delivers outcomes that are remarkably similar to the benchmark case where tests are unlimited. We provide theoretical underpinnings to the risk of becoming infected in macro-epidemiological models. Our methodology to reconstruct infection chains is not affected by curse-of-dimensionality problems. (JEL: E10, D62, I10)

1. Introduction

The outbreak of the COVID-19 pandemic set off a worldwide health and economic crisis of unprecedented proportions. Quickly expanding the capacity for testing, isolation, and contact tracing has been suggested by several experts to be a crucial

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step in alleviating the pandemic's toll on the economy and mortality.[1] For instance, South Korea has combined contact tracing, mass testing, and alternative containment measures to achieve one of the lowest infection rates in the world. Nevertheless, other countries, such as the U.S., have been considerably less successful, notwithstanding sizable investments made in contact tracing and mass testing. In this paper, we construct a macro-epidemiological model with asymptomatic transmission and limited testing capacity to study (i) the social value of a technology enabling policymakers to trace the close contacts of confirmed infected cases, (ii) why this technology may fall short of delivering the expected outcome, and (iii) how contact tracing can be combined with alternative containment policies to effectively control a pandemic.

We model contact tracing as a testing strategy that aims to reconstruct the newly symptomatic cases' *infection chain*—that is, the network of interactions that led a newly symptomatic case to become infected or to infect other agents. This reconstruction allows the policymakers to decide who to test. The objective of testing is to detect and quarantine as many asymptomatic spreaders as possible. The epidemiological parameters of the model and the availability of tests are calibrated to match the U.S. data during the COVID-19 pandemic.

Contact tracing can be unsuccessful because of an externality leading agents to expand economic and social interactions at rates exceeding policymakers' ability to trace, test, and isolate the close contacts of confirmed cases. Complementing contact tracing with timely deployed containment policies (e.g., social distancing or a tighter quarantine policy) allows policymakers to buy time to expand the tracing and testing scale so as to preserve the viability of the tracing and testing system. Our calibrated model predicts that U.S. testing availability during the COVID-19 pandemic was insufficient to ensure effective contract tracing without other containment policies.

If this externality is addressed properly by policymakers, contact tracing lowers the threshold number of infected agents needed to reach herd immunity by leveraging the information contained in the reconstructed infection chain of confirmed cases. In addition, the reconstruction of the confirmed cases' infection channel is critical to enable contact tracing to effectively detect asymptomatic spreaders at the early stages of a pandemic when there are only a few spreaders.[2] In virtue of these two attributes, contact tracing mitigates both the consumption drop due to the pandemic and its death toll, allowing policymakers to move beyond the traditional trade-off between saving human lives and mitigating the economic costs of the pandemic.

We show that preserving the functionality of contact tracing is optimal. When we solve the optimal social distancing problem, we find that the planner wants to

1. For instance, Dr. Anthony Fauci, the then director of the National Institute of Allergy and Infectious Diseases, said in an interview with Dr. Howard Bauchner, the editor of the *Journal of the American Medical Association*, in April 2020 that "The keys [to a successful response] are to make sure that we have in place the things that were not in place in January, that we have the capability of mobilizing identification—testing—identification, isolation, contact tracing."

2. This prediction is in line with empirical findings by Fetzer and Graeber (2021), who show quasi-experimental evidence that contact tracing is very effective in containing the spread of the virus.

tighten social distancing restrictions right before the tracing and testing system would collapse. Scaling up social distancing measures in that period corrects the externality that threatens the smooth functioning of contact tracing and, in doing so, leads to economic and health outcomes that are remarkably similar to the benchmark case where tests are assumed to be unlimited.

How critical is it for policymakers to be able to run contact tracing smoothly during a pandemic? Our calibrated model predicts that the social value of being endowed with a viable contact tracing and testing system is about $8.7 trillion. Given that a tracing technology is arguably cheap to develop for most countries, this result suggests that it may be cost-effective for policymakers to invest in such a technology, even if epidemics are expected to be rather infrequent events. A more comprehensive tracing technology enabling policymakers to trace contacts for one additional week further increases social welfare by $1.5 trillion.

Contact tracing has been used to control the spread of a long list of lethal diseases, such as tuberculosis, measles, sexually transmitted infections (including syphilis and HIV), blood-borne infections, Ebola, H1N1 (swine flu), avian influenza, SARS-CoV (SARS), and SARS-CoV-2 (COVID-19).[3] However, formally modeling contact tracing is very hard, as the number of contacts established by an infected subject quickly explodes as the number of past periods considered increases.

We solve this dimensionality problem by modeling the probability that a susceptible subject entertains a number of economic interactions with the pool of asymptomatic infected agents as a sequence of *Bernoulli trials*. The number of trials depends on how much susceptible agents consume (work), and the probability of success (i.e., meeting with an asymptomatic infected subject) is assumed to depend on the share of consumption (work) of asymptomatic infected people. It follows that the probability for a susceptible agent to have met a certain number of infected agents is a binomial distribution. This binomial distribution allows us to parsimoniously characterize the endogenous probability of a susceptible agent becoming infected in a given period. This probability turns out to be isomorphic to that in macro-epidemiological models (e.g., Eichenbaum, Rebelo, and Trabandt 2021), thereby providing theoretical underpinnings to that probability, which is typically assumed in those models.[4] Furthermore, this binomial distribution summarizes all of the necessary information to reconstruct the infection chains in our model, which is key to pinning down agents' probabilities of being traced and tested. This methodology to reconstruct the history of interactions relevant for contact tracing is general and can be applied to macro-epidemiological models with multiple sectors or heterogeneous agents.[5]

3. Contact tracing was originally proposed in 1937 by Surgeon General Thomas Parran for the control of syphilis in the U.S. and was implemented to control its spread in the following years (Parran 1937).

4. In the special case in which the virus cannot be spread through consumption and labor interactions, the infection probability is isomorphic to the canonical SIR model of Kermack and McKendrick (1927).

5. See Guerrieri et al. (2022) for an example of multisectoral models to study how an epidemic and social distancing affect aggregate demand and supply. See Kaplan, Moll, and Violante (2020) for an example of macro-epidemiological models with income and wealth inequalities.

Our paper belongs to the macro-epidemiological literature. This literature is quickly growing in many different directions. The directions more closely related to our paper are as follows: analyses of the trade-off between saving human lives and mitigating the recession (Gourinchas 2020; Hall, Jones, and Klenow 2020); models to study optimal social distancing (Atkeson 2020; Bethune and Korinek 2020; Alvarez, Argente, and Lippi 2021; Eichenbaum, Rebelo, and Trabandt 2021; Farboodi, Jarosch, and Shimer 2021; Moser and Yared 2022; Piguillem and Shi 2022); models to study more targeted and smarter policies, such as testing or targeted quarantines, as alternatives to indiscriminate social distancing measures (Akbarpour et al. 2020; Atkeson et al. 2020; Azzimonti et al. 2020; Baqaee et al. 2020a; Bognanni et al. 2020; Brotherhood et al. 2020; Favero, Ichino, and Rustichini 2020; Galeotti, Steiner, and Surico 2020; Glover et al. 2020; Acemoglu et al. 2021; Aum, Lee, and Shin 2021; Chari, Kirpalani, and Phelan 2021; Berger et al. 2022; Eichenbaum, Rebelo, and Trabandt 2022; Hornstein 2022; Krueger, Uhlig, and Xie 2022); studies of the distributional consequences of containment policies (Kaplan, Moll, and Violante 2020; Hacıoğlu-Hoke, Känzig, and Surico 2021; Lee, Park, and Shin 2021); and models to assess the efficacy of public policies—not based on tracing and testing—in controlling HIV (Greenwood et al. 2019).

The implementation of contact tracing is plagued by several bottlenecks. An important part of our analysis is to show that one potential bottleneck—that is, the limited availability of tests—may lead to the demise of the tracing and testing system and that this event would worsen the pandemic's economic and health outcomes considerably. We study a number of mitigation policies (optimal social distancing, a tighter quarantine policy, and a mask-wearing mandate) that can be deployed in a timely manner to shore up the resilience of the tracing and testing system. The macro-epidemiological literature has studied the dynamic complementarities of optimal social distancing with other factors: the limited capacity of the health system (e.g., Loertscher and Muir 2021), the arrival time of an effective vaccine (e.g., Iverson, Karp, and Peri 2022), and the arrival of an effective technology to test and quarantine infected subjects (e.g., Brotherhood et al. 2020).

Given the hurdles to formally modeling the infection chain of confirmed cases, all the papers we know take a reduced-form approach to contact tracing (e.g., Alvarez, Argente, and Lippi 2021; Piguillem and Shi 2022). Typically in these papers, a fraction of agents whose health status is unknown become tested by the government in every period.[6] Modeling contact tracing by taking into account the existence of infection chains as we do has three main advantages. First, the central result that a well-functioning contact tracing allows policymakers to improve both economic and health outcomes of a pandemics hinges upon the enhanced ability of contact tracing of successfully detecting asymptomatic spreaders, even at the onset of a pandemic when it is very hard to do so. We find this result because we take into account the existence of

6. Chari, Kirpalani, and Phelan (2021) study targeted testing assuming that infected agents are more likely to receive a signal about their health status. They interpret the signal as the outcome of a test.

infection chains. Second, our approach is preferable when one is concerned about the Lucas critique, which would arise, for instance, if one studies the efficacy of contact tracing under a mutating virus (e.g., a virus mutation resulting in more asymptomatic infections). Third, our structural analysis of contact tracing helps to calibrate smart testing in papers that take a more reduced-form approach.

Our paper is also related to the epidemiological literature that studies contact tracing. Hellewell et al. (2020) model contact tracing based on a branching process, which uses a negative binomial distribution to keep track of the number of secondary infections that a person infected with the virus could potentially produce (see also e.g., Ferretti et al. 2020). In our analysis, the binomial distribution is used to model the probability that an agent meets a number of times with asymptomatic infected subjects while consuming and working. This different approach has important implications: First, the probability for an agent to be traced is endogenous, depending on their consumption and labor decisions. Second, our binomial approach allows us to provide theoretical underpinnings to the infection rate in SIR and Macro-SIR models.

2. The Model

The model economy is populated by agents who consume and work, and firms that hire labor N_t from agents in a competitive market and produce output according to a linear production function in labor and productivity parameter A. The government levies taxes on consumption and remits transfers to agents. Labor and output are traded in competitive markets. Health authorities conduct contact tracing, administer tests, and can quarantine agents. Agents become infected through interactions with other agents. Following Eichenbaum, Rebelo, and Trabandt (2021), we assume there are three types of interactions through which the virus spreads out: consumption interactions, work interactions, and other interactions independent of agents' decisions.

Every period is organized as follows: First, agents consume, work, and engage in other interactions. Second, agents' health status can change: Agents can get infected or infected agents can recover or die. Third, health officials can administer tests. Tests deliver a binary outcome: positive or negative. Tests do not reveal if an agent has never been infected or has recovered.

There are six types of agents, who differ in their health status. The first type includes *susceptible agents* who have not contracted the disease, are not carriers, and are not immune. Infected agents can be divided into three types: *Untested asymptomatic agents* if they have not shown symptoms and have not tested positive, *tested-positive agents* if they are asymptomatic but they have tested positive, and *symptomatic infected agents* if they have shown symptoms regardless of whether they have previously tested positive. The remaining two types are the recovered agents, who have developed immunity. They are the *observed recovered agents*, who have shown symptoms or have tested positive and the *unobserved recovered agents*, who have recovered without having ever shown any symptoms or having ever tested positive.

Observability of Types' Health Status. Since the untested asymptomatic individuals are assumed not to show any symptoms of the disease, their health status is not observed by anyone in the model. The health status of susceptible agents and that of unobserved recovered subjects is also not observed even if they got tested at the end of the previous period. This is because tests only say whether the tested individual is currently infected or not. The health status of tested-positive, symptomatic infected, and observed recovered agents is publicly observed.

Quarantine. The tested-positive and the symptomatic subjects have their health status revealed and the health authorities immediately quarantine them.[7] Being quarantined means two things. First, in quarantine consumption and labor decisions are subject to restrictions, which are modeled as a consumption tax. Second, quarantined agents are isolated from other subjects and cannot infect anyone. Note that we use the word quarantine to mean a containment policy targeted to a single subject or a subset of subjects who have been uncovered by the government as potentially capable of spreading the virus. Thus, quarantine is different from social distancing, which refers to an economy-wide containment measure, affecting all subjects.

Meeting Probabilities. The virus in our model spreads out because susceptible agents may meet with untested asymptomatic agents while consuming, working, or engaging in other non-economic activities.[8] So, it is particularly important to characterize the probability that a susceptible individual meets with untested asymptomatic subjects. We make the following assumption to characterize this probability.

ASSUMPTION 1. Every random interaction of an agent with a set of agents of a specified type is modeled as a Bernoulli trial.

It then follows that the probability that an individual, who randomly meets $n > 0$ other agents in a period, meets k-times with agents of a certain type is given by the binomial distribution $\mathcal{B}(k, n, p) = \binom{n}{k} p^k (1-p)^{(n-k)}$, where p is the probability of meeting with agents of a certain type in one random meeting. In the Bernoullian jargon, there will be n random trials and in each of these trials the individual meets (success) or does not meet (failure) with a specified group of people. We make the following assumption about the probability of meeting with a specified group.

ASSUMPTION 2. The probability for an agent to meet with agents of a certain type

(a) in one random consumption interaction is given by the share of consumption of the agents of that type relative to the consumption of non-quarantined agents;

(b) in one random working interaction is given by the share of hours worked by the agents of that type relative to the hours worked by non-quarantined agents;

7. Untested asymptomatic agents are not quarantined because health authorities cannot distinguish them.

8. Other infected (tested-positive and symptomatic) people are quarantined and cannot infect anyone.

(c) in one random interaction not associated with either consumption or work is given by the share of agents of that type relative to the population of non-quarantined agents.

For instance, the probability of meeting an untested asymptomatic subject in one consumption interaction is given by the size of the consumption of untested asymptomatic people relative to aggregate consumption, in symbols, C_t^A/C_t, where C_t^A denotes total consumption of the untested asymptomatic agents and C_t stands for the aggregate consumption of non-quarantined agents. Analogously, the probability for a worker to meet an untested asymptomatic worker in 1 hour of work is assumed to be N_t^A/N_t, where N_t^A denotes total labor worked by the untested asymptomatic group and N_t stands for aggregate labor of non-quarantined agents. The probability for an individual to meet with an untested asymptomatic agent in one non-consumption, non-labor interaction is assumed to be equal to the share of untested asymptomatic agents: I_t^A/POP_t, where I_t^A denotes the size of the group of individuals who are untested asymptomatic and POP_t stands for the population size of non-quarantined agents.

ASSUMPTION 3. An individual of health status i who consumes c_t^i units of goods, works n_t^i number of hours at time t makes $\varphi_C : c_t^i \mapsto \mathbb{N} \cup \{0\}$ and $\varphi_N : n_t^i \mapsto \mathbb{N} \cup \{0\}$, respectively, number of interactions, where $\mathbb{N} \cup \{0\}$ denotes the set of natural numbers including zero. The same individual also makes a constant number of φ_O interactions when engaging in activities other than consumption and labor.

It follows that the total number of interactions a susceptible individual entertains to consume c_t^s, work n_t^s, and enjoy other activities, is given by $\varphi_C(c_t^s) + \varphi_N(n_t^s) + \varphi_O$. This gives us the number of Bernoulli trials due to these three activities in the time unit. We can think of the mappings φ_C and φ_N as monotonically increasing step functions.

Combining all these assumptions allows us to write the probability for a susceptible individual to meet k times with the set of asymptomatic subjects while consuming an amount c_t^s of goods as follows:

$$f_{c,t}(k) \equiv \mathcal{B}\left(k, \varphi_C(c_t^s), \frac{C_t^A}{C_t}\right) = \binom{\varphi_C(c_t^s)}{k} \left(\frac{C_t^A}{C_t}\right)^k \left(1 - \frac{C_t^A}{C_t}\right)^{\varphi_C(c_t^s)-k}, \quad (1)$$

$k \leq \varphi_C(c_t^s)$. We can analogously derive the probability for a susceptible individual to meet k-times with the asymptomatic subjects while working an amount n_t^s of hours

$$f_{n,t}(k) \equiv \mathcal{B}\left(k, \varphi_N(n_t^s), \frac{N_t^A}{N_t}\right) = \binom{\varphi_N(n_t^s)}{k} \left(\frac{N_t^A}{N_t}\right)^k \left(1 - \frac{N_t^A}{N_t}\right)^{\varphi_N(n_t^s)-k}, \quad (2)$$

$k < \varphi_N(n_t^s)$. Finally, the probability for any person to meet with people in the asymptomatic group k times while engaging in other types of interactions is

$$f_{o,t}(k) \equiv \mathcal{B}\left(k, \varphi_O, \frac{I_t^A}{\text{POP}_t}\right) = \binom{\varphi_O}{k}\left(\frac{I_t^A}{\text{POP}_t}\right)^k\left(1 - \frac{I_t^A}{\text{POP}_t}\right)^{\varphi_O - k}, \tag{3}$$

$k < \varphi_O$. Let us denote the number of random interactions due to consumption, work, and other activities as k_c, k_n, and k_o, respectively. The joint probability for a susceptible individual to have a triplet of random meetings (k_c, k_n, k_o) with untested asymptomatic people is defined as follows:

$$f_t(k_c, k_n, k_o) \equiv f_{c,t}(k_c) \cdot f_{n,t}(k_n) \cdot f_{o,t}(k_o). \tag{4}$$

ASSUMPTION 4. Conditional on meeting with an untested asymptomatic individual, a susceptible agent will become infected with probability $\tau \in (0, 1)$.

Since this probability of getting infected τ is assumed to be the same across the three different types of interactions (consumption, work, or others), a susceptible individual entertaining $k_c + k_n + k_o$ interactions with asymptomatic individuals will become infected with probability $1 - (1 - \tau)^{k_c + k_n + k_o}$; that is, one minus the probability that none of these interactions turns out to be infectious, that is, $(1 - \tau)^{k_c + k_n + k_o}$.

We can characterize the average probability for a susceptible individual to get infected conditional on consuming c_t^s and working n_t^s as follows:

$$\tau_t \equiv \sum_{k_c=0}^{\varphi_C(c_t^s)} \sum_{k_n=0}^{\varphi_N(n_t^s)} \sum_{k_o=0}^{\varphi_O} [1 - (1 - \tau)^{k_c + k_n + k_o}] f_t(k_c, k_n, k_o), \tag{5}$$

where $f_t(k_c, k_n, k_o)$ denotes the joint binomial distribution defined in equation (4).

The infection rate τ_t can be approximated to obtain

$$\tau_t \approx \Xi\left[\varphi_c \cdot c_t^s\left(\frac{C_t^A}{C_t}\right) + \varphi_n \cdot n_t^s\left(\frac{N_t^A}{N_t}\right) + \varphi_O\left(\frac{A_t}{\text{POP}_t}\right)\right], \tag{6}$$

where the coefficient $\Xi \equiv -\ln(1 - \tau)(1 - \tau)^{\bar{k}_c + \bar{k}_n + \bar{k}_o}$, with $(\bar{k}_c, \bar{k}_n, \bar{k}_o)$ denote the average number of interactions at steady state. Online Appendix E derives the approximation.

The approximated infection rate τ_t in equation (6) nests the rate in the canonical SIR model as the special case in which consumption and labor interactions do not transmit the virus. It is also isomorphic to other leading macro-epidemiological models, in which this rate is assumed (e.g., Eichenbaum, Rebelo, and Trabandt 2021). Since the infection rate in equation (6) stems from the choice of modeling economic interactions as binomial trials (Assumptions 1–4), our paper provides theoretical underpinnings to the infection rate used in those models.

Agents with Unknown Health Status. As discussed earlier, susceptible, untested asymptomatic, and unobserved recovered individuals do not know their health status. To keep the model tractable, we assume that these agents make consumption and labor decisions in the belief that they have never been infected and thereby are susceptible. While this assumption has a behavioral flavor, it has minimal implications for our conclusions because our analysis is primarily focused on dynamics at the beginning of a pandemic when the economy is far away from achieving herd immunity.[9] Conditional on the belief of having never been infected, agents' beliefs about future changes in their health status are model consistent. It follows that the agents who do not know their health status choose their consumption c_t^s, and labor n_t^s so as to maximize

$$V_t^S = \max_{c_t^s, n_t^s} u\left(c_t^s, n_t^s\right) + \beta\left[(1-\tau_t)V_{t+1}^S + \tau_t\left\{\pi_{P,t}^T V_{t+1}^P + \left(1-\pi_{P,t}^T\right)V_{t+1}^A\right\}\right], \tag{7}$$

where the utility function $u(c_t, n_t) = \ln c_t - (\theta/(1/\eta))n_t^{1/\eta}$ and β denotes the discount factor. We denoted all the variables in equation (7) with the superscript S because these agents believe they are susceptible.

These agents expect to be infected with probability τ_t, which is defined in equation (5). Conditional on this event, the agents expect with probability $\pi_{P,t}^T$ to test positive at the end of period t and thereby to receive the utility V_{t+1}^P of the tested-positive agents in period $t+1$. This value function will be defined in Section 2. With probability $(1-\pi_{P,t}^T)$, the agents expect to become untested asymptomatic and receive the utility V_{t+1}^A, which, in period t, is given by

$$\begin{aligned} V_t^A = {} & u\left(\tilde{c}_t^s, \tilde{n}_t^s\right) \\ & + \beta\left[\pi_{IS}V_{t+1}^{IS} + \pi_R V_{t+1}^{UR} + (1-\pi_{IS}-\pi_R)\left(\pi_{P,t}^A V_{t+1}^P + \left(1-\pi_{P,t}^A\right)V_{t+1}^A\right)\right], \end{aligned} \tag{8}$$

where $\tilde{c}_t^s$ and $\tilde{n}_t^s$ denote the optimal solution to the problem in equation (7) since untested asymptomatic agents do not know their health status. Conditional on becoming untested asymptomatic in period $t+1$, they expect to become infected symptomatic in the next period with probability π_{IS} and receive utility V_{t+2}^{IS}—defined in Section 2. They expect to become unobserved recovered with probability π_R and to receive the utility V_{t+2}^{UR}, which is defined for the period t as $V_t^{UR} = u(\tilde{c}_t^s, \tilde{n}_t^s) + \beta V_{t+1}^{UR}$. The unobserved recovered agents have never shown any symptoms and hence do not know their health status. Hence, they choose consumption and labor by solving the problem in equation (7). If the untested asymptomatic agents neither develop symptoms nor recover, then they expect to test positive at the end of period $t+1$ with probability $\pi_{P,t+1}^A$ and receive the utility function V_{t+2}^P in the next period. The probabilities of

9. Solving the imperfect information problem under full rationality requires keeping track of when agents were tested last and therefore is very cumbersome.

testing positive for a newly infected agent, $\pi^T_{P,t}$, and for an asymptomatic agent, $\pi^A_{P,t}$, are characterized in Section 3.

The problem is subject to the budget constraint for non-quarantined agents: $(1+\mu^S_{c,t})c^s_t = w^S_t n^s_t + \Gamma^L_t$, where $\mu^S_{c,t}$ denotes a tax on consumption proxying the effects of a government-imposed social distancing on consumption and labor. By reducing consumption and labor, social distancing curtails agents' economic interactions. In doing so, social distancing reduces the probability to become infected (τ_t) and, as we shall show, the number of traceable contacts health authorities have to test at the end of the period. The consumption tax revenue is rebated to the agents the tax is levied on, Γ^L_t. The equilibrium wage w^S_t equals the agent's labor marginal productivity.

Tested-Positive Agents. Tested-positive agents are individuals who know they are infected even though they do not have symptoms. They choose consumption, c^P_t and labor n^P_t so as to maximize

$$V^P_t = \max_{c^P_t, n^P_t} u\left(c^P_t, n^P_t\right) + \beta\left[\pi_{IS} V^{IS}_{t+1} + \pi_R V^{OR}_{t+1} + (1-\pi_{IS}-\pi_R)V^P_{t+1}\right], \quad (9)$$

where the tested-positive individual can develop symptoms with probability π_{IS} and, in this case, the individual will receive the utility V^{IS}_{t+1} in the next period. The health status of the tested-positive individual can also change to observed recovered with probability π_R and, in this case, the individual will receive the utility V^{OR}_{t+1} in the next period. If the tested-positive individual neither develops symptoms nor recovers, they will remain in their current status. Tested-positive agents are subject to quarantine until they recover. Thus, the maximization problem for these agents is subject to the following budget constraint: $(1+\mu^Q_c + \alpha\mu^S_{c,t})c^P_t = w^P_t n^P_t + \Gamma^Q_t$, where μ^Q_c proxies the effects of imposing a quarantine on individuals' consumption and labor decisions. Social distancing is assumed to affect consumption of quarantined subjects as well. The parameter $\alpha \in (0,1)$ controls the additional effects of social distancing on quarantined agents' consumption. The tax is rebated to them, Γ^Q_t.

Infected Symptomatic Agents. As the symptoms of the disease develop, agents observe their health status, which becomes infected symptomatic. An infected symptomatic subject chooses consumption c^{IS}_t and n^{IS}_t so as to maximize

$$V^{IS}_t = \max_{c^{IS}_t, n^{IS}_t} u\left(c^{IS}_t, n^{IS}_t\right) + \beta\left[\pi_R V^{OR}_{t+1} + \left(1-\pi_R-\pi_D\right)V^{IS}_{t+1}\right], \quad (10)$$

subject to the budget constraint for quarantined subjects, which is the same as for the tested-positive agents. The probability π_R denotes the probability that the health status of the infected symptomatic individual changes to observed recovered and the individual will receive V^{OR}_{t+1} in the next period. The probability π_D denotes the probability that the infected symptomatic individual dies and, in this case, they will get zero utility forever. If neither event happens, the infected symptomatic individual will not change their health status in the next period. The equilibrium wage paid to the

agents is determined by the agent's marginal productivity of labor, which is assumed to be lower when the symptoms of the disease have developed. This penalty on labor productivity is given by $\phi < 1$.

Observed Recovered Agents. Observed recovered agents are agents who know they have been infected at some point in the past either because they tested positive or they showed the symptoms of the disease. Since they have become immune to the virus, their health status will never change again and their decision problem reads

$$V_t^{OR} = \max_{c_t^{OR}, n_t^{OR}} u\left(c_t^{OR}, n_t^{OR}\right) + \beta V_{t+1}^{OR}, \tag{11}$$

subject to the same budget constraint as for the non-quarantined subjects.

The Government Budget Constraint. The government balances its budget in every period by satisfying the conditions

$$\mu_{c,t}^{S}\left[C_t + \alpha\left(C_t^{IS} + C_t^{P}\right)\right] = \Gamma_t^{L}\left(S_t + I_t^{A} + R_t^{U} + R_t^{O} + (1-\alpha)\left(I_t^{S} + P_t\right)\right), \tag{12}$$

$$\mu_c^{Q} \cdot C_t^{IS} = \Gamma_t^{Q} \cdot I_t^{S}, \quad \text{and} \quad \mu_c^{Q} \cdot C_t^{P} = \Gamma_t^{Q} \cdot P_t, \tag{13}$$

where we denote the share of susceptible individuals with S_t, the share of untested asymptomatic individuals with I_t^A, the share of symptomatic infected individuals I_t^S, the share of tested-positive individuals with P_t, the share of unobserved recovered with R_t^U, and the share of observed recovered individuals with R_t^O. Recall that C_t denotes consumption of non-quarantined agents. $C_t^{IS} \equiv c_t^{IS} I_t^S$ and $C_t^P \equiv c_t^P P_t$ stand for total consumption of the infected symptomatic agents and that of the tested-positive agents, respectively. There is no fiscal redistribution. The revenues of the social distancing and quarantine taxes are rebated to the agents these taxes are levied on.[10]

Dynamics of Agents' Types. We now describe the evolution of the six types of agents. The law of motion for the share of susceptible agents reads $S_{t+1} = S_t - T_t$, where T_t denotes the share of newly infected subjects in period t. This share is defined using the law of large numbers as follows: $T_t = \tau_t \cdot S_t$, where τ_t is the expected probability for susceptible individuals to become infected—defined in equation (5).

The size of untested asymptomatic agents evolves according to the law of motion

$$I_{t+1}^{A} = \left(1 - \pi_{P,t}^{T}\right)T_t + \left(1 - \pi_{P,t}^{A}\right)(1 - \pi_{IS} - \pi_R) I_t^{A}, \tag{14}$$

This set of agents is given by those who were untested asymptomatic I_t^A at the end of the previous period and have not developed symptoms, recovered, or tested positive

10. We abstract from fiscal policy in this study. Bianchi, Faccini, and Melosi (2020), Mitman and Rabinovich (2021), and Hagedorn and Mitman (2020) study how fiscal policy should respond to pandemic recessions.

at the end of the current period. Moreover, subjects who have become infected in this period, T_t, and have not tested positive will also join the set of untested asymptomatic subjects in the next period.

The pool of tested positive subjects is given by

$$P_{t+1} = (1 - \pi_{IS} - \pi_R)P_t + \pi^T_{P,t}T_t + \pi^A_{P,t}(1 - \pi_{IS} - \pi_R)I^A_t. \tag{15}$$

Tested-positive subjects in the current period are people who had this health status at the end of the previous period and have neither developed symptoms nor recovered. The infected agents who have just tested positive also join the tested-positive pool.

The pool of infected symptomatic people is: $I^S_{t+1} = (1 - \pi_R - \pi_D)I^S_t + \pi_{IS}(I^A_t + P_t)$. A fraction of infected symptomatic agents recovers or dies in the period and the remainder remain infected symptomatic. Untested asymptomatic and tested-positive agents can develop symptoms and become symptomatic infected subjects.

The share of unobserved recovered evolves as follows: $R^U_{t+1} = R^U_t + \pi_R I^A_t$. This health status is an absorbing state and increases with the set of untested asymptomatic agents who recover in every period. The share of observed recovered evolves as follows: $R^O_{t+1} = R^O_t + \pi_R(P_t + I^S_t)$. This health status is also an absorbing state and the magnitude of this set of agents increases as tested-positive and infected symptomatic agents recover. The measure of population is given by the sum of these six groups. Note that the population size may vary because infected people die. The share of agents who have died by period $t + 1$ is given by $D_{t+1} = D_t + \pi_D I^S_t$.

The only two variables we have not yet defined are the probability of testing positive for newly infected agents, $\pi^T_{P,t}$, and untested asymptomatic agents, $\pi^A_{P,t}$. The characterization of these probabilities is the object of the next section.

3. Contact Tracing and Testing

Health officials test subjects whose health status is unknown; that is, susceptible, untested asymptomatic, and unobserved recovered agents. In our model, an agent can be infected and remain asymptomatic throughout their entire infection. These agents are undiscovered spreaders who keep infecting susceptible agents until they recover or get quarantined because they test positive or become symptomatic. Tests do not reveal when a positive agent was infected or whether a negative agent is still susceptible to getting infected or has recovered. Results can be false-negative.

Contact tracing is a testing strategy whose aim is to ex-post reconstruct as much as possible of the newly symptomatic cases' *infection chain*; that is, the network of interactions that led a newly symptomatic case to become infected or to infect other agents. How much of the infection chain can be known by health officials defines the efficiency of the contact tracing technology. We consider two levels of efficiency of the tracing technology: a technology that allows health officials to trace only those contacts that have occurred during the current week and a more comprehensive technology that allows them to trace contacts up to one week back. When we say contact tracing, we

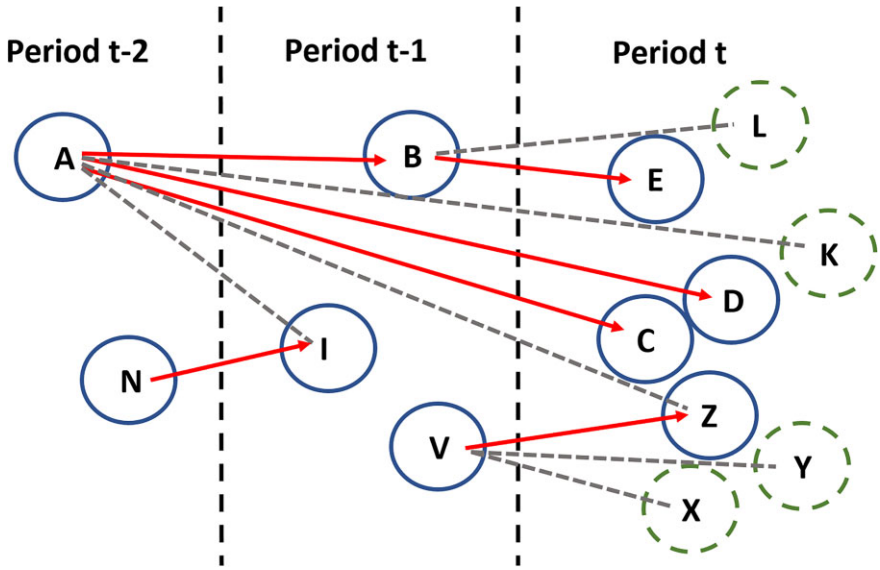

FIGURE 1. Example of an infection chain. The blue solid circles indicate an asymptomatic person. The green dashed circles are susceptible or recovered agents. The red lines describe an interaction that leads to an infection, while the gray lines describe an interaction that does not lead to an infection.

generally refer to the first technology. When we say *comprehensive contact tracing* or simply comprehensive tracing, we mean the second technology.

It is useful to resort to a graphical example to illustrate how contact tracing works in the model. In Figure 1, agent A, who caught the virus in period $t-2$, infects agent B in period $t-1$. In the next period, agent A infects further two agents, who are denoted by C and D. At the same time, agent B also infects agent E. In period t, agent A also met subject Z, who was however infected by subject V. The gray line connecting subject A and Z means that this was a non-infectious meeting. The other subjects, who are denoted by dashed green circles, are agents that were not infected by meeting with one of the untested asymptomatic subjects, who are denoted by blue solid circles.

Let's assume that subject A turns symptomatic in period t. The contact tracing technology would allow health officials to trace the newly infected subjects C, D, and Z. However, subjects B and E, who belong to the same infection chain originated by subject A, cannot be traced. It is important to note that subject Z does not belong to agent A's infection chain as subject Z was infected by subject V. However, subject Z has randomly met with subject A in period t and is therefore traceable. If the comprehensive tracing technology is available, then subject B can also be traced.

Let's suppose that subject B turns symptomatic in period t, while subject A is still untested asymptomatic. The tracing technology would discover subject E. By allowing subject B's contacts to be traced in the earlier period $t-1$, the comprehensive technology allows health authorities to find out the asymptomatic spreader A. Since subject A infected subject B, the detection of subject A is called *backward tracing*.

The contact tracing technology does not allow health authorities to trace backward as it takes at least one period for newly infected subjects to become symptomatic.

It is important to note that the contact tracing technology can catch asymptomatic agents who went untested in the previous periods only if these agents meet randomly with a subject who turns symptomatic in the current period. These random meetings are fairly rare, as we later show. In contrast, the comprehensive technology allows the health authorities to leverage the infection chain of the newly symptomatic agents to detect asymptomatic spreaders that were not caught in previous periods. An example is the backward tracing of agent A when agent B turns symptomatic.

Health authorities could also launch a second round of tests by reconstructing the network of contacts of those agents who tested positive in the first round. We deal with this extension in Section 6.

Testing Probabilities. The probability of catching a spreader depends on (i) the probability of tracing this subject; (ii) the tracing and testing capacity in period t, Υ_t, relative to the number of people traceable E_t; and (iii) the probability of a false negative (π_F). As we will show, the efficiency of the tracing technology influences the probability of being traced and the number of traceable subjects in a given period.

Formally, for a given efficiency of the tracing technology, the probability that a newly infected subject infected ($i = T$) or an untested asymptomatic subject ($i = A$) tests positive in period t is

$$\pi^i_{P,t} = \pi^i_{C,t} \cdot \pi_{T,t} \cdot (1 - \pi_F), \quad i \in \{T, A\}, \tag{16}$$

where the probability $\pi^i_{C,t}$ denotes the probability of being traced for a subject of type i and the probability $\pi_{T,t}$ denotes the probability of being tested conditional on being traced by the government. As we shall explain, this probability depends on the tracing and testing capacity Υ_t, and the number of agents that are traceable E_t. This decomposition implies that a subject has to be traced before being tested. The case in which all the traced subjects are quarantined is discussed in Section 5.4.

The variable Υ_t should be interpreted broadly as the intensive margin of tracing and testing as opposed to the extensive margin, which is determined by the efficiency of the tracing technology. While the extensive margin affects the number of traceable agents ($\pi^T_{C,t} + \pi^A_{C,t}$), the intensive margin, Υ_t, reflects the government's capacity to process all the necessary information to test these traceable contacts and quarantine those who test positive. Henceforth, we will refer to Υ_t as testing capacity because this is how we will calibrate the model. This choice reflects the absence of data regarding this broader concept of intensive margin in tracing and testing.

Externality and the Collapse of the Testing System. The magnitude of the variable Υ_t relative to the number of traceable people, E_t, plays the role of a critical bottleneck that can lead to the collapse of the tracing and testing system in our model. Agents fail to realize that their consumption and labor decisions have externality on the number of traceable subjects, E_t, that health authorities will have to test a few periods later. This is for two reasons. First, those agents whose health status is unknown do not appreciate

that as they increase their consumption or labor, the overall amount of interactions in the economy will increase and, thereby, newly symptomatic agents will end up having more traceable contacts. Second, untested asymptomatic subjects fail to realize that as they consume or work more, more people will become infected, raising the number of newly symptomatic cases in every period. A larger number of newly symptomatic cases enlarges the pool of subjects who met with them and are, therefore, traceable.

This externality may lead the number of traceable contacts E_t to rise to the point at which the testing system collapses, with very severe consequences for the economy. When the number of traceable contacts largely exceeds the testing capacity, Υ_t, the probability for traceable people to be tested ($\pi_{T,t}$) falls and, with it, the probability for untested asymptomatic subjects to test positive, ($\pi^i_{P,t}$, $i \in \{T, A\}$). Consequently, the number of asymptomatic spreaders starts increasing out of control and the spread of the virus accelerates. The economy contracts sharply as the heightened probability of becoming infected, τ_t, causes non-quarantined agents to want to reduce economic interactions so as to minimize the probability of catching the virus and dying.[11]

Eichenbaum, Rebelo, and Trabandt (2021) consider the case in which individuals do not internalize the limited availability of beds in hospitals when they decide how much to consume and work (medical preparedness). While both that externality and the one studied in our paper are about the existence of a bottleneck agents do not internalize, how these two types of externality affect the economic and health outcomes of a pandemic is quite different. When tests are running short, the efficacy of contact tracing falls, the effective reproduction number of the virus soars, and the threshold of recovered agents needed to reach herd immunity increases. As a result, the consumption loss and the number of deaths due to the pandemic worsen considerably. In contrast, the medical-preparedness externality leads to a larger consumption loss and a heavier death toll because the mortality rate sharply rises if there are not enough beds to treat ill agents.

It is also important to note that putting in place a viable system of contact tracing is an effective tool to address the medical-preparedness externality. As we shall show, when we solve the optimal social distancing problem, the planner wants to scale up social distancing measures to shore up the tracing and testing system so as to keep the number of infected cases low. If we expanded the model to introduce medical preparedness, the planner would still want to tighten social distancing in similar fashion to preserve the tracing and testing system. If the planner did not do that, more subjects would become infected and more stress would be put on the health system. An implication of this argument is that the externality concerning medical preparedness becomes less relevant for policymakers when the externality threatening the functionality of the tracing and testing system is properly addressed.

11. There is another source of externality in the model. Agents do not internalize that their consumption and labor decisions affect how many people will become infected in the economy and, hence, ultimately the probability of getting infected. Eichenbaum, Rebelo, and Trabandt (2021) study the implications of this externality in great detail. In our model with contact tracing, that externality does not play any significant role.

In the next section, we will characterize the probability of being traced and tested ($\pi^{i}_{C,t}$ and $\pi_{T,t}$) under the assumption that health authorities can trace only those contacts that has occurred in the current week. We show how to obtain those probabilities for the case of the comprehensive tracing technology in Online Appendix A.

3.1. The Probability of Being Traced

Contact tracing allows health authorities to trace only those contacts that occur in the current week. It is useful to combine the binomial distributions in equations (1), (2), and (3) to obtain the probability for an agent who does not know their health status to meet k-times with the set of untested asymptomatic subjects while consuming, working, and performing other activities:

$$f_t(k) \equiv \sum_{i=0}^{k} \sum_{j=0}^{k-i} f_{c,t}(i) f_{n,t}(j) f_{o,t}(k-i-j). \tag{17}$$

Conditional on meeting k asymptomatic subjects in period t, the probability that at least one of these subjects becomes symptomatic in the same period is $1-(1-\pi_{IS})^k$. Thus, the probability for a subject who does not know the health status to be traced is

$$\pi^{S}_{C,t} = \pi^{A}_{C,t} = \pi^{UR}_{C,t} = \sum_{k=0}^{\varphi_C(c^s_t)+\varphi_N(n^s_t)+\varphi_O} [1-(1-\pi_{IS})^k] f_t(k), \tag{18}$$

implying that the probability of being traced is the same for the three unobserved types: susceptible (S), untested asymptomatic (A), and unobserved recovered (UR). This is because these agents consume and work the same amount as shown in Section 2. As a result, they will have the same number of total interactions $\varphi_C(c^s_t)+\varphi_N(n^s_t)+\varphi_O$ and the same probability of meeting with k untested asymptomatic agents.

We now work out the probability for a newly infected subject to be traced, $\pi^{T}_{C,t}$. Newly infected subjects are susceptible at the beginning of the period and become infected because they have met an untested asymptomatic individual. Thus, we have to condition the probability distribution that a susceptible agent has met k untested asymptomatic subjects in period t $-f_t(k)$ defined in equation (17)—on the fact that the newly infected agent has met at least one untested asymptomatic subject, that is, the agent who infected them. To do so, we apply the Bayes theorem to obtain

$$f^{T}_t(k) = \frac{f_t(k)\tilde{\tau}(k)}{\tau_t}, \tag{19}$$

where $\tilde{\tau}(k) \equiv 1-(1-\tau)^k$ is the probability of getting at least one infectious contact out of k interactions, and recall that τ_t stands for the average probability for susceptible subjects to become infected in period t, which is defined in equation (5). Following the same reasoning behind the probability in equation (18), we characterize the probability

for a newly infected individual to be traced as

$$\pi^T_{C,t} = \sum_{k=0}^{\varphi_C(c^s_t)+\varphi_N(n^s_t)+\varphi_O} [1-(1-\pi_{IS})^k] f^T_t(k). \tag{20}$$

As noted at the beginning of this section where we analyzed Figure 1, an untested asymptomatic subject can only be traced if they have met a newly symptomatic subject randomly. The application of the Bayes theorem adjusts the probability distribution $f^T_t(k)$ to factor in that the newly infected subject belongs to the infection chain of an agent who was untested asymptomatic at the beginning of the period. This is important as this untested asymptomatic agent may turn symptomatic with probability π_{IS}. The event that the subject who infected the newly infected agent turns symptomatic is more likely than the joint event that an untested asymptomatic agent has randomly met another untested asymptomatic agent ($\sum_{k>1} f_t(k)$) *and* the latter agent turns symptomatic. Therefore, an untested asymptomatic agent is less likely to be traced than a newly infected agent under the contact tracing technology ($\pi^T_{C,t} > \pi^A_{C,t}$).

In Online Appendix I, we show the unconditional and conditional distributions $f_t(k)$ and $f^T_t(k)$ in one simulation where the tracing technology leads to successful control of the pandemic. As one can see, the probability of catching an untested asymptomatic subject is dwarfed by the fact that these subjects are very unlikely to meet randomly with other untested asymptomatic agents, who can turn symptomatic. Conditioning on the fact that newly infected agents have met at least one untested asymptomatic subject causes the mode of the probability $f^T_t(k)$ to shift from $k = 0$ to $k = 1$, making tracing more likely. This result underscores the importance of exploiting the existence of the infection chain to increase the chance of detecting newly symptomatic agents.

3.2. The Conditional Probability of Being Traced

The contact tracing technology endows health authorities with the list of contacts of the newly symptomatic agents in period t. Health authorities look at the contacts with individuals whose health status is unknown (i.e., contacts with observed recovered individuals are discarded). We call this set of traceable individuals *the exposed*. The measure of this set is given by

$$E_t = \pi^S_{C,t} \cdot S_t + \pi^A_{C,t} \cdot (1-\pi_{IS}) I^A_t + \pi^{UR}_{C,t} \cdot R^U_t, \tag{21}$$

where $\pi^S_{C,t}$, $\pi^A_{C,t}$, and $\pi^{UR}_{C,t}$ are the probabilities of being traced for the three types of agents who do not know their health status. These probabilities were defined in equation (18). We adjusted the share of the untested asymptomatic subjects who were exposed by taking out those who have revealed symptoms ($\pi_{IS} I^A_t$) in period t.

Health authorities do not know the health status of susceptible, untested asymptomatic, and unobserved recovered individuals and hence they cannot tell these types of subjects apart when it comes to deciding who to test. Thus, the probability of

TABLE 1. Calibration.

Parameters	Sign	Value	Target / source
(a) Economic parameters			
Discount factor	β	$0.96^{1/52}$	Conventional discount factor
Labor disutility	θ	0.13%	Weekly working hours of 28
Productivity	A	39.84	Yearly income \$58,000
Frisch labor elasticity	φ	0.5	Literature
(b) Epidemiological parameters			
Interaction via consumption	φ_C	0.99%	Consumption-based interactions 33%
Interaction via labor	φ_N	0.39	Labor-based interactions 33%
Interaction independently	φ_O	10	Basic reproduction number $R_0 = 2$
Probability of infection	τ	5%	World Health Organization (2020)
Recovery rate	π_R	7/18	Average recovery rate = 18 days
Symptomatic rate	π_{IS}	7/18	Share of symptomatic cases = 50%
Mortality rate	π_D	0.6%	Infection fatality rate = 0.3%
False negative outcome	π_F	0	False positive probability = 0
Quarantine policy	μ^Q	1	Quarantine lowers C and L by 30%
Productivity symptomatic	ϕ	0.8	Eichenbaum et al. (2021)
Social distancing effect on quarantine	α	0	No impact besides quarantine
Initial infection	ϵ	0.1%	Infections March 16, 2020

testing a traceable contact does not depend on the contact's health status and is

$$\pi_{t,T} = \min\left(1, \frac{\Upsilon_t}{E_t}\right), \tag{22}$$

where recall $\Upsilon_t \geq 0$ denotes the testing capacity of policymakers in every period, which is an exogenous variable. We substitute equations (20) and (22) into equation (16) to obtain the probability of testing positive for newly infected subjects, $\pi^T_{P,t}$. Substituting both the probability $\pi^A_{C,t}$ of equation (18) and the conditional probability of being tested of equation (22) into equation (16) allows us to pin down the probability of testing positive for subjects infected in earlier periods, $\pi^A_{P,t}$. The probabilities $\pi^A_{P,t}$ and $\pi^T_{P,t}$, in turn, pin down the dynamics of types in equations (14) and (15) for the contact tracing technology.

4. Model Solution and Calibration

We use the model to study the response of epidemiological and economic variables following a surprise shock that initially infects a tiny share of the population. To this end, we solve the model iteratively with a numerical root finder that computes the sequence of policy functions and the evolution of the measure of agent types for a given number of periods. More details are in Online Appendix D.

The calibrated parameters of the model are summarized in Table 1. The economic parameters are calibrated based on Eichenbaum, Rebelo, and Trabandt (2021). We set

the weekly discount factor to $0.96^{1/52}$. This number is standard and implies the value of a statistical life of roughly 10 million 2019 U.S. dollars, which is in line with what other studies assume (e.g., Eichenbaum, Rebelo, and Trabandt 2021). Productivity, A, is set to match a yearly income of $58,000. The scale parameter of labor disutility, θ, is calibrated so that agents work on average 28 hours per week. The Frisch labor elasticity φ is 0.5.

The epidemiological parameters are calibrated to the recent COVID-19 crisis in the US. A key epidemiological parameter is τ, which is the probability that one interaction with an infected subject results in an infection. We set this parameter to 5% based on evidence from the World Health Organization (2020). The parameters φ_C, φ_N, and φ_O determine the number of interactions required to support levels of individual consumption c_t^s, labor n_t^s, and other non-economic activities, respectively. The original step functions $\varphi_C(c_t)$ and $\varphi_N(n_t)$ are shown in Online Appendix I. We set the parameters φ_C and φ_N so that consumption- and labor-based transmissions of the virus account for a share of 1/3 each when consumption and labor decisions are fixed to the pre-pandemic level. The values are consistent with the influenza study by Ferguson et al. (2006).

The parameter φ_O is set to target a basic reproduction number R_0 of 2 in line with the evidence about the early transmission of COVID-19 (Li et al. 2020.).[12] The calibration implies a total amount of 30 interactions in the pre-epidemic economy, which is consistent with surveillance data (e.g., Pung et al. 2020). In line with evidence from the World Health Organization (2020), we choose that an agent recovers on average after 18 days. We calibrate the probability of developing symptoms (π_{IS}), so that 50% of infected agents develop symptoms at some point of the pandemic crisis, which is in line with the symptomatic rate estimated by Baqaee et al. (2020b).[13] A key metric in parameterizing an SIR model is the infection fatality rate, which measures the amount of deaths relative to all infectious cases. The mortality rate π_D is the infection fatality rate divided by the share of symptomatic agents. This rate is calibrated to target an infection fatality rate of 0.3% as in Hortaçsu, Liu, and Schwieg (2021).[14]

In the model, symptomatic agents are subject to a labor productivity penalty, ϕ. We calibrate the penalty $\phi = 0.8$ based on Eichenbaum, Rebelo, and Trabandt (2021). Furthermore, infected symptomatic agents and tested-positive agents are quarantined, which is modeled as a tax on consumption, μ_c^Q. This tax implies that at steady state the consumption and labor of a tested-positive agent is lower than those of non-quarantined (non-recovered) agents by approximately 30%. We assume that quarantined agents are not affected by social distancing. We set the probability of a false negative outcome π_F to 0. The initial share of infected agents ϵ is set to 0.1% and is divided evenly between asymptomatic and symptomatic agents. Following Berger et al. (2022), this

12. This is the total number of infections caused by one infected person in their lifetime in a population where everybody is susceptible and no containment measures are taken.

13. There is mixed evidence about this rate as discussed in Online Appendix J.

14. Fernández-Villaverde and Jones (2022) estimate a rate of 1%.

can be interpreted as the amount of infections adjusted for unreported cases on March 16, 2020.

5. Quantitative Analysis of Contact Tracing

To better understand the results shown in this section, it is useful to define an epidemiological variable that gauges the speed at which the virus is spreading: the effective reproduction number, R_t^E, which is defined as

$$R_t^E = \left(1 - \pi_{P,t-1}^T\right) \sum_{j=0}^{\infty} \left(\tau_{t+j} (1 - \pi_{IS} - \pi_R)^j \prod_{k=0}^{j} \left(1 - \pi_{P,t+k}^A\right)\right). \tag{23}$$

This number captures how many susceptible people an untested asymptomatic agent infects on average during the spell of their illness. An effective reproduction number above 1 indicates a situation in which the virus is infecting more and more people over time, while a number below 1 signifies that the virus is retreating. The efficiency of the tracing technology and the testing capacity affect the reproduction number R_t^E through the probability for newly infected subjects and for untested asymptomatic subjects to test positive; that is, $\pi_{P,t}^T$ and $\pi_{P,t}^A$, respectively. Social distancing lowers this number R_t^E primarily by reducing the infection rate, τ_t.

It is important to note that the reproduction number is more sensitive to changes in the probability for a newly infected agent to test positive, $\pi_{P,t-1}^T$, than to changes in the future probability for an untested asymptomatic agent to test positive, $\pi_{P,t+k}^A$. The reason is that asymptomatic agents may turn symptomatic or recover in every future period and, when they do, they will stop infecting other people. The transitory nature of being asymptomatic, which is captured by the term $(1 - \pi_{IS} - \pi_R)$, implies that increasing the probability of catching asymptomatic agents further in the future has decreasing effects on the reproduction number.

5.1. Contact Tracing with Unlimited Testing Capacity

It is interesting to start with a scenario in which tests are always sufficient to cover all the contacts of newly symptomatic subjects. This scenario sheds light on the efficacy of contact tracing technologies in the most favorable environment where policymakers do not face any bottleneck when tracing and testing people. In addition, this exercise will show us how many tests would be needed to make contact tracing work best.

In this scenario, we also consider random testing as an alternative to contact tracing, which has been advocated by Romer (2020) among other scholars.[15] It is assumed that random testing is run on a weekly testing capacity of 10% of the initial population over the entire simulation horizon. This implies a daily testing capacity of close to

15. The formalization of random testing in our model is explained in Online Appendix C.

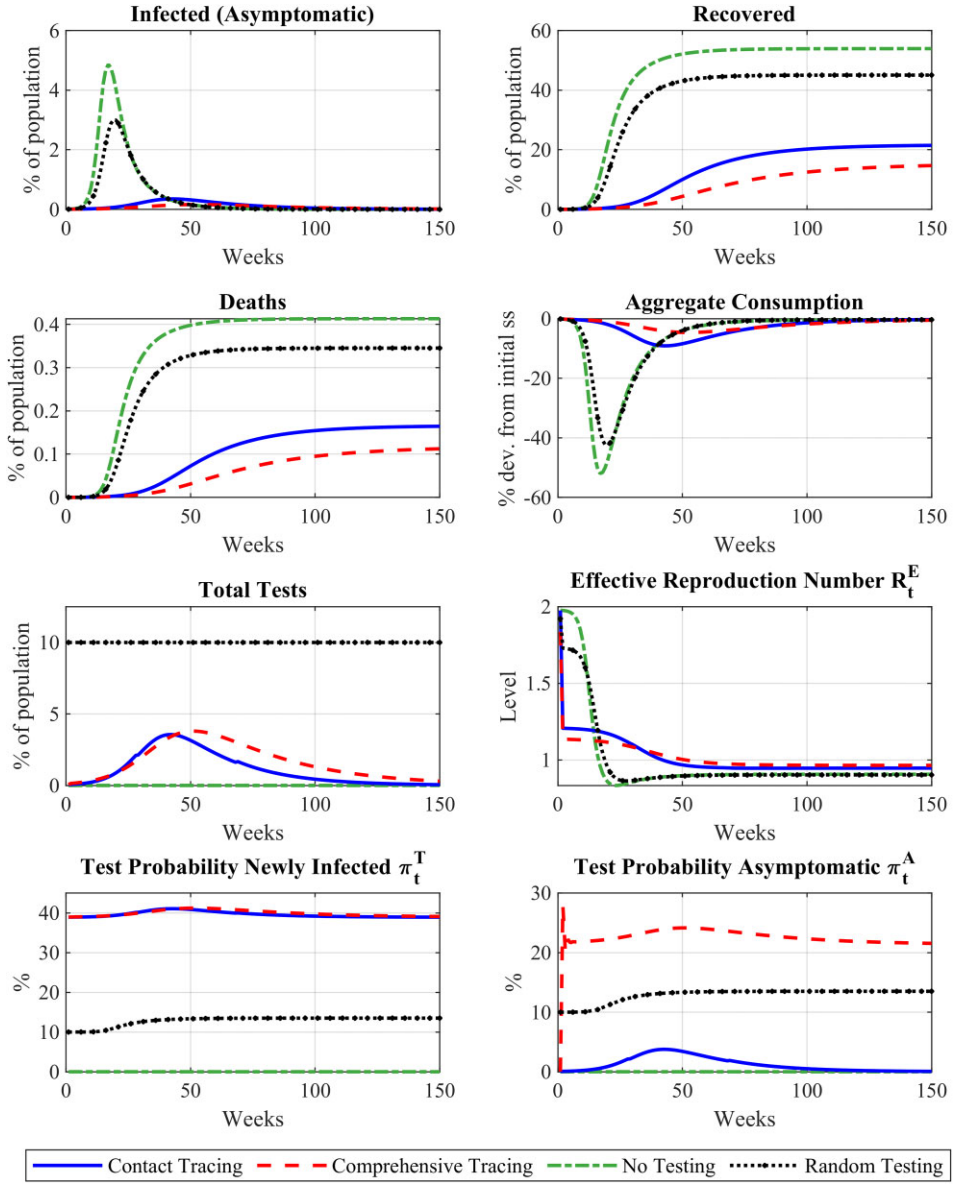

FIGURE 2. Comparison of different testing strategies with unconstrained number of tests for contact tracing and comprehensive contact tracing. The amount of tests used in random testing is 10% of the entire population each week.

5 million tests. To put this number in perspective, 1 million tests were administered per day in September 2020 in the U.S. We also consider the case in which no testing is performed.

Figure 2 shows the evolution of the key epidemiological, economic, and testing variables. Beginning with the case in which no one is tested (the green dashed–dotted line), the pandemic spreads very fast and causes many people to become infected. The

pandemic crisis fades away when 60% of the population becomes infected and herd immunity is reached. In total, 0.4% of the population dies because of the pandemic. In response to the surge in the infection probability, agents reduce their interactions by drastically lowering consumption and labor. As a consequence, the economy goes through an extreme recession, with aggregate consumption contracting by up to 50%.

The introduction of the contact tracing technology hugely improves outcomes by slowing the spread of the virus and reducing the death toll by more than 50% (solid blue line in Figure 2). As the virus spreads less quickly (lower reproduction number), the chances of getting infected are reduced, leading agents to lower their consumption and labor less dramatically compared to the case of no testing. The reproduction number quickly drops and eventually falls below 1. As a result, herd immunity is reached with around 20% of infected agents—three times less in the case of no testing.

The comprehensive contact tracing technology, which allows tracing of contacts up to one week back, (the red dashed line in Figure 2) further mitigates the severe consequences of the pandemic crisis.[16] However, the improvement is only marginal relative to what is already achieved by the contact tracing technology. Both tracing technologies require testing at most 4% of the population in a week, which is substantially less than the number of tests we assume for random testing. The timing of the testing varies somewhat across these two tracing technologies. The contact tracing technology requires more tests to be performed a few periods after the pandemic has started (around period 30) relative to the comprehensive one.

While this result may seem odd at first, it is important to recall that the contact tracing technology is less effective than the comprehensive technology in detecting untested asymptomatic subjects. The contact tracing technology can only trace these subjects through random meetings. As explained in Section 3.1, these types of meetings are quite rare.[17] As a result, in the lower right panel of Figure 2, the share of untested asymptomatic subjects detected by the contact tracing technology is very low compared to the levels attained by the comprehensive technology. Thus, the effective reproduction number is initially higher in the case of the contact tracing technology, which justifies a faster increase in the number of traceable subjects, E_t, and hence more tests performed a few periods after the pandemic has started (around period 30). In short, under the contact technology, you trace and test fewer people at the onset of the pandemic and this requires you to test more people later on.

Even though random testing (the black dotted line in Figure 2) is assumed to have an implausibly large testing capacity, it proves to be fairly ineffective in mitigating the outcomes of the pandemic. Even if 5 million people could be randomly tested every day, the pandemic would lead to a severe contraction and would kill 0.35% of the entire population—-more than twice as many deaths as under contact tracing.

What Explains the Spectacular Failure of Random Testing? To answer this question, one should look at the two bottom graphs of Figure 2, which show the share of newly

16. The formal derivation of comprehensive contact tracing is explained in Online Appendix A.

17. The probabilities of such meetings are shown in Online Appendix I Figure I.2 for periods 20 and 40.

infected asymptomatic subjects and the share of untested asymptomatic subjects who are detected and quarantined in every period under random testing and under the two tracing technologies. Even though many more tests are performed, random testing can detect only around 10% of the newly infected subjects in every period. Random testing is rather effective in capturing untested asymptomatic subjects. Even so, random testing fails to reduce the reproduction number, underscoring the importance of detecting and quarantining the newly infected cases to attain a successful containment of the virus. This last intuition is reinforced by observing that even though the tracing technology largely fails to detect untested asymptomatic subjects, it fares relatively well in containing the economic costs and mortality of the pandemic.

That the probability of catching the newly infected asymptomatic subjects turns out to be key to controlling the pandemic should not come as a surprise. We already noted that the reproduction number defined in equation (23) is more sensitive to changes in the probability for newly infected agents to test positive, $\pi^T_{P,t}$, than to changes in the probability for untested asymptomatic subjects to test positive, $\pi^A_{P,t}$.

Why is Contact Tracing so Successful? By leveraging the information contained in the reconstructed infection chains, contact tracing allows policymakers to break the positive relation between the probability of detecting newly infected agents $\pi^T_{P,t}$ and the infection rate τ_t. In doing so, contact tracing resolves an important challenge faced by random testing: at the beginning of a pandemic—when the infection rate τ_t is low—infected agents who can spread the virus are only a few and are therefore hard to detect. As explained before, the ability of detecting and quarantining newly infected agents has a large effect on reducing the effective reproduction number, allowing contact tracing to nip the pandemic in the bud. Hence, social distancing is not required to quash a surge in the number of infections. Rather, these measures are only adopted if needed to address the externality associated with consumption and labor. The challenges posed by this externality are shown in the next section, where we impose an upper bound on the number of tests that can be performed in every period.

5.2. Contact Tracing with Limited Testing Capacity

In the previous section, we showed that the contract tracing technology does a great job in controlling the spread of the virus. The comprehensive tracing technology improves outcomes only marginally. In this section, we show that this is not the case when the testing capacity, Υ_t, is calibrated to the amount of tests performed in the U.S. from March 16, 2020, through October 4, 2020. The U.S. health authorities had a daily capacity of only 30,000 tests available at the onset of the pandemic crisis. This capacity then increased linearly up to 1 million tests 28 weeks later.[18] Afterward, the capacity is assumed to increase at a steady pace until week 52, after which it stays put.

18. The US conducted 231,081 tests between 16 and 22 of March (approximately 33,000 daily tests). Between September 28 and October 4, the U.S. conducted 6,936,961 tests (around 991,000 daily tests).

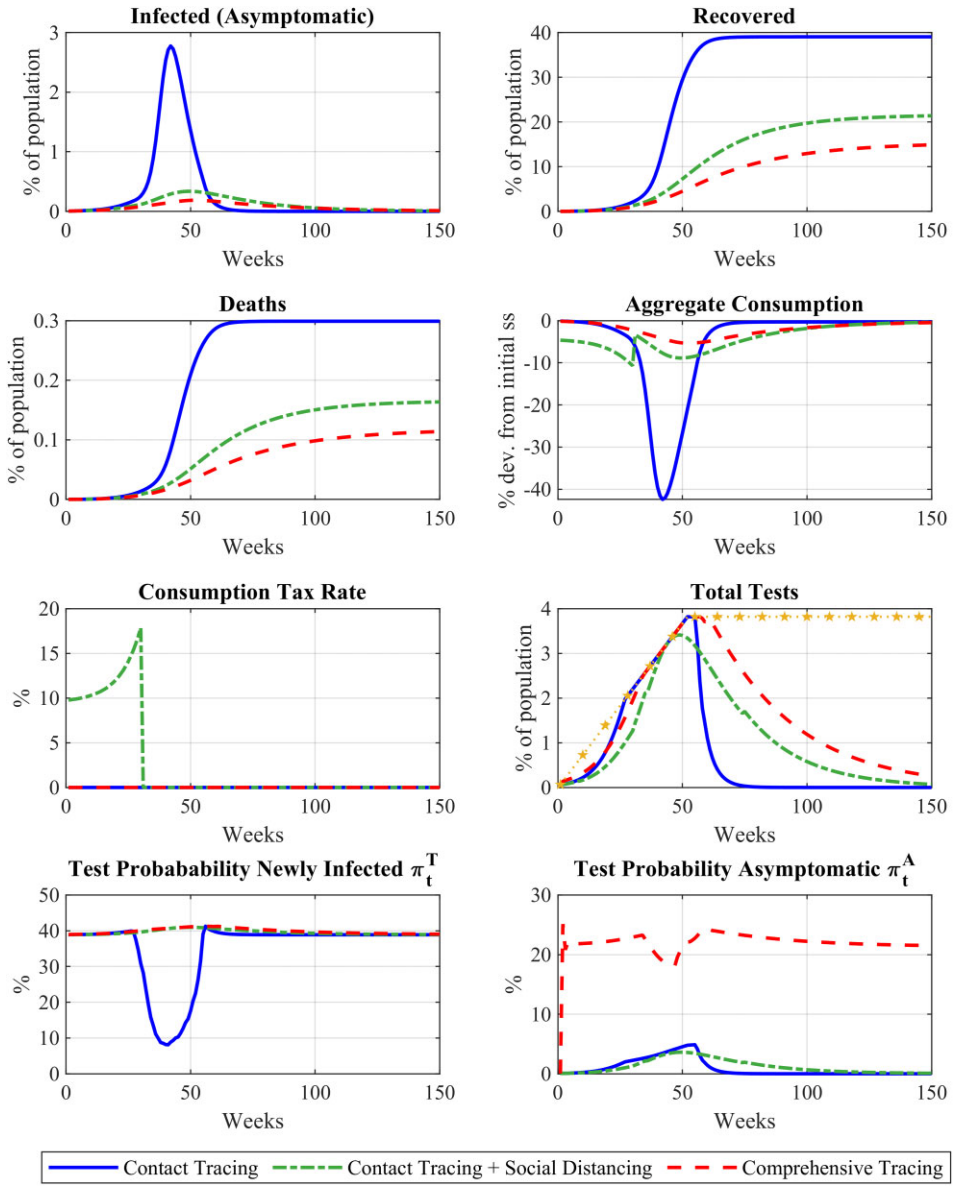

FIGURE 3. Comparison of different testing strategies with limited testing capacity: contact tracing (blue solid line), contact tracing combined with social distancing for 30 periods (green dash–dotted line), and comprehensive tracing (red dashed line). In the sixth plot, the yellow starred line shows the testing capacity Υ_t.

Looking at the third left plot in Figure 3, the contact tracing technology (blue solid line) requires testing to accelerate after period 30 to compensate for its inability to catch untested asymptomatic subjects, as reflected in the low value of $\pi_{P,t}^A$ in the lower right plot of the figure. However, the testing capacity is not growing fast enough and

the blue solid line hits the yellow starred line, denoting the U.S. testing scale (Υ_t). As the testing capacity becomes binding, the testing system collapses, as captured by the rapid drop in the probability of catching a newly infected subject ($\pi^T_{P,t}$). The effective reproduction number increases then and agents cut their consumption and labor in response to the higher risk of getting infected.

The comprehensive tracing technology (the red dashed line in Figure 3) delivers the best outcome among the considered strategies. This better tracing technology allows health authorities to detect and isolate roughly 20% of untested asymptomatic agents in every period via backward tracing (see the bottom right graph). In doing so, this technology keeps the path of exposed subjects lower, reducing the number of tests required. Consequently, the number of tests performed does not accelerate after period 30 as in the case of the contact tracing technology. Thus, under the comprehensive tracing technology, the number of required tests does not become constrained by the limited testing capacity so early and the testing system remains viable.[19]

5.3. Complementarity with Other Containment Policies

In Section 5.1, we showed that a well-functioning tracing and testing system allows policymakers to reduce both the consumption loss and the death toll of a pandemic. However, actual implementation of contact tracing turned out to be very challenging for a variety of reasons in many countries across the world. We showed that one reason that can impair the correct functioning of contact tracing is the scarcity of tests, which can be more broadly interpreted as the inability of coordinating tracing and tests when the number of traced close contacts grows too large. In this section, we study how to remedy this situation that leads contact tracing to fail. We consider three containment policies that the government can deploy to shore up a tracing system at risk of collapse. The first policy is social distancing, the second one is a tighter quarantine, and the third one is to randomly allocate the excess testing capacity.

Table 2 summarizes the outcomes and compares them with those studied in the earlier sections. The case of "All exposed quarantined" will be explained in Section 5.4 and will be used to isolate the social value of testing. The table shows the welfare losses expressed as consumption equivalents relative to the non-pandemic economy. It also shows the average consumption loss over the entire considered horizon of 250 periods relative to the non-pandemic economy, the cumulative mortality rate and the recovery rate at the end of the pandemic. The social costs of the different scenarios are expressed in trillions of dollars. Online Appendix F shows the derivation of consumption equivalents and the social costs.

Before evaluating the three cases, it is important to notice that, in the idyllic case of unlimited testing capacity (no externality), contact tracing reduces the share of

19. Nevertheless, the testing availability becomes binding later on, lowering the probability of testing asymptomatic subjects, π^A_t, somewhat in subsequent periods. Because of the pecking order (explained in Online Appendix A), there is no effect on the probability of detecting newly infected agents, π^T_t, which, as already pointed out, is essential to contain the pandemic. Thus, the effective reproduction number hardly budges.

TABLE 2. Welfare, economic, and health outcomes of various containment policies.

	Welfare CE %[a]	Consumption %[b]	Mortality %[c]	Recovered %[d]	Social costs trillion $[e]
Contact tracing with *limited* testing capacity					
No social distancing	−2.07	−3.22	0.30	39	9.67
Optimal social distancing (short)	−1.06	−2.55	0.17	22	4.93
Optimal social distancing (long)	−0.92	−6.56	0.12	16	4.27
Tighter quarantine	−1.06	−1.92	0.17	22	4.94
Alternative contact tracing scenarios					
Unlimited testing capacity	−1.05	−1.89	0.17	22	4.91
Comprehensive tracing	−0.74	−1.38	0.12	15	3.44
All exposed contacts quarantined	−1.40	−2.95	0.21	28	6.51
No contact tracing					
No testing	−2.93	−4.25	0.41	54	13.64
No testing + optimal social distancing	−2.87	−6.76	0.39	51	13.39
Random testing	−2.40	−3.67	0.35	45	11.18

a. Welfare gain/loss expressed as consumption equivalent relative to a non-pandemic economy.
b. Cumulated consumption loss at the end of the pandemic relative to a non-pandemic economy.
c. Cumulated mortality rate at the end of the pandemic.
d. Fraction of recovered agents at the end of the pandemic.
e. Social costs in trillion $ relative to a non-pandemic economy.

recovered agents needed to reach herd immunity by 32 percentage points. Compare the column reporting the cumulative percentage of fully recovered agents at the end of the pandemic in the case of Unlimited testing capacity (under Alternative contact tracing scenarios) with the No testing (under No contact tracing scenarios) in Table 2. This result arises because tracing and testing permanently lower the effective reproduction number of the virus—as shown in Section 5.1—decreasing the threshold of recovered people needed to attain herd immunity.

Now we turn to the less idyllic case in which contact tracing is threatened by an externality due to limited testing capacity. In this context, we will show how containment policies can be combined with contact tracing to deliver welfare, economic, and health outcomes that are remarkably similar to those obtained under the idyllic case of unlimited testing capacity (no externality).

Optimal Social Distancing. We solve for the optimal path of the consumption tax rate $\mu^S_{c,t}$. As standard in this literature, the planner sets the consumption tax to maximize the welfare of the economy at the beginning of the pandemic. Online Appendix F describes the welfare criteria and the Ramsey problem in detail. For a reason that will be clarified below, we consider two scenarios: The government can either commit its social distancing policy over a period of either 30 weeks (labelled Optimal social distancing (short) in Table 2) or 150 weeks (labelled Optimal social distancing (long) in the table). The green dash–dotted line in Figure 3 shows the dynamics of the macro and epidemiological variables under the optimal short social distancing policy.

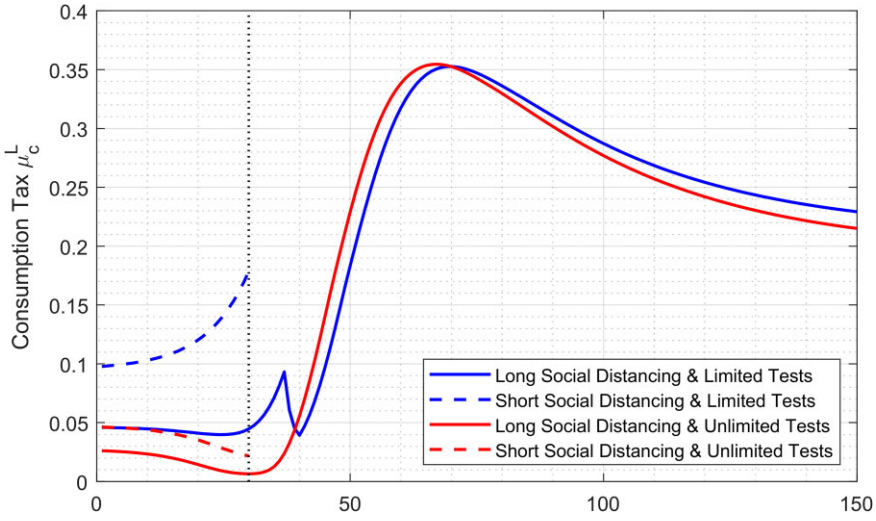

FIGURE 4. Optimal social distancing—the planner's optimal path of consumption tax rates is shown for different scenarios in an economy with contact tracing. The test availability is either limited (blue lines) or unlimited (red lines). We consider two horizons over which the government can commit to maneuver the tax rate: a long horizon of 150 periods (solid lines—long social distancing) or a short horizon of 30 periods (dashed lines—short social distancing).

As shown in Figure 3, when we solve for the optimal path of consumption tax rates over the first 30 periods, the collapse of the tracing and testing system is averted by implementing social distancing before the testing capacity would become binding. See the tax increases over the 30 periods aimed to curtail the amount of consumption and labor interactions. By lowering the amount of economic interactions early on, social distancing reduces the number of tests required, preventing the testing capacity from becoming binding later on. Hence, the effective reproduction of the virus is successfully reduced, allowing the economy to reach herd immunity with fewer cases, as shown in Table 2 (see optimal social distancing (short) for limited testing capacity).

Remarkably, the optimal *short* social distancing policy leads to a cumulative mortality rate and welfare gains that are very similar to those achieved under no constraint on testing (unlimited testing in Table 2), where, by construction, no externality threatens the functioning of contact tracing. As Figure 3 shows, the lower aggregate consumption path at the beginning due to the tightening of social distancing is more than compensated by a higher consumption level throughout the pandemic, relative to the case in which the tracing and testing system collapses.

How can the government avert the collapse of the tracing and testing system? This is shown in Figure 4, in which the optimal tax rate from the Ramsey problem is displayed. Under both time horizons considered (blue solid and dashed lines), the optimizing tax rate is increased in the run-up to period 37 when the system would have collapsed in the absence of this measure. Yet, if we assume unlimited testing capacity (the red solid and dashed lines), the externality studied in this paper does not

arise, the tracing and testing system does not collapse, and the optimal tax rate is not characterized by any increase from period 30 through period 37.

Why is the optimal tax rate increased a second time when we consider a longer commitment period (the solid lines in Figure 4)? The optimal consumption path is raised to sufficiently slow down the spreading of the virus to attain herd immunity gradually over time. This result is not new, and Eichenbaum, Rebelo, and Trabandt (2021) have explained it thoroughly.[20] If one compares the consumption loss and the mortality rate in the case of limited testing capacity and short social distancing with those in the case of limited testing capacity and long social distancing in Table 2, one can see that the second tax hike leads to a quite dramatic contraction in consumption to push the death toll down only a bit. This result is in line with other studies that calibrate the costs of a statistical life similarly to the way we do in our paper.

Importantly, while, of course, social welfare increases relative to the case of the short social distancing policy, much of the welfare gains are reaped in the short run. This can be seen by comparing the first column in Table 2 for the cases No social distancing, Optimal social distancing (short), and Optimal social distancing (long) under "Contact tracing with limited testing capacity". This finding highlights the importance of the type of externality studied in this paper.

To sum up, we showed that (i) a combination of mitigation policies (in this case contact tracing and testing + social distancing) is welfare improving; (ii) it is optimal to use mitigation policies to lower social interactions right before tests are running short; and (iii) most of the welfare gains are reaped by only correcting the externality studied in our paper—that is, by implementing the *short* optimal social distancing policy. Welfare gains from addressing the other externality in the model are relatively small.

Tighter Quarantine Policy and Limited Testing Capacity. To keep the tracing and testing system afloat when tests are running short, policymakers decide to quarantine all the agents for whom no test is available because the testing capacity constraint is binding. When the testing capacity constraint is not binding, policymakers quarantine only subjects who test positive, exactly as in the baseline case. For computational reasons, we assume that the duration of the quarantine for the untested agents is stochastic. Agents who were tested before being quarantined leave the quarantine when they test negative, as assumed in the baseline case. The outcomes of this mix of policies is shown in Table 2 as "Tighter quarantine."

The more aggressive quarantine policy leads to welfare, economic, and health outcomes that are remarkably similar to the case of unlimited testing capacity and to the case of (short) optimal social distancing policy under limited testing capacity. The reason is that by quarantining more people, policymakers avert the collapse of contact tracing. Nevertheless, outcomes are slightly worse than those under unlimited testing

20. The second tax hike needed to address the externality related to achieving herd immunity is much larger than the first hike intended to address the externality studied in our paper. This relatively large tax hike is due to the quite large value the literature typically attributes to a human life in the calibration. The magnitude of the first tax hike primarily depends on how many tests are available.

capacity because the lack of tests prevents policymakers from knowing the true health status of those agents who are quarantined under the tighter quarantine regime. Thus, some subjects who leave quarantine are still asymptomatic and able to infect others. As a result, consumption falls and mortality increases. Furthermore, consumption falls because more agents are quarantined and quarantined agents consume less. However, the effects on consumption are rather small quantitatively, as shown in Table 2. Indeed, the tighter quarantine policy leads to a better consumption outcome than the optimal *short* social distancing policy, which, to be effective, has to lower the consumption path considerably in the early stages of the pandemic as shown in Figure 3.

Random Testing in Combination with Contact Tracing. When random testing is combined with contact tracing, the marginal contribution of allocating tests randomly is negligible. We combine these two testing strategies by assuming that when the testing capacity exceeds the number of traced subjects to be tested, this excess of tests is allocated randomly across the population. The negligible marginal contribution of random testing is due to the inability of this testing strategy to significantly lower the effective reproduction number beyond what contact tracing already achieves. This failure is largely due to the low probability that asymptomatic spreaders can be detected through their random meetings with newly symptomatic cases, as explained in Section 5.1 and shown graphically in Online Appendix I. More details on the random testing in combination with contact tracing are shown in Online Appendix C.

We conclude that both optimal social distancing and a tighter quarantine policy are suitable tools to preserve the viability of the tracing and testing system, while random testing is not. Indeed, when the government has a limited ability to commit to optimal (short) social distancing, the welfare implications of the two approaches are virtually identical, as shown in Table 2. Even when the government has the ability to commit for a longer period of time, optimal social distancing policy leads to a quite small increase in social welfare. And this slightly higher level of welfare can be achieved by sacrificing much more consumption than what the tighter quarantine policy engenders.

5.4. The Value of Tracing and Testing

We now use our model to study the social value of tracing and testing. To this end, we compare the case of unlimited testing capacity plus tracing to the case of no tracing and testing in Table 2. This comparison shows that testing and tracing more than halve the consumption loss and the mortality rate. According to our model, the social gains from running a viable tracing and testing system are of the order of $8.7 trillion. This result underscores the importance of preserving the tracing and testing system.

Let us now focus on the gains from testing alone (conditional on being able to trace the contacts of confirmed cases in the current week). For this, we construct a counterfactual case in which there is no test and hence policymakers have to quarantine all the traced contacts.[21] This requires to quarantine lots of susceptible subjects, and

21. We assume that quarantine has a stochastic duration in the absence of tests for computational reasons.

since tests are not available, some infected agents may leave quarantine still being asymptomatic and infect more susceptible subjects. Furthermore, without testing, subjects who did not develop symptoms during quarantine do not know their health status. This lack of information lowers welfare. The case of no testing is called "All exposed contacts quarantined" in Table 2. If one compares this case with of unlimited testing capacity, the value of having enough tests to check the health status of all the traced contacts is valued by the model to be equal to $1.6 trillion.

Furthermore, we show that being able to trace contacts for one additional week (comprehensive contact tracing) will further lower the mortality rate (−0.05 percentage points) and the consumption loss (−0.051 percentage points). The value of a more comprehensive tracing system is roughly $1.5 trillion.

6. Extensions

Our objective was to construct a macro-epidemiological model to serve as a general framework to study the efficacy (or lack thereof) of contact tracing and testing. With this goal in mind, we tried to keep the model as clean as possible. That said, our model can be extended in a number of interesting directions. First, an interesting extension could be the case of superspreaders—a small number of carriers ending up infecting many individuals. Second, we could extend our methodology to study multiple rounds of contact tracing and testing. However, this extension would not change our main conclusions because any gain from performing additional rounds of tracing and testing can only be incremental relative to an already close-to-optimal control of the virus with the comprehensive tracing technology. Third, a more stringent mask-wearing mandate could be another tool to shore up contact tracing. Finally, the government could implement a furlough scheme to contain the economic losses of quarantined agents. Details on the latter two policies and related simulations are shown in Online Appendix G.

7. Concluding Remarks

We study contact tracing in a macro-epidemiological model in which some of the infected agents remain asymptomatic for a number of periods, during which they contribute to spreading the virus. In the model, agents' consumption and labor decisions have externality on the number of subjects that will need to be traced and tested. This externality can threaten the correct functioning of contact tracing. Timely deployed containment policies—social distancing or tightening quarantine policies—may correct this externality, allowing policymakers to move beyond the traditional pandemic trade-off between saving human lives and mitigating the economic costs of pandemics. Indeed, we showed that the complementarity between contact tracing and these containment policies is so strong that policymakers can achieve welfare, consumption, and health outcomes that are remarkably similar to the idyllic case in which no externality threatens the implementation of contact tracing.

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Supplementary Material

Supplementary data are available at *JEEA* online.