Pandemic Recessions and Contact Tracing

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Introduction

- The COVID-19 pandemic set off a worldwide health and economic crisis
- Progress to reach herd immunity against the coronavirus seems to languish
- Major long-lasting obstacles to end the pandemic
  - Low global vaccination rates and breakthrough infections
  - Emergence of new variants of the coronavirus
- Important to understand tools that can contrast this long-running pandemic

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- Important to understand tools that can contrast this long-running pandemic

$\Rightarrow$ This paper: The efficacy of contact tracing to combat a pandemic crisis

- Testing strategy based on tracing and testing the contacts of confirmed infected cases
- Rests on reconstructing the network of interactions and infection chain

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A macro-epidemiological model with asymptomatic transmission and contact tracing

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  - Contact tracing aims to reconstruct the interactions of confirmed positive cases
- Agents' decisions have an externality on the number of subjects to be traced
  - This externality can cause the tracing and testing system to become overburdened
- The collapse of the system can be averted by
  - A sufficiently comprehensive tracing technology
  - A complementary lockdown aimed at buying time to expand the tracing and testing scale

The Importance of Reconstructing the Infection Chains

A typical challenge of uninformed or random testing

- At the onset of an epidemic or a new variant of the virus, spreaders are only a few

$\rightarrow$ Detecting and isolating enough spreaders to prevent flare-ups is challenging

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→ Contact tracing can prevent flare-ups of infections if tracing externality is mitigated

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$\rightarrow$ Our approach is general and can be extended to a broad set of epi-mac models

Overview of the Model

- Agents consume and work

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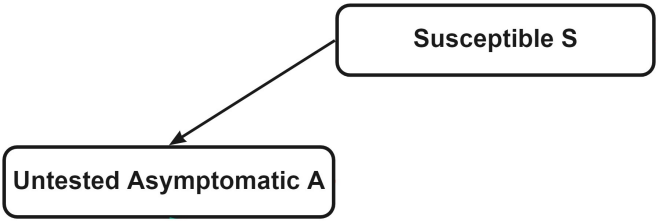
- Consuming and working require agents to interact with other agents
- Susceptible agents may become infected through interactions with infected agents
- The govt administers tests, quarantine infected agents, and can enact lockdowns

Change in Health Status

Change in Health Status



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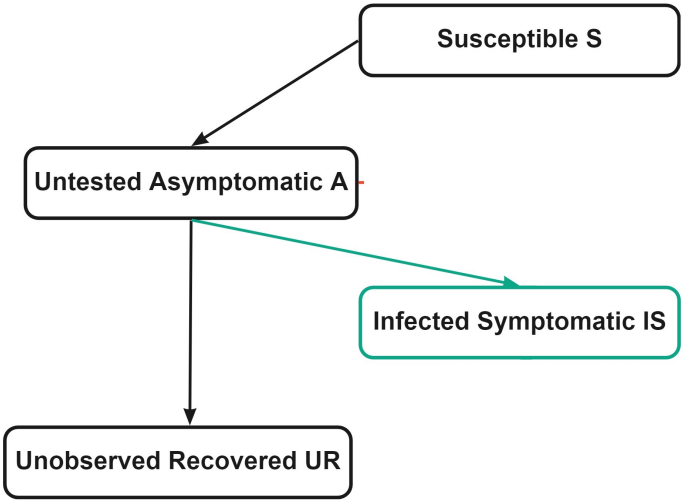

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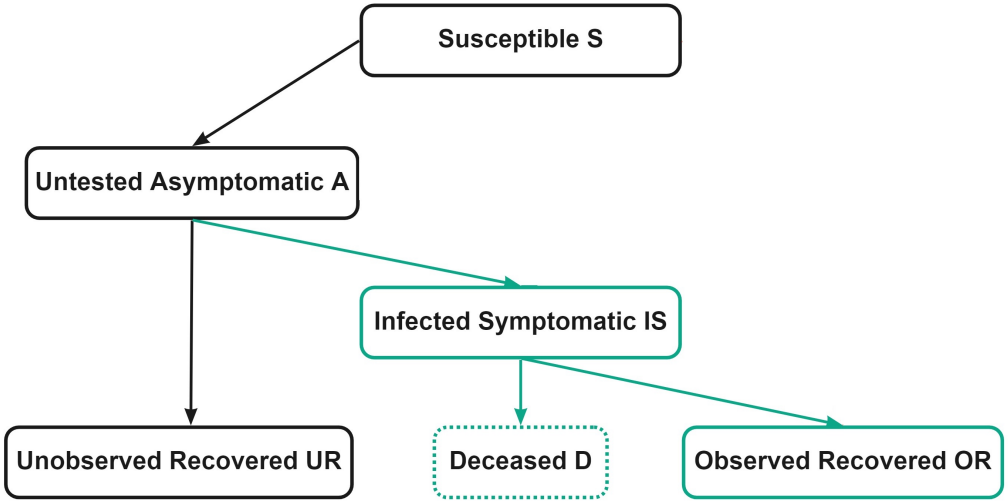

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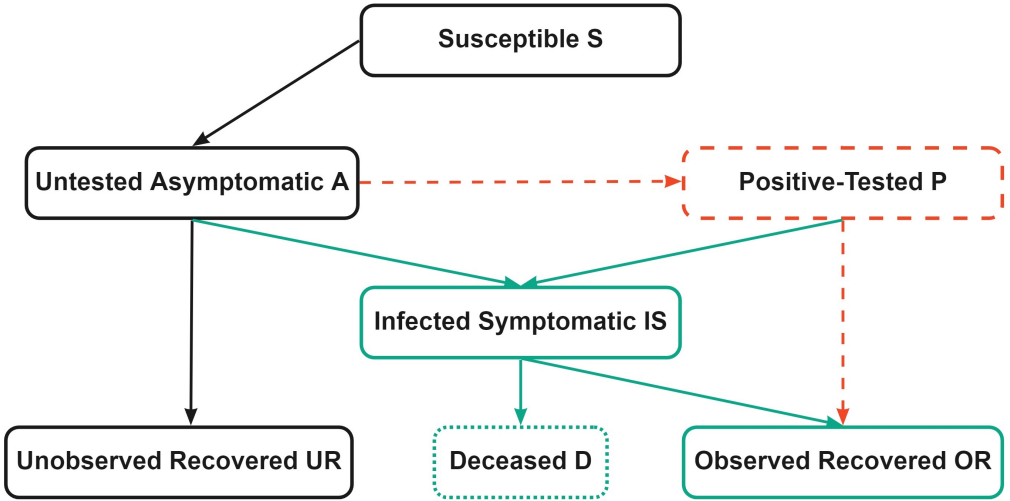

Observability of Health Status, Tracing, and Testing

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  - → The contacts of those agents who turn symptomatic are traced and tested
- Tests deliver a binary outcome: positive or negative (can be false negative)

Infection and Testing Probabilities

To close the model we need to characterize

1. The probability of becoming infected
2. The probability of being traced and tested
    - Endogenous network of interactions characterizes these probabilities

The Probability of Random Meetings

- The probability for an agent to randomly meet with k asymptomatic agents when consuming is given by the Binomial distribution $\mathcal{B}$

$$f_{c,t}(k) \equiv \mathcal{B}(k, \overbrace{\varphi_C(c_t^s)}^{\text{n}}, \underbrace{\frac{C_t^A}{C_t}}_{\text{p}}) = \binom{\varphi_C(c_t^s)}{k} \left(\frac{C_t^A}{C_t}\right)^k \left(1 - \frac{C_t^A}{C_t}\right)^{\varphi_C(c_t^s)-k}$$

- Similarly defined probabilities for labor interactions and other interactions

Probability of Becoming Infected

- If the agent is susceptible, the probability of becoming infected in one meeting is τ
- The probability of becoming infected for a susceptible agent that chooses c_t^s and n_t^s

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

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- Linearized version is isomporhic to SIR and Macro-SIR models Details

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

Testing Probabilities

- The probability for an infected agent to test positive:

  1. Probability of tracing infected agents
  2. Testing capacity Υ_t relative to number of traceable people E_t
  3. Accuracy of tests due to false negative outcomes with probability π_F

$$\pi^i_{P,t} = \pi^i_{C,t} \cdot \min\left\{\frac{\Upsilon_t}{E_t}, 1\right\} \cdot (1 - \pi_F)$$

where i captures the difference for newly infected and previously infected, resp.

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- This is also the fraction of asymptomatic spreaders quarantined in period t

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- This network contains the **the infection chain** – chain of interactions that led a newly symptomatic case to become infected or to infect other agents
- The reconstruction of the infection chain improves the efficacy of testing
  1. Exploiting the infection chain raises the chance of detecting asymptomatic agents
  2. Random meetings between asymptomatic agents of different infection chains are rare

Model Solution and Calibration

- The model studies response of epidemiological and economic variables
  - Initial surprise shock that infects tiny share of population
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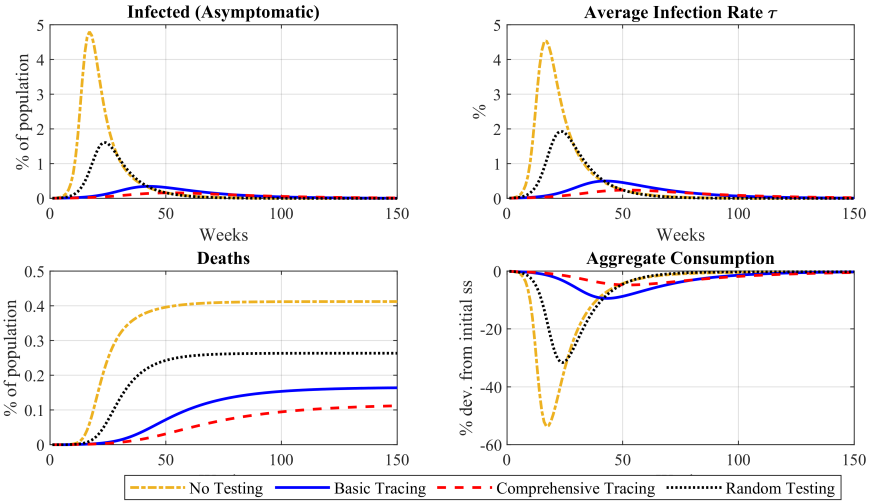
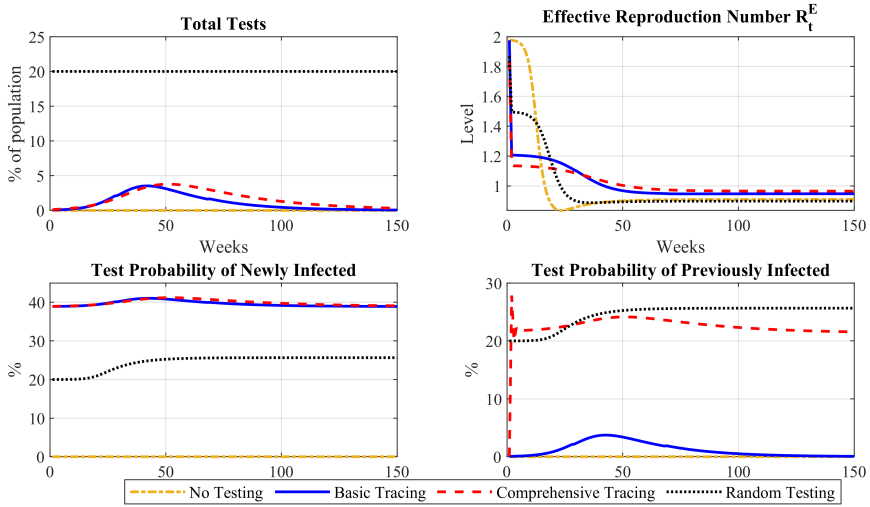
- Calibration
  - Economic parameters are set in line with literature
  - Probability that interaction results in infection τ is 5% (WHO, 2020)
  - Share of different transmission (consumption, labor, other) is $1/3$ (Ferguson et al. 2006)
  - Basic Reproduction number is 2 (e.g. Zhang et al, 2020)
  - Share of infected agents with symptoms is 50% (e.g. Baqaee et al., 2020)
  - Agents recover after 18 days on average (WHO, 2020)
  - Infection fatality rate of 0.3% (Hortascu, Liu, Schwieg, 2020)
  - False negative outcome $\pi_F = 0$

Contact Tracing with Unconstrained Testing I



Contact Tracing with Unconstrained Testing II



Contact Tracing with Unconstrained Testing: Summary

- Contact tracing does considerably better than random testing
  - Random testing does not leverage the existence of infection chains
  - Contact tracing leads to a sudden, rapid fall in the reproduction number, averting the flare-up of infections
- Basic and comprehensive contact tracing technologies lead to comparable outcomes
  - Similar efficacy in detecting the newly infected
  - effective reproduction number is much more sensitive to catching newly infected than agents who were infected in previous periods Details

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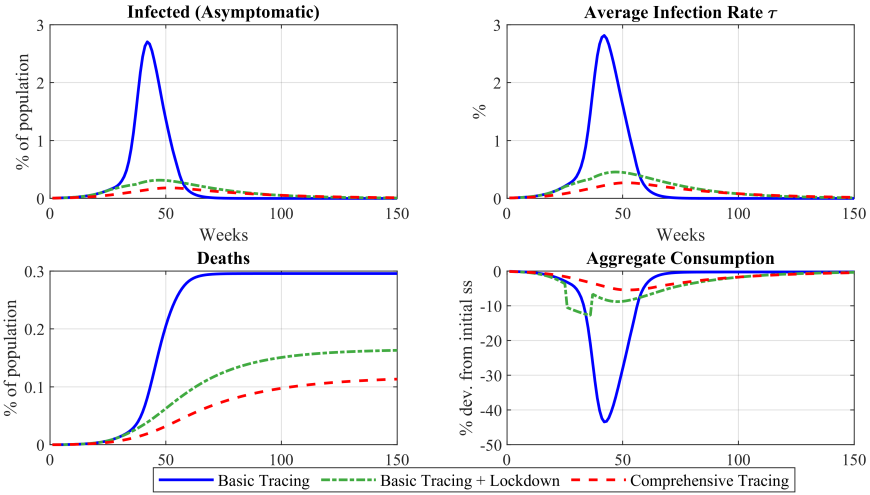

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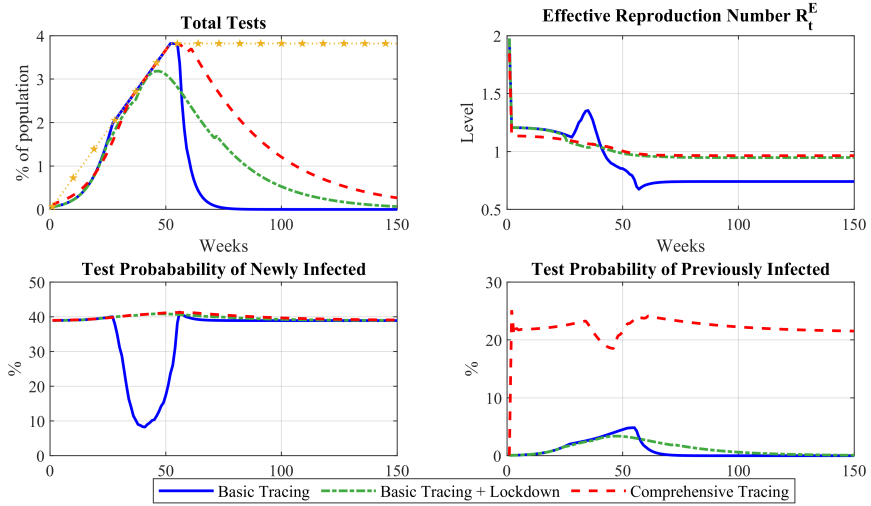

Contact Tracing with Constrained Testing: Summary

- The comprehensive tracing technology delivers the best outcome
  - Agents infected in period $t-1$ can be traced using the reconstructed infection chains
  - Early on, more spreaders are quarantined, preventing E_t from getting ahead of Υ_t
  - Eventually testing capacity Υ_t becomes constrained, lowering the ability of detecting previously infected agents. But the reproduction number hardly budges

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  - Early on, more spreaders are quarantined, preventing E_t from getting ahead of Υ_t
  - Eventually testing capacity Υ_t becomes constrained, lowering the ability of detecting previously infected agents. But the reproduction number hardly budges
- The basic contact tracing technology alone cannot avert the flare-up of infections
  - Tracing externality causes the testing capacity to become constrained
  - A complementary lockdown, timed to avoid the testing capacity from becoming constrained, averts the collapse of the tracing system and the ensuing deep recession

Concluding Remarks

- Contact tracing is a valuable tool to keep long-lasting epidemics under control
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Concluding Remarks

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  - Key to its success is the exploiting of the infection chain to trace and isolate asymptomatic spreaders
- However, tracing externality combined with critical bottlenecks of the tracing and testing system may require to complement this tool with a well-timed lockdown
- A general methodology to characterize the network of interactions and to study contact tracing in large set of epi-mac models

Agents with Unknown Health Status

- Susceptible S, untested asymptomatic A and unobserved recovered UR individuals do not know their health status
  - Assumption: These agents believe that they are susceptible
  - Conditional this belief, agents compute model-consistent probabilities

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- Agents choose consumption c_t^s and labor n_t^s to maximize utility V_t^S

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

$$\text{s.t.} \quad \left(1+\mu_{c,t}^L\right) c_t^s = w_t^s n_t^s + \Gamma_t^L$$

  - Agents expect to be newly infected with τ_t
  - Newly infected agents get tested positive with $\pi_{P,t}^T$
  - $\mu_{c,t}$ denotes a tax on consumption (proxy for lockdown) that is rebated Γ_t^L

Agents with Unknown Health Status (cont'd)

- Continuation value conditional of becoming asymptomatic V_t^A:

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

  - π_{IS} is the probability to get infected-symptomatic
  - π_R is the probability to become unobserved recovered
  - $\pi_{P,t}^A$ is the probability to test positive conditionally on staying asymptomatic

- Continuation value conditional of becoming an unobserved recovered agent V_t^{UR}:

$$V_t^{UR} = u(\tilde{c}_t^s, \tilde{n}_t^s) + \beta V_{t+1}^{UR}.$$

Agents with Known Health Status

- The utility function of tested-positive Agents P

$$V_t^P = \max_{c_t^P, n_t^P} u\left(c_t^P, n_t^P\right) + \beta\left[\pi_{IS} V_{t+1}^{IS} + \pi_R V_{t+1}^{OR} + (1 - \pi_{IS} - \pi_R) V_{t+1}^P\right]$$

$$\text{s.t.} \quad \left(1 + \mu_c^Q + \alpha \mu_{c,t}^L\right) c_t^P = w_t^P n_t^P + \Gamma_t^Q,$$

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- Infected symptomatic agents IS

$$V_t^{IS} = \max_{c_t^{IS}, n_t^{IS}} u\left(c_t^{IS}, n_t^{IS}\right) + \beta\left[\pi_R V_{t+1}^{OR} + (1 - \pi_R - \pi_D) V_{t+1}^{IS}\right],$$

  - Similar budget constraint but penalty on labor $\phi < 1$

Agents with Known Health Status (cont'd)

- Observed recovered agents *OR*

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

$$\text{s.t.} \quad (1 + \mu_{c,t}^{L}) c_t^{OR} = w_t^{OR} n_t^{OR} + \Gamma_t^{L}$$

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$$\text{s.t.} \quad (1+\mu_{c,t}^L) c_t^{OR} = w_t^{OR} n_t^{OR} + \Gamma_t^L$$

$\Rightarrow$ To close the model, we need calculate following key objects Law of Motions for Types

- τ_t: Average probability of getting infected
- Probabilities of testing positive for newly infected $\pi_{P,t}^T$ and previously infected asymptomatic $\pi_{A,t}^T$

Dynamics of Agents' Types I

- The law of motion for the share susceptible agents reads

$$S_{t+1} = S_t - T_t$$

- Newly infected subject in period t

$$T_t = \tau_t \cdot S_t$$

- Untested asymptomatic agents evolves according to the law of motion

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

Back

Dynamic of Agents' Types II

- The pool of tested positive subjects is given by

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

- The pool of infected symptomatic people evolves as follows:

$$I^S_{t+1} = (1 - \pi_R - \pi_D)I^S_t + \pi_{IS}(I^A_t + P_t)$$

Back

Microfoundation of SIR and Macro-SIR Models

- Average probability of getting infected τ_t for a susceptible individual is as follows:

$$\tau_t = \sum_{k=0}^{\varphi_C(c_t^S)} \underbrace{\left[1-(1-\tau)^k\right]}_{\substack{\text{Prob. of getting infected} \\ \text{cond. on k interactions}}} \times \underbrace{f_{t,c}(k)}_{\substack{\text{Prob. of k} \\ \text{interactions}}}$$

- Linearized version is isomporhic to SIR and Macro-SIR models

$$\tau_t \approx \Xi\left[\varphi_C c_t^s \left(C_t^A / C_t\right)\right]$$

- Extending this expression with labor and other interactions nests this to the formulation of Eichenbaum, Rebelo and Trabandt (2020) Back

Effective Reproduction Number and Contact Tracing

- Key epidemiological number: Effective Reproduction Number

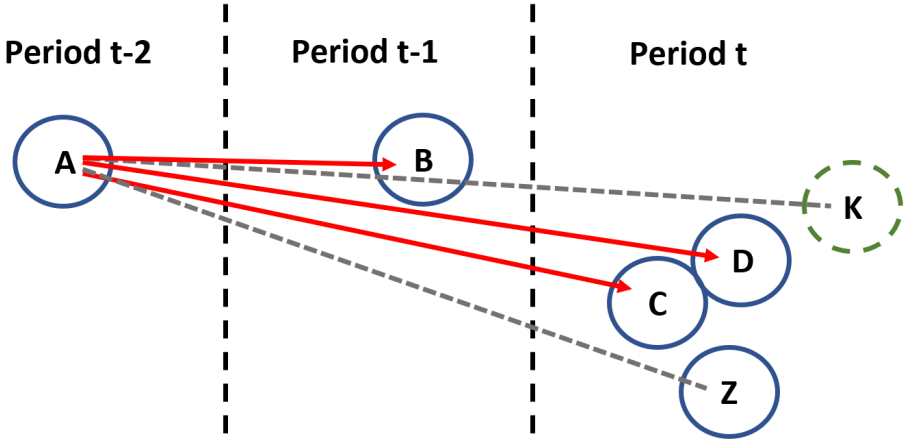
$$R_t^E = (1-\pi_{t-1}^T)\big[\tau_t + (1-\pi_{IS}-\pi_R)\left(1-\pi_t^A\right)\tau_{t+1} + (1-\pi_{IS}-\pi_R)^2\left(1-\pi_t^A\right)(1-\pi_{t+1}^A)\tau_{t+2}+\dots\big]$$

$$= (1-\pi_{P,t-1}^T)\sum_{j=0}^{\infty}\left(\tau_{t+j}(1-\pi_{IS}-\pi_R)^j \Pi_{k=0}^j \left(1-\pi_{P,t+k}^A\right)\right)$$

- Testing infrastructure affects R_T^E directly via testing newly infected π_{t-1}^T and testing asymptomatic infected earlier π_t^A
- Basic technology operates mostly over π_{t-1}^T, while comprehensive relies also on π_t^A
- Lockdowns lower the reproduction number via the infection rate τ_t Back

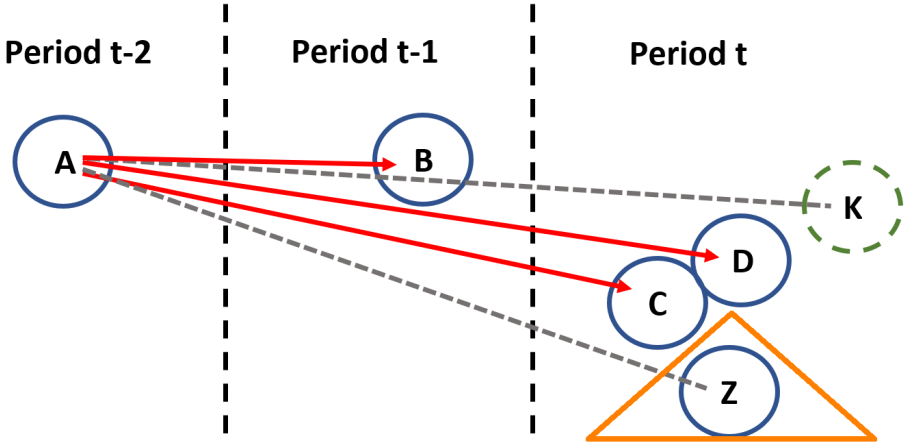
Example of a Network of Interactions

- Network of interactions and infection chain of Agent A



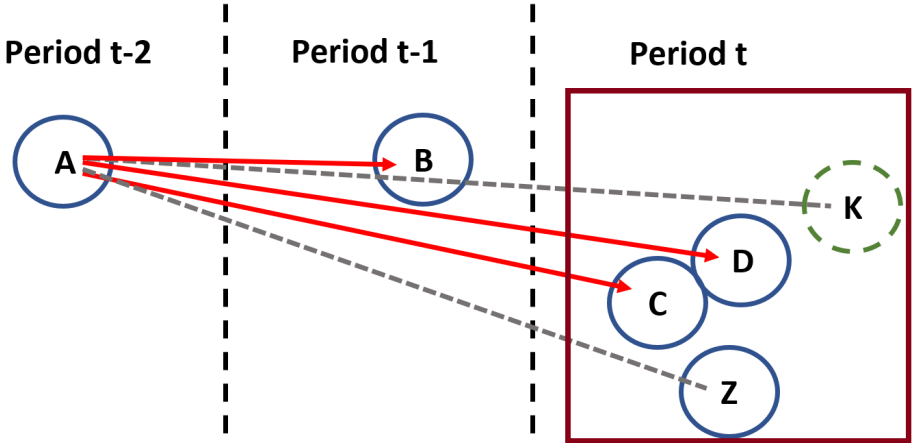
Example of a Network of Interactions

- Random meetings with asymptomatic agents from different infection chain Back



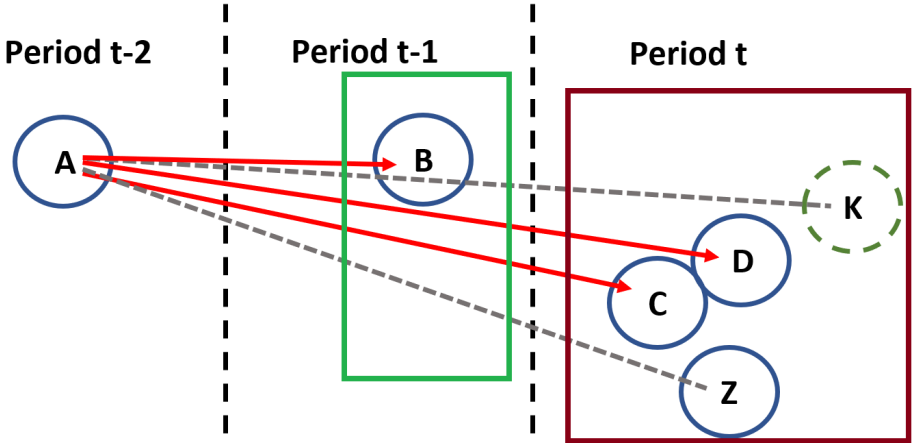
Example of a Network of Interactions

- **Basic tracing**: Current week contacts Back



Example of a Network of Interactions

- **Comprehensive tracing**: Current week contacts and previous week contacts Back



What Type of Lockdowns?

- Lockdowns are typically enacted in response to flare-ups of infection – often to prevent hospitals from becoming overburdened.

- We suggest a different strategy: moderate lockdowns as preemptive tools
  1. These lockdowns are generally **less stringent**
  2. The timing of these lockdowns is chosen so as to move ahead of the infection curve
  3. The objective is to keep the testing system viable while policymakers ramp up the testing capacity

Back

Tracing Probabilities - Basic Tracing

- Agents get traced if at least one of their k asymptomatic contacts becomes symptomatic: $1-(1-\Pi_{IS})^k$

- Tracing probability for previously infected asymptomatic agents $\pi^A_{C,t}$

$$\pi^A_{C,t} = \sum_{k=0}^{K(c_t^S, n_t^S)} \underbrace{\left[1-(1-\pi_{IS})^k\right]}_{\substack{\text{Prob. of contact getting} \\ \text{symptomatic cond. on k contacts}}} \times \underbrace{f_t(k)}_{\substack{\text{Prob. of k} \\ \text{contacts}}}$$

Tracing Probabilities - Basic Tracing (cont'd)

- Tracing probability for a newly infected agent T is different $\pi^A_{C,t}$

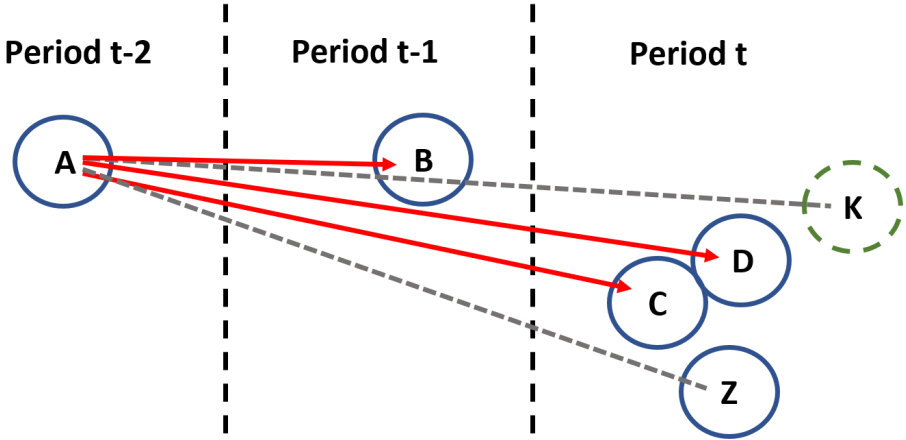
$$f_t^T(k) = \frac{f_t(k)\tilde{\tau}(k)}{\tau_t} = \frac{f_t(k)\overbrace{\left[1-(1-\tau)^k\right]}^{\text{Probability to get at least 1 infectious contact}}}{\tau_t}$$

- Characterization of the probability for a newly infected individual to be traced

$$\pi^T_{C,t} = \sum_{k=0}^{K(c_t^S, n_t^S)} \underbrace{\left[1-(1-\pi_{IS})^k\right]}_{\substack{\text{Prob. of contact getting} \\ \text{symptomatic cond. on k contacts}}} \times \underbrace{f_t^T(k)}_{\substack{\text{Prob. of k contacts} \\ \text{for a newly infected}}}$$

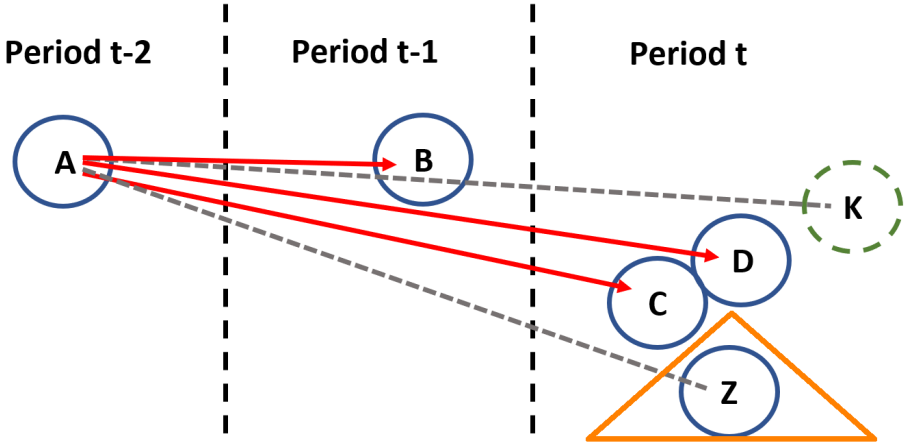
Example of a Network of Interactions

- Network of interactions and infection chain of Agent A



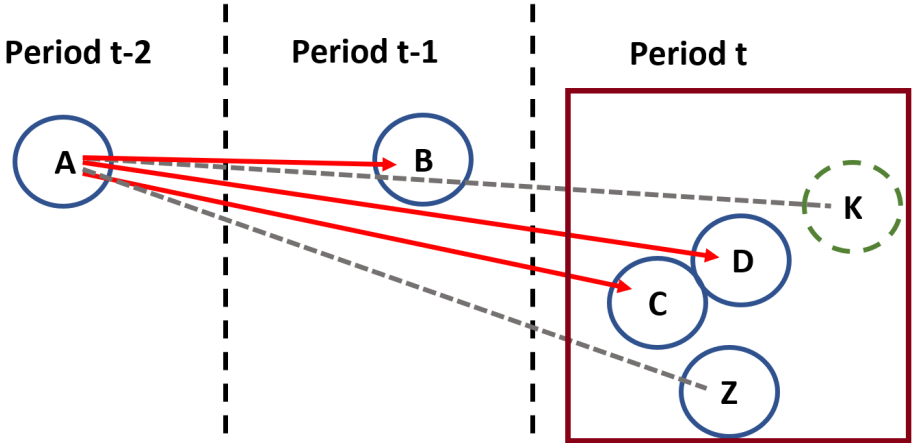
Example of a Network of Interactions

- Random meetings with asymptomatic agents from different infection chain



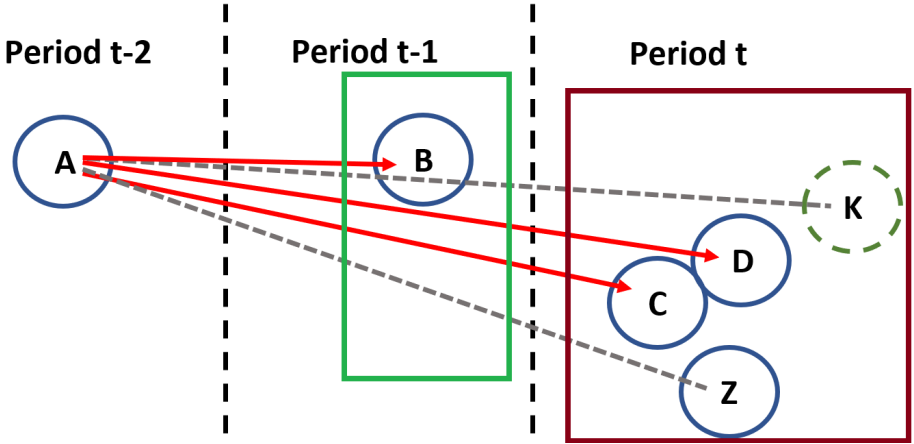
Example of a Network of Interactions

- **Basic tracing**: Current week contacts

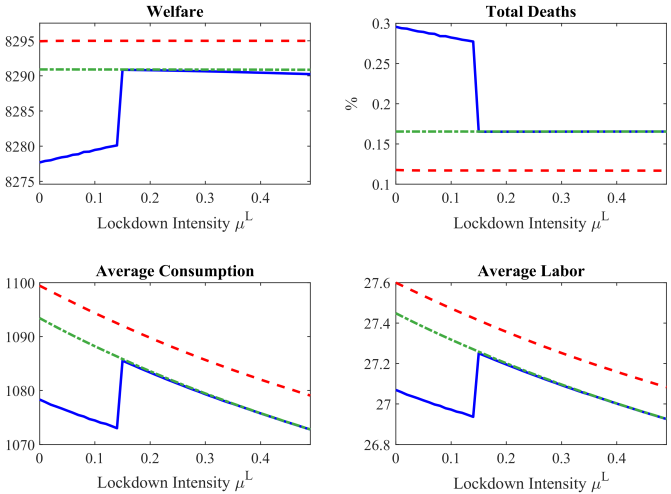


Example of a Network of Interactions

- **Comprehensive tracing**: Current week contacts and previous week contacts



Optimal Stringency of Lockdowns



Random Meetings are Rare