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Supplementary information

The effectiveness of backward contact tracing in networks

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Supplementary Information: The effectiveness of backward contact tracing in networks

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Supplementary analysis

Temporal delays are a major source of failures in contact tracing. We can incorporate the role of delays in our PGF formalism by calculating a tracing probability P and a failure probability f of contact tracing per node. These probabilities P and f should be calculated to correspond to a given continuous-time epidemic model. For example, one interesting calculation accounts for incubation, contact tracing, and infection rates but assumes that they all follow Poisson processes. With Poisson processes, we can simplify the integration over all times by noting that the probability that a Poisson process with rate a occurs before one with rate b is $a/(a+b)$. More specifically, consider that an index case causes a first secondary infection, and a contact tracing is initiated with rate c. If the infection rate from the index case is β, what is the probability that the contact tracing from the first secondary case prevents the additional infection from the index case? The probability of a transmission occurring during some time τ can be obtained by discretizing time τ in $\tau/\delta t$ time steps of length δt:

$$T(\tau) = 1 - \lim_{\delta t \to 0}(1-\beta\delta t)^{\tau/\delta t} = 1 - \exp^{-\beta\tau} \ . \tag{1}$$

To calculate the probability that contact tracing takes a given value of time τ, we first consider its cumulative distribution

$$F(\tau) = 1 - \lim_{\delta t \to 0}(1-c\delta t)^{\tau/\delta t} = 1 - \exp^{-c\tau} \ , \tag{2}$$

from which we derive the distribution of time for possible transmission $f(\tau)$,

$$f(\tau) = \frac{dF(\tau)}{d\tau} - c\exp^{-c\tau} \ . \tag{3}$$

The total probability of transmission before contact tracing is thus

$$P_T = \int_0^\infty T(\tau)f(\tau)d\tau = \frac{\beta}{\beta+c} \ , \tag{4}$$

note that we do not have to explicitly account for the recovery of the index case (occurring at rate α) since we are operating on the percolated network where transmission occurring before recovery was already controlled for through the transmission probability T.

We can then apply the same logic to subsequent competing Poisson processes. Using this result and assuming that the root node has infected one of its neighbors, we want to calculate the probability f that the neighbor fails to initiate successful contact tracing to protect one of its siblings. We are therefore following two sequences of Poisson processes: one for contact tracing (the newly infectious node traces backward to the root and the root traces to the sibling, both at rate c) and one for infection (the root infects the sibling at rate β which goes through an incubation period at rate σ). The probability that the infection sequence completes before the contact tracing sequence is:

$$f = \frac{\beta}{\beta+c}\left(\frac{\sigma}{\sigma+c} + \frac{c}{\sigma+c}\frac{\sigma}{\sigma+c}\right) + \frac{c}{\beta+c}\frac{\beta}{\beta+c}\frac{\sigma}{\sigma+c} \ . \tag{5}$$

The first term accounts for infection occurring before the first contact tracing, which will lead to successful contact tracing if incubation occurs before the first contact tracing as well (first term in parenthesis) or after the first trace but before the second (second term in parenthesis). The second term accounts for the backward contact tracing to occur before infection of the sibling but for infection and incubation to occur before forward tracing and therefore isolation. A similar but much simpler calculation would also give us that the probability of contact tracing being initiated by a COVID-19 case before its recovery (at rate γ) would simply be $P = c/(c + \gamma)$.

Of course, this calculation is independent of the PGF formalism itself and could therefore include additional processes, contact tracing coverage, or non-Markovian dynamics if needed. This would be done by calculating the integrals above for every competing process independently.