A Mathematical Model of Manual and Digital Contact Tracing

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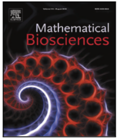

Original Research Article

An SEIR network epidemic model with manual and digital contact tracing allowing delays

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This work was included in my PhD thesis, defended in June 2024.

Introduction: Contact Tracing

Contact tracing (CT) interrupts chains of transmission - aims at identifying infected individuals early and preventing further transmission. It was widely used during Covid-19.

Manual CT

- Interviews conducted by public health agencies or self-reporting (in Sweden).
- Identified cases are asked to report their contacts and advise them to test (and self-quarantine).
- Mainly among close contacts (family, workplace, friends)

Digital CT

- Contact tracing apps were introduced during Covid-19 in certain countries.
- Smartphone-based proximity notifications
- Instantaneous alerts between app-users

Start with an SEIR network epidemic model with random contacts

- Initially, the number of infectious individuals $I(0) = 1$ and the number of susceptibles $S(0) = n - 1$. (size of population n)
- Infectious individuals make two types of contacts:
    - **local contacts** with each neighbour in G (represented by a configuration model having degree distribution $D \sim \{p_k = \mathbb{P}(D = k), k = 0, 1, 2, \ldots\}$ with finite mean μ) at rate β_L;
    - **random (global) contacts** with individuals chosen uniformly from the entire population (neighbors or not) at rate β_G;
- If a contacted individual is susceptible then they are infected and become exposed for a random period T_L, otherwise nothing happens.
- Once T_L ends, they become infectious for a period $T_I \equiv \tau_I$, after which they are recovered (becomes immune).
- All random quantities above are mutually independent. The epidemic goes on until first time T when $I(T) = 0$.

Network SEIR epidemic: early epidemic approximation

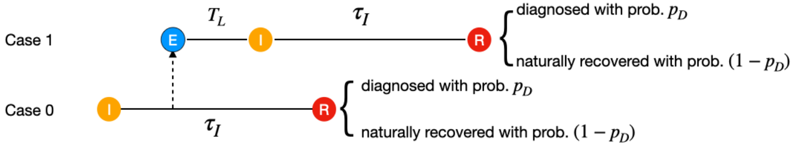
- **If population size n is large**, then all infectious contacts at the beginning will be with susceptibles (with large probability); local and global infections behave independently.
- So for large n, during the **early stage** of the epidemic, the epidemic behaves like a **two-type branching process**, with
  - **type-L**: infected through the network (by a local contact)
  - **type-G**: infected by a global contact
- Then we can compute the **basic reproduction number** R_0, which is the largest eigenvalue of the corresponding **next-generation matrix** $M = (m_{ij})$ with m_{ij} of type-j offsprings produced by a type-i individual, for $i, j = L, G$ [1]. When $D \sim Poi(\mu)$, it has a "simple" expression: $R_0 = \beta_G \tau_I + \mu(1 - e^{-\beta_L \tau_I})$

Important threshold property:

A major outbreak can occur with positive probability if and only if $R_0 > 1$, while a minor outbreak occurs with probability 1 when $R_0 \leq 1$.

Introducing diagnosis

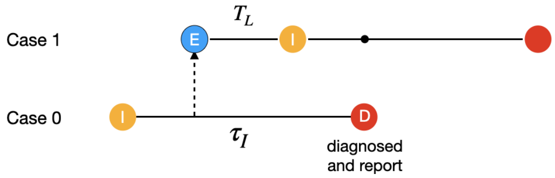
- We assume that diagnosis is the only trigger for CT.
- After infectious period τ_I, an infective is
  - diagnosed with probability p_D
  - otherwise we say the infective is naturally recovered.



"E" = "Exposed", "I" = "Infectious", "R" = "Removed"

Manual CT on network with delay

- **Forward, only for network contacts:** upon diagnosis, the infective is interviewed and reports each of their *infectee neighbours* with probability p_M independently.
- **Tracing delay:** If such reported neighbours are infectious/latent after a delay period of time T_D, they are isolated (stop spreading) and said to be traced. (No assumption about the form of T_D, suppose the distribution is known.)
- **Non-iterative:** Only diagnosed person can perform manual CT.
- The random delays of all infectees with the same infector are mutually independent.



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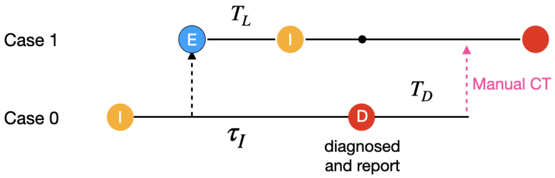

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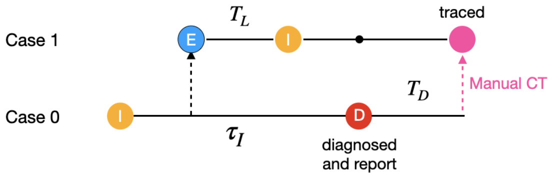

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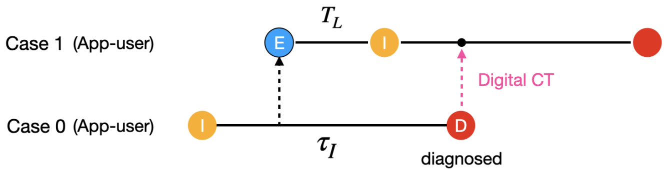
Instantaneous Digital CT on network and global contacts

- **A fraction π_A of individuals use the tracing app** (and follow the recommendations); and we assume random mixing between app-users and non-app-users.
- **Forward, instantaneous:** Once infectious app-users are diagnosed, all app-users they infected (neighbours or not, including those who are latent) will be *immediately* notified and self-isolated (hence stop spreading).
- **Non-iterative:** As for manual CT, we also assume that only the diagnosed app-users could trigger digital CT.



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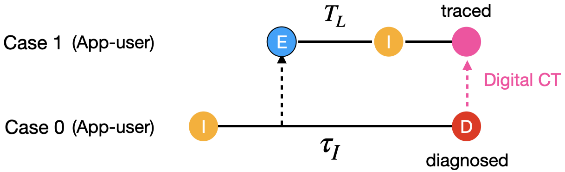

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Introducing both Manual and Digital CT

- There is an app-using fraction π_A.
- Upon removal, **if the non-app-users are diagnosed**, each of the neighbours infected by them is reported with probability p_M. Among the reported infectees, those who are infectious or latent after a delay period of time T_D are isolated and stop spreading.
- **If an app-user is diagnosed**, all of their app-using infectees (neighbours or not) will be traced immediately; meanwhile each of non-app-using infectee neighbours is reported with probability p_M.
- Only the diagnosed individuals could trigger CT (manual and/or digital CT).

Next slides: approximation of the early epidemic with CT - multi-type branching processes

Key assumptions enabling the branching process approximation

- **Challenge:** With CT, infected individuals usually do not behave independently $\Rightarrow$ branching process approximation typically breaks down.

- **Our key modelling assumptions restore independence:**
    - The infectious period is **deterministic**: $T_I \equiv \tau_I$
    - CT is triggered **only** when an individual is diagnosed

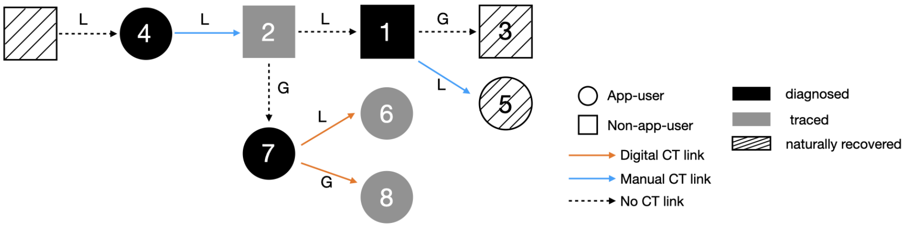
- **Consequence:** For a diagnosed infector with k infectees that have a CT link (manual or digital), the infection times of these infectees are independent and uniformly distributed over the infectious period:

$$U_1, \dots, U_k \overset{i.i.d}{\sim} \mathrm{Uniform}(0, \tau_I)$$

- **Why this matters:** If T_I were random, then the U_i's would become dependent $\Rightarrow$ loss of independence between offspring $\Rightarrow$ **branching process approximation fails**.

Early epidemic approximation: epidemic with combined CT

Assuming large population, we can approximate the initial phase of epidemic by a **eight-type branching process**.
Example of an infection tree containing the eight types ("L" = "local contact", "G" = "global contact"):



Reproduction number R_{MD} is the largest eigenvalue of the corresponding next-generation (8-by-8) matrix.

Reproduction numbers for manual/digital CT only

One straightforward approach: setting $R_M = R_{MD}(\pi_A = 0)$ and $R_D = R_{MD}(p_M = 0)$.

Alternatively, we can have the similar branching process approximation for each:

Manual CT only:

Assuming large population, we can approximate the initial phase of epidemic by a **three-type branching process**. Reproduction number R_M is the largest eigenvalue of the corresponding next-generation (3-by-3) matrix.

Digital CT only:

Approximated by a **six-type branching process**. Reproduction number R_D is the largest eigenvalue of the corresponding next-generation (6-by-6) matrix.

Numerical Illustrations

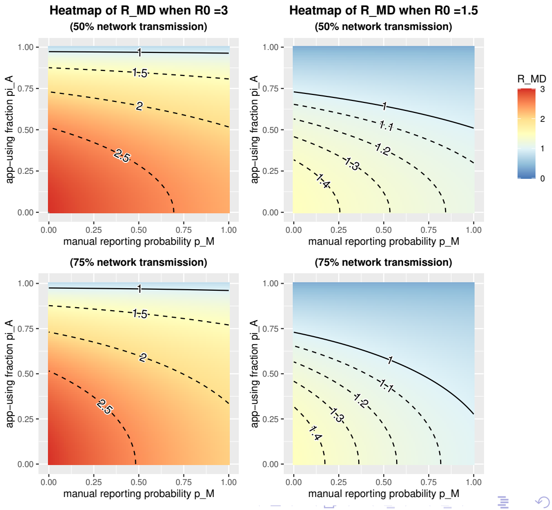
We quantify the effectiveness of CT numerically through the reduction of the reproduction number.

Parameter	Values
Degree distribution	$D \sim Poi(\mu)$ with mean degree $\mu = 5$ [6] (average household size in EU (2019) was 2.3; one meets 3 more at work etc.)
Latent period	$T_L \equiv 4$ days [3, 4]
Infectious period	$\tau_I = 5$ days [4]
Tracing delay	$T_D \equiv 3$ day [5]

Contact rates β_L, β_G are chosen so that there are $\alpha = 50\%$ and 75% transmissions on the network when $R_0 = 3$ and $R_0 = 1.5$. We also fix the probability of diagnosis $p_D = 0.8$, if not specified.

Heatmaps of R_{MD} as function of (p_M, π_A)

- As expected, **the reproduction number for combined CT** R_{MD} is monotonically decreasing in both **manual reporting probability** p_M and **app-using fraction** π_A.



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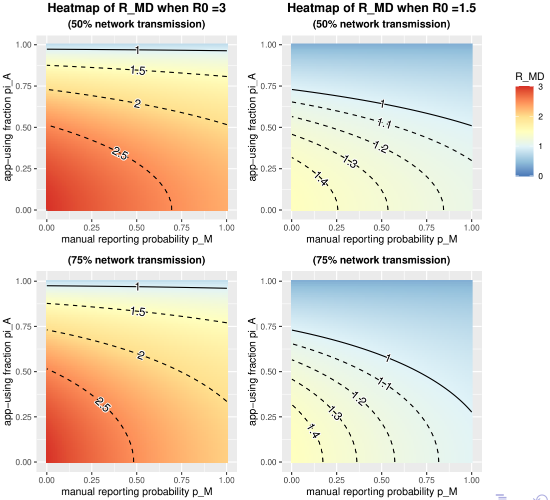
- When $R_0 = 3$, realistic values of p_M and π_A cannot bring R_{MD} below 1.



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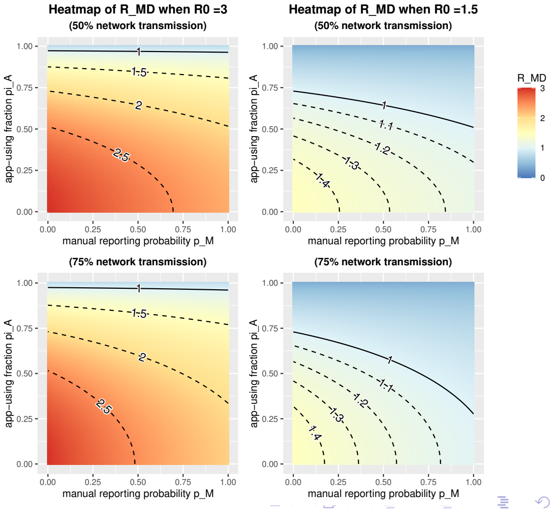
- When $R_0 = 3$, realistic values of p_M and π_A cannot bring R_{MD} below 1.
- Even if $R_0 = 1.5$, a fairly large app-using fraction is still required to prevent a major outbreak.



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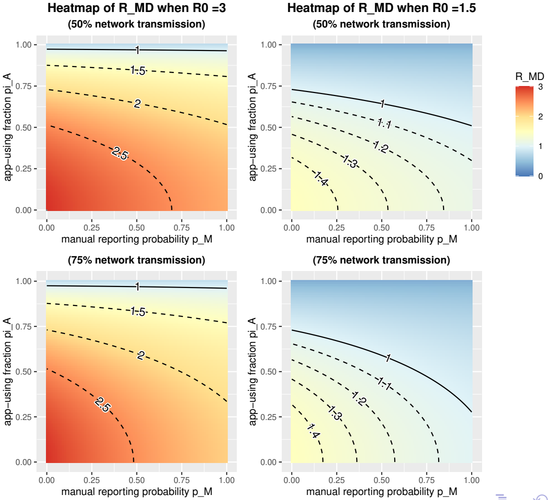
- When $R_0 = 3$, realistic values of p_M and π_A cannot bring R_{MD} below 1.
- Even if $R_0 = 1.5$, a fairly large app-using fraction is still required to prevent a major outbreak.
- With 75% of infections occurring through the network, $R_{MD} < 1$ is achievable with strong manual CT and moderate app usage.



Combined effect in comparison with the two separate effects

Let r_M, r_D and r_{MD} be the **relative reductions in** R_0 attributed to manual, digital and both types of CT, respectively:

$$R_M = R_0(1 - r_M), R_D = R_0(1 - r_D), R_{MD} = R_0(1 - r_{MD}).$$

If manual and digital CT would have acted *independently*, then $R_{MD} \stackrel{?}{=} R_0(1 - r_M)(1 - r_D)$

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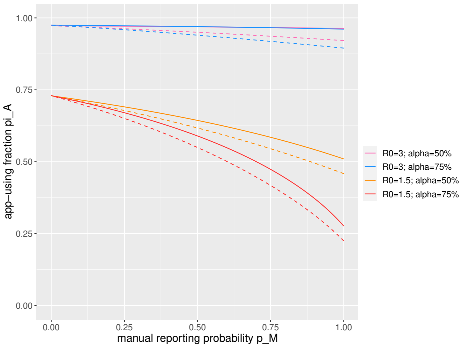

Critical (p_M, π_A) - curves: $R_{MD} = 1$ (solid),
$R_0(1 - r_M)(1 - r_D) = 1$ (dashed)

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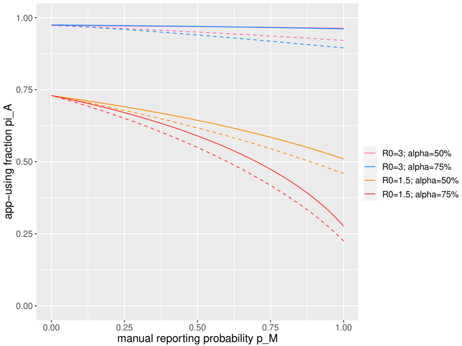

Critical (p_M, π_A) - curves: $R_{MD} = 1$ (solid), $R_0(1 - r_M)(1 - r_D) = 1$ (dashed)

The effect of combining manual and digital CT is actually smaller than the product of their separate effect!

Comparison with other CT models

- **Earlier CT models** [7, 2]: both manual and digital CT are forward, backward, and iterative without delay (*highly optimistic scenario*).
- **This CT model** [8]: forward, non-iterative CT, manual CT with delay (*more conservative assumptions*)

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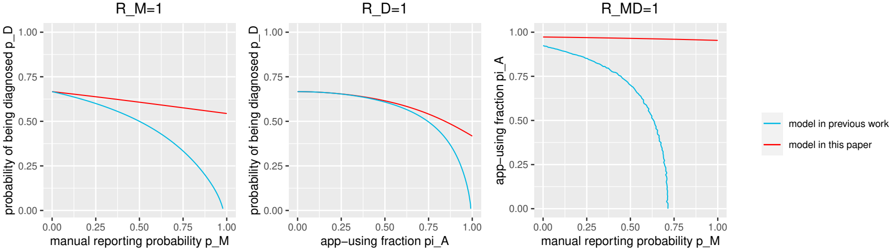
Plots of critical combinations of (p_D, p_M), (p_D, π_A) and (p_M, π_A) such that R_M, R_D and R_{MD} equal 1:



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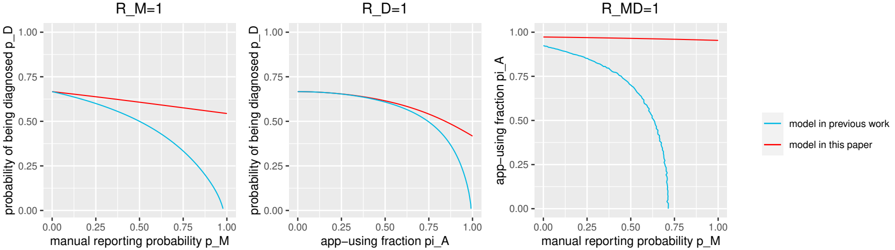

Real-world outcomes may lie somewhere in between!

Conclusion and possible extensions

Main conclusion:

- The models for manual, digital and combined CT could be approximated by different multi-type branching processes.
- The corresponding effective reproduction numbers could be derived.
- App-using fraction plays an essential role in the overall effectiveness of CT.
- The combined CT model would achieve a better effect if manual and digital CT acted independently.

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Interesting extensions:

- Incorporating CT within household structures, where manual tracing may be more effective.
- Allowing for assortative mixing in app adoption, reflecting that app-users tend to cluster within social networks.

Thanks for your attention!

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