Network epidemic models with digital and manual CT allowing delay

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Introduction: Contact tracing

Manual CT

- Performed by public health agencies or self-reporting (in Sweden)
- Interview identified cases and then call their reported contacts to advise them to test (and self-quarantine).

Digital CT

- Contact tracing app's were introduced during Covid-19 in certain countries.
- Once an app-user is confirmed as infectious, warning messages will be sent out to all the app-users who have been recently in close proximity for a sufficient duration with the confirmed case.

One challenge of modelling CT:
the standard branching process approximations breaks down: my infectious period would depend on how/when my infector is recovered.

Epidemic models incorporating CT

Earlier work [1, 2]

- Markovian SIR epidemic model with diagnosis in a homogeneous mixing population (size n fixed)
- Instantaneous manual CT and digital CT
- Forward and backward, iterative CT: once traced, those who are infectious or recently recovered by then, trigger CT, and so on.

We focus on the **early stage of epidemic** in a large population:

- infected individuals no longer behave independently (branching process approximation impossible)
- But if consider *to-be-traced components* as "macro-individuals" which behave independent of each other, we can analyse the branching process of to-be-traced components.

[1] Dongni Zhang and Tom Britton (2022), Analysing the Effect of Test-and-Trace Strategy in an SIR Epidemic Model, *Bulletin of Mathematical Biology*, 84(10):105.

[2] Dongni Zhang and Tom Britton (2022), Epidemic models with digital and manual contact tracing, *arXiv preprint*, arXiv:2211.12869.

Epidemic models incorporating CT

Now (inspired by [3])

- ~~SIR~~ SEIR epidemic model with diagnosis ~~in a homogeneous mixing population~~ on a network but also allowing random contacts
- ~~Instantaneous~~ manual CT with tracing delay and instantaneous digital CT
- Manual CT only on network, but digital CT works on both network and random contacts.

For mathematical tractability, we "make a compromise":

- Forward ~~and backward~~ ~~iterative~~ one-step CT
- constant infectious period

We focus on the early stage of epidemic: multi-type branching process approximations

[3] Ball, Frank G and Knock, Edward S and O'Neill, Philip D (2015), Stochastic epidemic models featuring contact tracing with delays, *Mathematical biosciences*, 266:23-35.

Network SEIR epidemic model with global contacts

- **SEIR** epidemic in a fixed population of size n on a configuration model network G with degree distribution $D \sim \{p_k\}$ (mean μ);
- **local** infectious contacts with each susceptible neighbor in G randomly in time according to independent Poisson processes with rate β_N;
- **global** infectious contacts with all other susceptible individuals (neighbors or not) independently at rate β_G;
- Once contacted with an infective, a susceptible becomes an exposed individual for a random period T_L, which has arbitrary but specified distribution;
- Each infective remains infectious for a *constant* period τ_I, after which the infective is **diagnosed** with probability p_D, otherwise we say the infective is naturally recovered.
- All the contact processes and the random variables describing T_L and D are assumed to be mutually independent.

Manual CT on network with delay

- **Forward, on network only:** upon diagnosis, the infective is interviewed and reports each of his/her *infectee neighbours* with probability p_M independently.
- **With delay:** If such reported neighbours are infectious 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.)
- If reported contacts are still latent after T_D, they will also be traced, i.e. they would infect no one.
- **Non-iterative:** Only diagnosed person can perform manual CT.
- The random delays of all infectees with the same infector are mutually independent.

Instantaneous digital CT on network and global contacts

- There is a fraction π_A of individuals use the tracing app (and follow the recommendations).
  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.

The combined CT (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 his/her 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 perform manual CT (and digital CT if an app-user).

Early epidemic approximation: epidemic with no CT

The process of infectives in the early stage of an epidemic can be approximated by a **two-type branching process** [4] with

- **type-L**: infected through network (by local contacts)
- **type-G**: infected by global contacts

The corresponding next-generation matrix M is given by

$$M = \begin{pmatrix} m_{LL} & m_{LG} \\ m_{GL} & m_{GG} \end{pmatrix} = \begin{pmatrix} \mathbf{E}[\tilde{D}-1](1-e^{-\beta_N \tau_I}) & \beta_G \tau_I \\ \mathbf{E}[D](1-e^{-\beta_N \tau_I}) & \beta_G \tau_I \end{pmatrix}, \tag{1}$$

with m_{ij} the mean number of secondary infections of type j produced by a single infected individual of type i, for $i, j = L, G$; $P(\tilde{D} = k) = kp_k/\mu$.
Basic reproduction number is the largest eigenvalue of M:

$$R_0 = \frac{m_{LL} + m_{GG}}{2} + \sqrt{\frac{(m_{LL} + m_{GG})^2}{4} - (m_{LL} m_{GG} - m_{LG} m_{GL})}$$

Early epidemic approximation: epidemic with manual CT

Start with $2^2 = 4$ types:

type	manual CT-link	infected
1	0 (without)	0 (locally)
2	0	1 (globally)
3	1 (with)	0
~~4~~	~~1~~	~~1~~

Manual CT on network only $\Rightarrow$ individuals who are infected by global contacts will never be reported.

Early epidemic approximation: epidemic with manual CT

Assuming large population, we can approximate the initial phase of epidemic by a **three-type branching process** with

type	manual CT-link	infected
1	0 (without)	0 (locally)
2	0	1 (globally)
3	1 (with)	0

Reproduction number R_M is the largest eigenvalue of the corresponding next-generation (3-by-3) matrix.

Early epidemic approximation: epidemic with digital CT

Start with $2^3 = 8$ types:

type	non-/app-user	digital CT-link	infected
1	0 (non-app)	0 (without)	0 (locally)
2	0	0	1 (globally)
~~3~~	~~0~~	~~1 (with)~~	~~0~~
~~4~~	~~0~~	~~1~~	~~1~~
5	1 (app)	0	0
6	1	0	1
7	1	1	0
8	1	1	1

However, non-app-users will never get digital CT-link $\Rightarrow$ two impossible types.

Early epidemic approximation: epidemic with digital CT

Assuming large population, we can approximate the initial phase of epidemic by a **six-type branching process** with

type	non-/app-user	digital CT-link	infected
1	0 (non-app)	0 (without)	0 (locally)
2	0	0	1 (globally)
3	1 (app)	0	0
4	1	0	1
5	1	1 (with)	0
6	1	1	1

Reproduction number R_D is the largest eigenvalue of the corresponding next-generation (6-by-6) matrix.

Early epidemic approximation: epidemic with combined CT

Start with $2^4 = 16$ types:

type	individual	infected through	digital CT-link	manual CT-link

Note:

- Digital CT can only take place between two app-users.
- Manual CT only on network: non-app-users infected through network can only be reached by manual CT.

Early epidemic approximation: epidemic with combined CT

Start with $2^4 = 16$ types:

type	individual	infected through	digital CT-link	manual CT-link

Note:

- Digital CT can only take place between two app-users.
- Manual CT only on network: non-app-users infected through network can only be reached by manual CT.

$\Rightarrow$ There are **7 impossible types**: (NA, homogeneous/network, with digital CT-link, with/without manual CT-link), (NA, homogeneous, without digital CT-link, with manual CT-link), (A, homogeneous, with/without digital CT-link, with manual CT-link);

Early epidemic approximation: epidemic with combined CT

Start with $2^4 = 16$ types:

type	individual	infected through	digital CT-link	manual CT-link

First, there are **7 impossible types** $\Rightarrow 16 - 7 = 9$ types

Then we can **merge two types**: one is the app-user infected on network with digital CT-link and manual CT-link; another is all the same but without manual CT-link, into one type. (traced by digital CT at the first place, no matter if has manual CT-link or not).

Early epidemic approximation: epidemic with combined CT

Assuming large population, we can approximate the initial phase of epidemic by a **eight-type branching process** with

type	individual	infected through	digital CT-link	manual CT-link
1	0 (NA)	0 (Network)	0 (No)	0 (No)
2	0 (NA)	0 (Network)	0 (No)	1 (Yes)
3	0 (NA)	1 (Homogeneous)	0 (No)	0 (No)
4	1 (A)	0 (Network)	0 (No)	0 (No)
5	1 (A)	0 (Network)	0 (No)	1 (yes)
6	1 (A)	0 (Network)	1 (yes)	0/1
7	1 (A)	1 (Homogeneous)	0 (No)	0 (No)
8	1 (A)	1 (Homogeneous)	1 (yes)	0 (No)

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

Numerical Illustrations

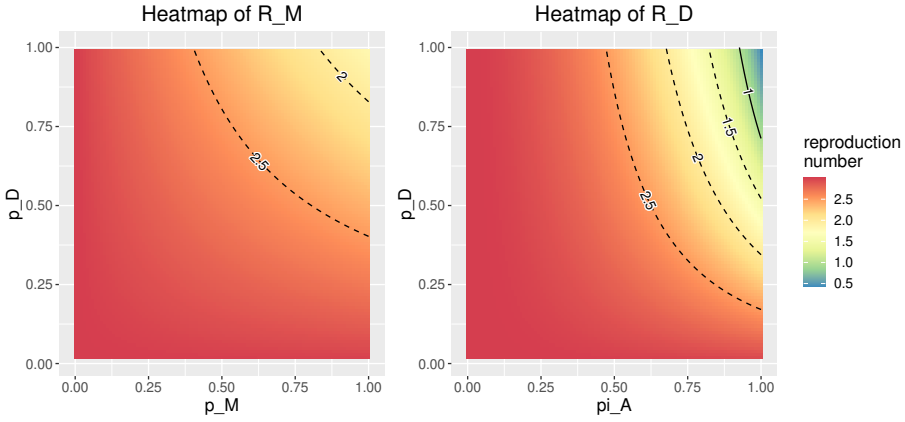
Parameter values used for the numerical results:

Parameter	Values
degree distribution	$D \sim Poi(\mu)$ with $\mu = 5$ [5]
contact rate on network	$\beta_N = 0.06$ [6]
rate of global contacts	$\beta_G = 0.3$
latent period	$T_L \equiv 4$ days [7, 8]
infectious period	$\tau_I = 5$ days [8]
tracing delay	$T_D \equiv 1$ day [3]

In this case, we have $R_0 \approx 3$.

Next, we plot the heatmap of R_M (R_D) as a function of p_D: the probability of being diagnosed and of p_M: the manual reporting probability (π_A: the app-using fraction)

The separate effect of manual and digital CT

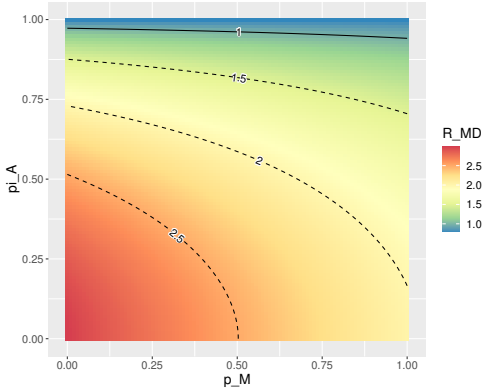


R_M is still above 1, even with $p_M, p_D \approx 1$.

π_A seems to be more influential in reducing R_D as compared with p_D.

The combined effect of manual and digital contact tracing

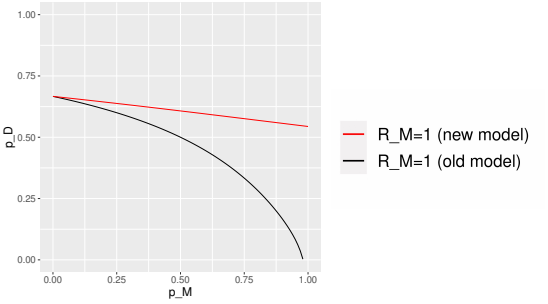
Here, we fix $p_D = 0.8$, then p_M and π_A quantify the effectiveness of the combined CT.

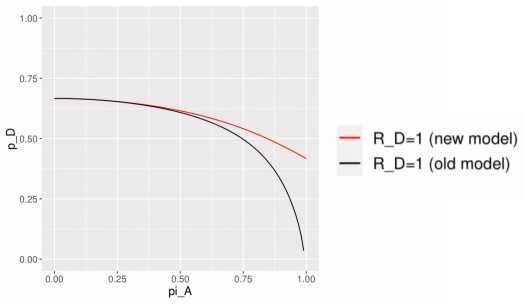


Even with more implementation from manual CT, we still need larger app-using fraction to control the epidemic.

Comparison with earlier model: manual/digital CT only

Plots of two critical curves:

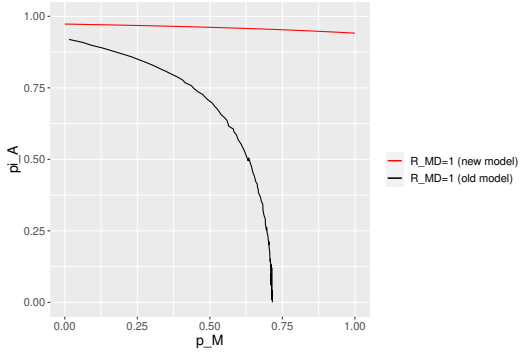




For manual CT, the difference is bigger since here we have also introduced a delay and that CT only on network.

Comparison with earlier model: combined CT

Fix $p_D = 0.8$.



Our earlier model assumptions: full, iterative CT, without delay;
This work: forward, non-iterative CT, manual CT with delay.

Conclusion

- The network epidemic models with Manual, Digital and Combined CT could be approximated by different multi-type branching processes.
- The corresponding individual reproduction numbers are derived.
- The underlying combined model is *pessimistic* by only having one step CT and even introducing a delay for manual CT, whereas our earlier model in [2] is *over-optimistic* by assuming iterative CT without any delay.
  Real world should lie somewhere in between.

Thanks for your attention!

References I

[1] Dongni Zhang and Tom Britton.
Analysing the effect of test-and-trace strategy in an sir epidemic model.
Bulletin of Mathematical Biology, 84(10):105, 2022.

[2] Dongni Zhang and Tom Britton.
Epidemic models with digital and manual contact tracing.
arXiv preprint arXiv:2211.12869, 2022.

[3] Frank G Ball, Edward S Knock, and Philip D O'Neill.
Stochastic epidemic models featuring contact tracing with delays.
Mathematical biosciences, 266:23–35, 2015.

[4] Frank Ball and Peter Neal.
Network epidemic models with two levels of mixing.
Mathematical biosciences, 212(1):69–87, 2008.

References II

[5] Stefan Thurner, Peter Klimek, and Rudolf Hanel.
A network-based explanation of why most covid-19 infection curves are linear.
Proceedings of the National Academy of Sciences, 117(37):22684–22689, 2020.

[6] Anjalika Nande, Ben Adlam, Justin Sheen, Michael Z Levy, and Alison L Hill.
Dynamics of covid-19 under social distancing measures are driven by transmission network structure.
PLoS computational biology, 17(2):e1008684, 2021.

[7] Laura Di Domenico, Giulia Pullano, Chiara E Sabbatini, Pierre-Yves Boëlle, and Vittoria Colizza.
Impact of lockdown on covid-19 epidemic in île-de-france and possible exit strategies.
BMC medicine, 18(1):1–13, 2020.

References III

[8] Stephen M Kissler, Christine Tedijanto, Edward Goldstein, Yonatan H Grad, and Marc Lipsitch.
Projecting the transmission dynamics of sars-cov-2 through the postpandemic period.
Science, 368(6493):860–868, 2020.