Epidemic Models with Manual and Digital Contact Tracing

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Epidemic models incorporating conact tracing

Ultimate goal: Analyse an epidemic model with:

- Manual as well as digital contact tracing
- not all manual CT successful and not all ind using app
- Random infectious contacts as well as contacts "on" population structure (e.g. network)
- Delay between diagnosis and successful manual contact tracing
- Iterative CT if infectious or recently recovered are discovered (but with delay for testing, i.e. iteration)
- Manual tracing only on social structure (not random contacts)

Epidemic models incorporating contact tracing: so far

What we have managed so far: Analyse an epidemic model with:

- Manual as well as digital contact tracing
- not all manual CT successful and not all ind using app
- Random infectious contacts ~~as well as contacts "on" population structure~~ (~~e.g. network~~)
- ~~Delay between diagnosis and successful manual contact tracing~~
- Iterative CT if infectious or ~~recently~~ recovered are discovered (~~but with delay for testing, i.e. iteration~~)
- ~~Manual tracing only on social structure~~ (~~not random contacts~~)

And: We only analyse initial phase of epidemic ...

Epidemic model

Focus: Stochastic **SIR-epidemic** in a large but finite (size n) fixed population

Simplest epidemic model: Homogeneous Markovian SIR epidemic

– Infectious individuals have infectious contacts at rate β

– Each contact with a uniformly chosen individual. If contacted person is susceptble s/he becomes infected and infectious, otherwise nothing happens

– Infectious individuals recover (and become immune) at rate γ

– All random quantities above are mutually independent

Initiation: $(S(0), I(0), R(0)) = (n-1, 1, 0)$

Termination: Epidemic goes on until first time T for which $I(T) = 0$. Then epidemic stops

Well-known result: $R_0 = \beta/\gamma$ and major outbreak possible iff $R_0 > 1$.

Properties of Epidemic model

If n is large, then all infectious contacts in beginning will be with susceptibles (w.l.p)

So in beginning infectious individuals infect new individuals at rate β and recover at rate γ

$\Longrightarrow$ epidemic behaves like a branching process (B-D process) with birth rate β and death rate γ

$\Longrightarrow$ we can compute $P(\text{minor outbreak}) = P(\text{extinction})$, and other quantities determined during start of epidemic

"beginning" = e.g. up until $\sqrt{n}$ have been infected

Introducing manual contact tracing (CT)

In order for any CT to happen an individual must test positive ("diagnosed")

So now infectious individuals stop spreading because they recover naturally (at rate γ) **or** if they are diagnosed (at rate δ)

With diagnosis rate reproduction number equals $R = \beta/(\gamma + \delta)$. For comparison I call this R_0: $R_0 = \beta/(\gamma + \delta)$.

Manual contact tracing: an individual who is diagnosed is instantaneously questioned for its contacts, and each such contact is reached and tested immediately, with prob p. Those that test positive (including recovered) are in turn contact traced immediately, and so on.

Model parameters

β transmission rate
γ recovery rate
δ diagnosis rate
p prob of a contact being successfully contact traced

So p, quantifies the effectiveness of the manual CT

Introducing digital contact tracing

In certain countries app's were introduced during Covid-19. An app-user who is diagnosed would result in warnings among recent contacts

Model

Same assumption as in manual CT that individuals are diagnosed at rate δ, and $R_0 = \beta/(\gamma + \delta)$.

A community fraction π have the app and follow its instructions. We assume random mixing between app-users and non-app-users

Digital contact tracing: if an app-users is diagnosed all his/her contacts are instantaneously informed, tested and diagnosed if infected (infectious or recovered). Such diagnosed individuals iterate the digital CT.

Model parameters

β transmission rate
γ recovery rate
δ diagnosis rate
π fraction of individuals using the App

So π quantifies the effectiveness of the digital CT (π^2 more relevant)

Manual and digital CT

It is of course possible to consider both types of CT simultaneously

Model
Same diagnosis model as before: individuals are diagnosed at rate δ, and $R_0 = \beta/(\gamma + \delta)$.

Manual and Digital CT: Any individual who is diagnosed is immediately CT reaching each contact with prob p. App-users that are diagnosed are additionally immediately CT traced by each app-using contact being traced. All traced individuals are tested and if infected CT is iterated.

Model parameters
β transmission rate
γ recovery rate
δ diagnosis rate
p prob of a contact being successfully contact traced
π fraction of individuals using the App

So p and π quantify the effectiveness of the combined CT

How to analyse CT models?

When (manual or digital) CT is present, then infected individuals no longer behave indepenently so branching process approximation not possible ...

However: if we instead consider to-be-traced components as "macro-individuals" then these behave independent of each other and we can analyse the branching process of to-be-traced components

Epidemic with manual CT:

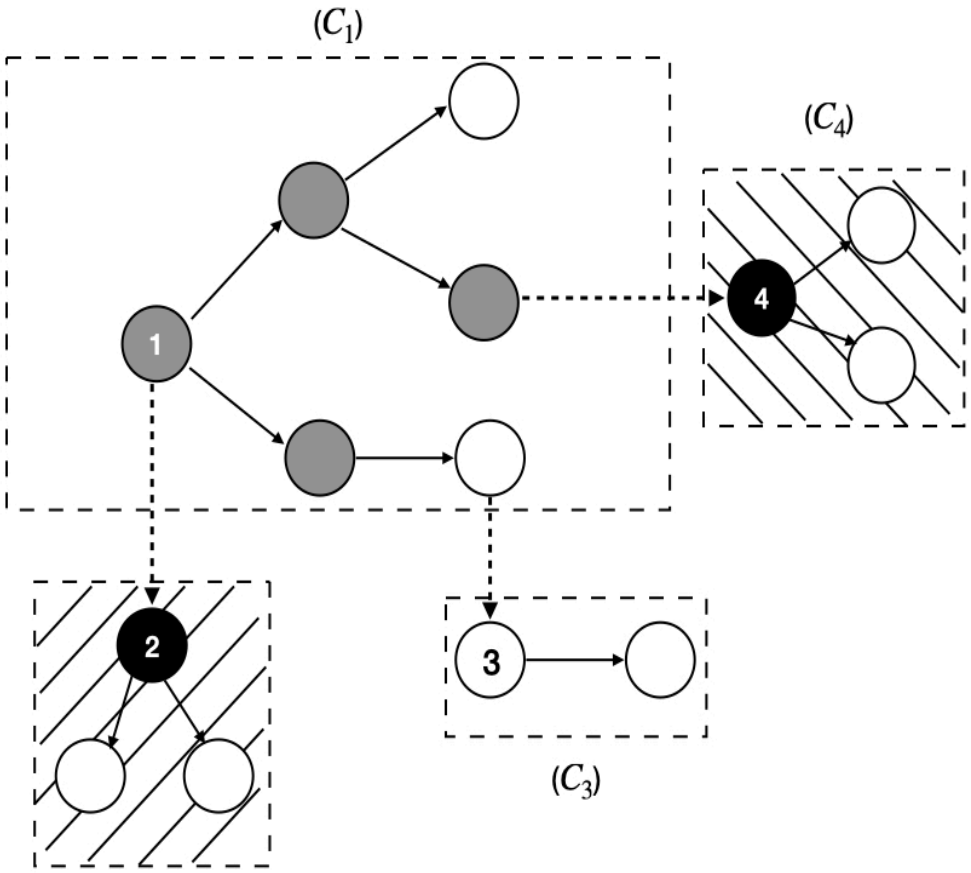
Whether or not CT will happen can be determined already at infection

Those with CT belong to same component and those without CT start new components

Manual CT: to be traced components

White = infectious, grey = naturally recovered, black = diagnosed

Solid arrow = infection and manual CT, Dashed arrow = infection but no manual CT



Manual CT: to be traced components

Consider a to-be-traced component and let s denote the time since birth (an individual gets infected without manual CT)

$X(s) :=$ current number of **infectious** individuals in component. Then

$X(s)$ increases with 1 at rate $\beta p X(s)$

$X(s)$ decreases with 1 at rate $\gamma X(s)$

$X(s)$ drops to 0 at rate $\delta X(s)$

$X(s)$ gives birth to new components at rate $\beta(1-p)X(s)$

$\Longrightarrow Z :=$ # born new components until next jump
$\sim Geo((\beta p + \gamma + \delta)/(\beta + \gamma + \delta))$

$R_M^{(Comp)} =$ Component reproduction number for Manual CT $=$ expected number of new components produced by a component before it dies $(X(s) = 0)$

$R_M^{(Comp)} = E\left(\sum_{i=1}^{N} Z_i\right) = E(N)E(Z)$, where $N =$ # jumps a component makes until $X(s) = 0$

Manual CT: to be traced components

$R_M^{(Comp)}$ = expected number of new *components* that one *component* infects

Can one define an individual reproduction number?

It is possible to compute μ_{Comp} = average number of infected individuals in a to-be-traced component

All individuals except the index case have been infected within the component, so $\mu_{Comp} - 1$ internal infections, and $R_M^{(Comp)}$ externally infected individuals

So expected total number of infections $= R_M^{(Comp)} + \mu_{Comp} - 1$, and the expected number of infections per individual in a component hence equals

$$R_M^{(ind)} = \frac{R_M^{(Comp)} + \mu_{Comp} - 1}{\mu_{Comp}}$$

This is not the "true" resproduction number, but still a threshold parameter

To-be-traced components for Digital CT

For the model with digital CT there are two types of individuals: App-users and non-App-users.

To-be-traced components are built up of app-users that infect each other. These app-user components can also infect non-app-users

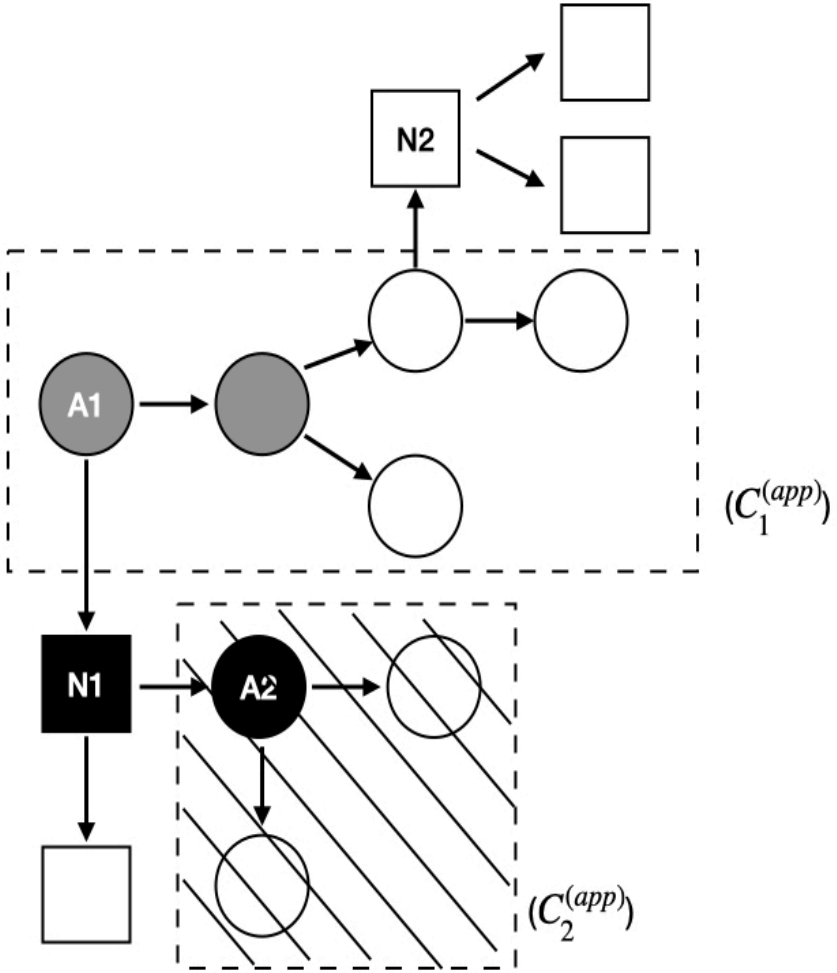
Non-app-users infect other non-app-users AND new App-using components

The branching process consist of two types: app-using components and non-app-users

Digital CT: to-be-traced component illustration

Circles are app-users, boxes non-app-users

White = infectious, grey = naturally recovered, black = diagnosed



Limiting branching process for Digital CT

Two-type branching process:

Type 1: app-using component

Type 2: non-app-user

$M = (m_{ij}) =$ next generation matrix

$m_{11} = 0$

m_{12} obtained similarly as with manual (but a bit more complicated)

$m_{21} = \beta\pi/(\gamma + \delta)$ and

$m_{22} = \beta(1 - \pi)/(\gamma + \delta)$

Reproduction number for Digital CT: R_M is largest eigenvalue of M

To-be-traced components for Manual and Digital CT

For the model with manual digital CT there are two types of individuals: App-users and non-App-users.

Infections where both are not app-user may also lead to CT

To-be-traced components can contain both app-users and non-app-users (each infection within a component is either manual or digital CT)

A to-be-traced components gives birth to new components when a) app-user infect non-app-users with no manual CT, and b) when non-app-users infect any individual with no manual CT

Every new component is a new to-be-traced component, but its distribution depends on if index case is app-user or not

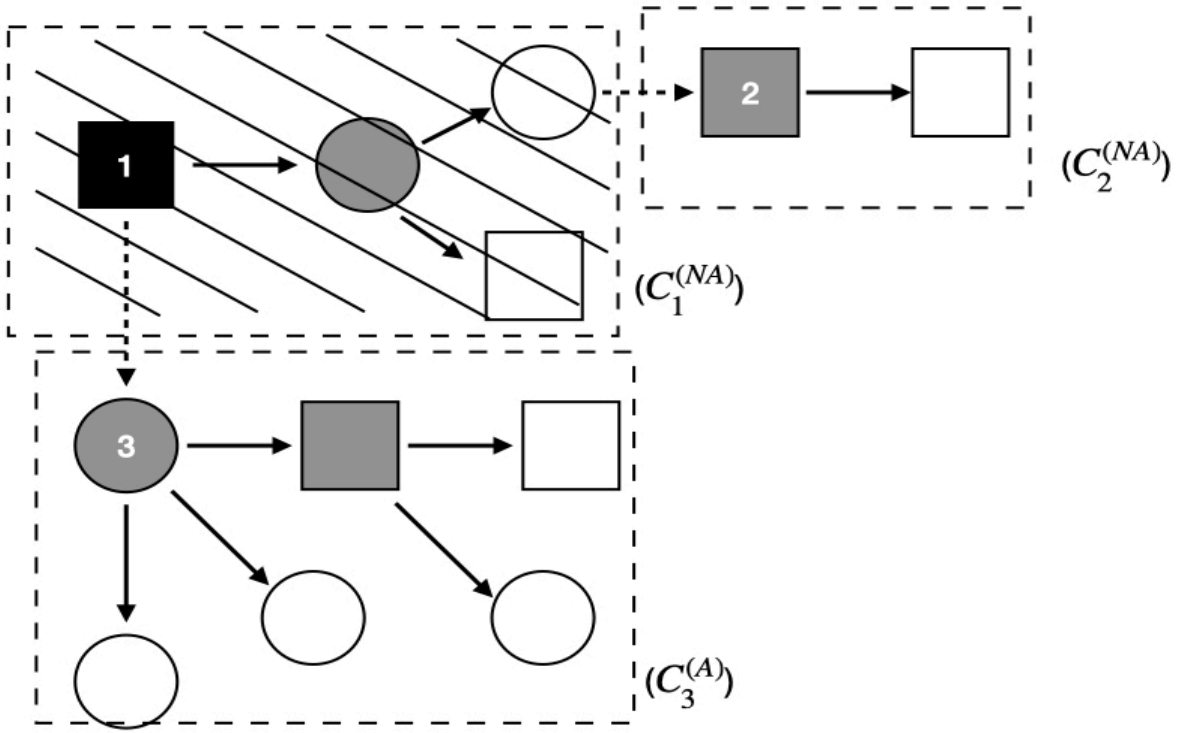
The branching process consist of two types: To-be-traced component with an app-user as index and To-be-traced component with non-app-user as index

Manual and Digital CT: to-be-traced component illustration

Circles are app-users, boxes non-app-users

Solid edges: infection with some CT, dashed edges: infection without CT

White = infectious, grey = naturally recovered, black = diagnosed



Limiting branching process for Manual and Digital CT

Two-type branching process:

Type 1: to-be-traced component with non-app-using index

Type 2: to-be-traced component with app-using index

$M = (m_{ij}) =$ next generation matrix

m_{ij} have more complicated expressions

Reproduction number for Manual and Digital CT R_{MD} is largest eigenvalue of M

Manual CT: component and individual reproduction number

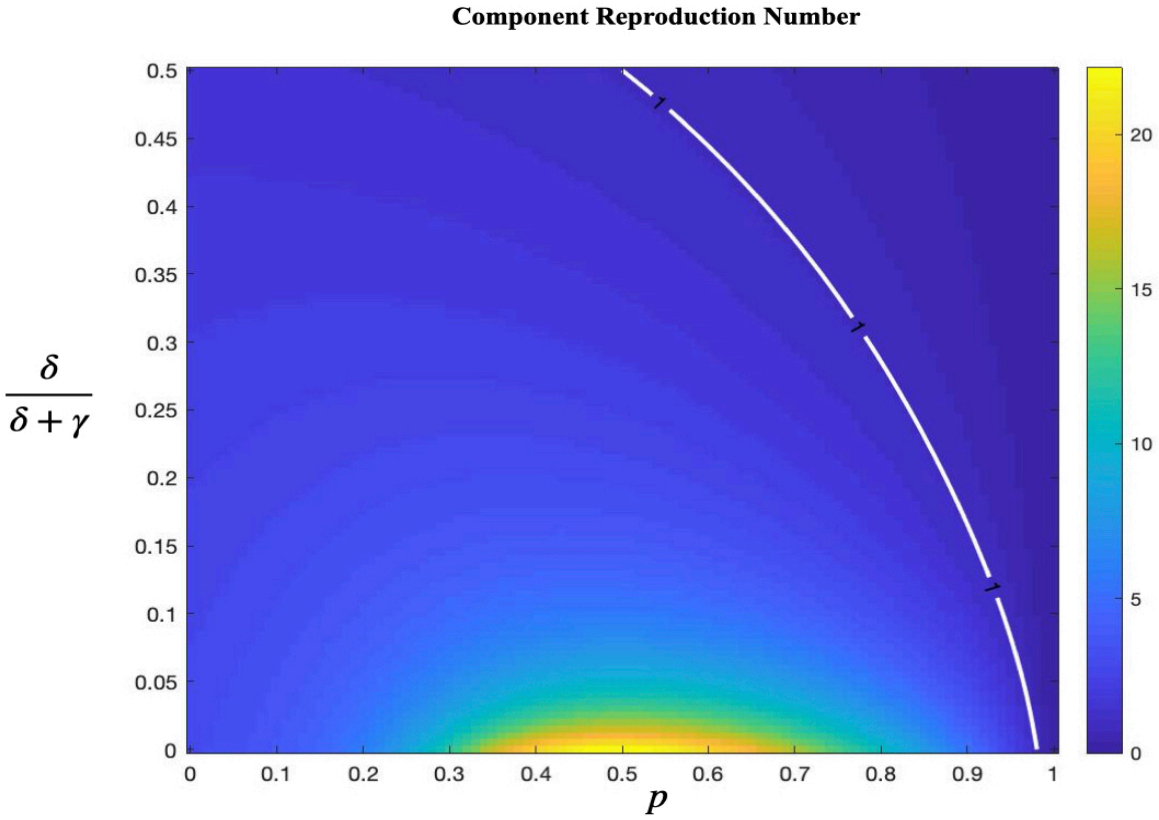
Now numerical illustrations

In all models CT initiated when an infectious individual is diagnozed (rate δ)

The fraction of individuals that are diagnozed rather than naturally recovered (and undiagnozed) equals $\delta/(\delta+\gamma)$

Next slide: heatmap of $R_M^{(Comp)}$ as a function of fraction diagnosed $\delta/(\delta+\gamma)$ and of $p =$ fraction of contacts that are successfully contact traced

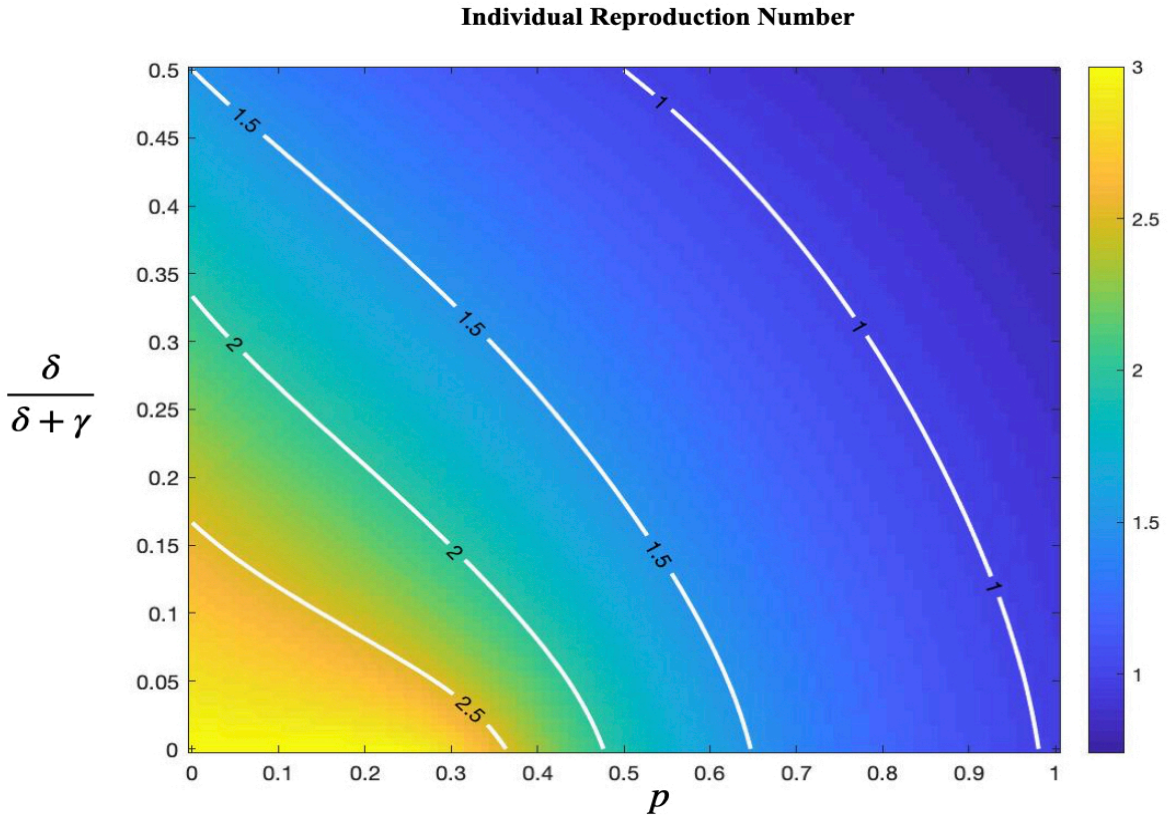
Heatmap of $R_M^{(Comp)}$ as function of $\delta/(\delta+\gamma)$ and p



Not monotonically decaying in p!!! When $\delta/(\delta+\gamma)$ is small, increasing fraction of successful CT can increase the reproduction number ...?

How about individual reproduction number?

Heatmap of $R_M^{(Ind)}$ as function of $\delta/(\delta+\gamma)$ and p



Individual reproduction number behaves as expected

Explanation: When $\delta/(\delta+\gamma)$ is small, increasing p may lead to more infected components. But the components also become smaller!

Digital CT: effectiveness compared with manual

Clearly, the higher usage π of App the more effective (true but not illustrated directly)

How does the method compare with Manual CT?

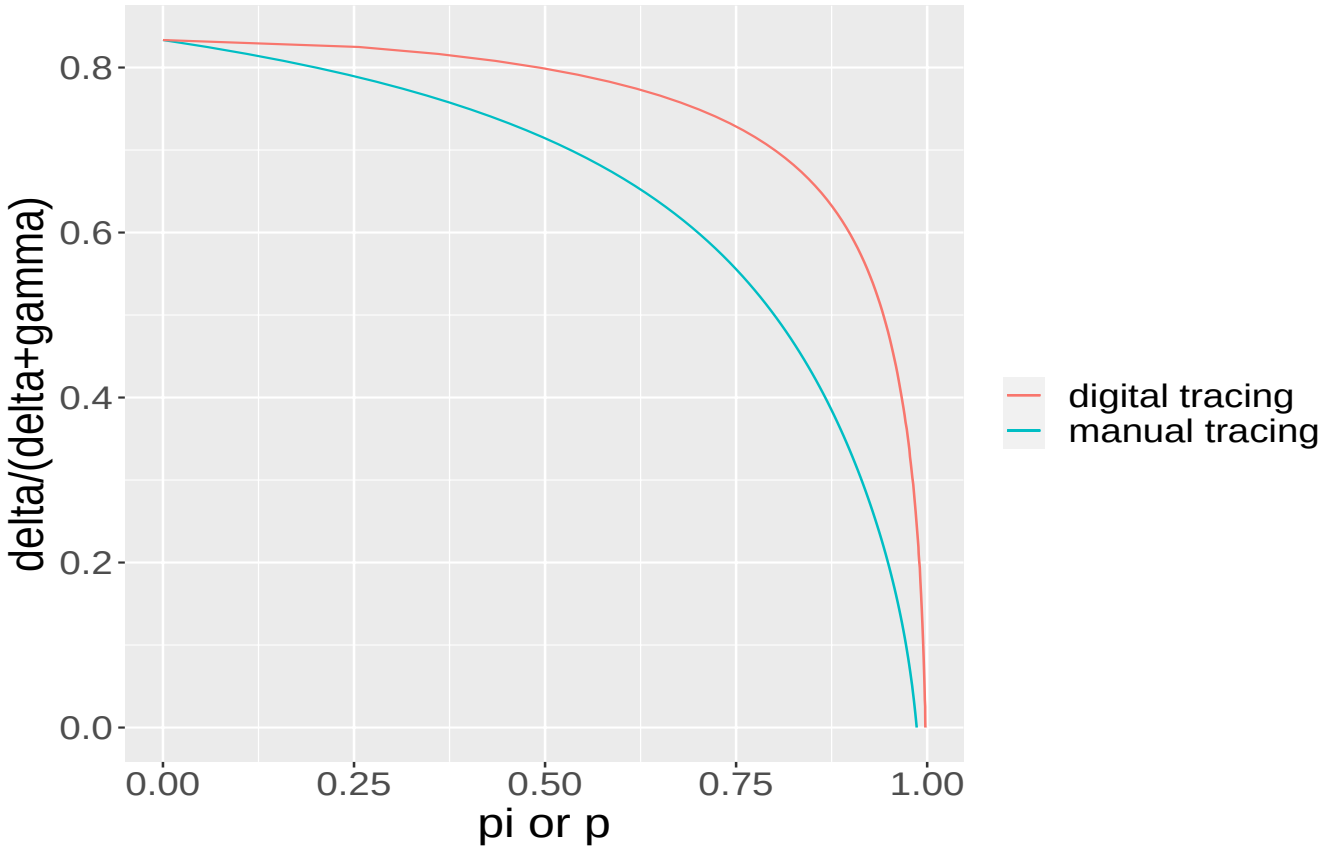
π in Digital different from p in manual

Also, the two reproduction numbers are not comparable: Manual CT has $R_M^{(Comp)}$ and $R_M^{(Ind)}$, but digital has R_D for a 2-type Br pr

Instead we compute necessary π and p, given $\delta/(\delta+\gamma)$, to become sub-critical

(Also Digital CT has in individual reproduction number $R_D^{(Ind)}$ (not discussed further))

Critical π in Digital CT and critical p in Manual CT



π has to be larger than p. Quite natural since Digital CT require both infector and infecteee to use App (prob π^2)

Closer but not identical curves if π^2 used

Manual and Digital CT: effectiveness compared with separate effects

How is the combined effect in comparison with the two separate effects?

Fix $\delta/(\delta+\gamma)$, p and π. Suppose r_M, r_D and r_{MD} denote the reduction of the three reproduction numbers: $R_M = (1-r_M)R_0$, $R_D = (1-r_D)R_0$ and $R_{MD} = (1-r_{MD})R_0$

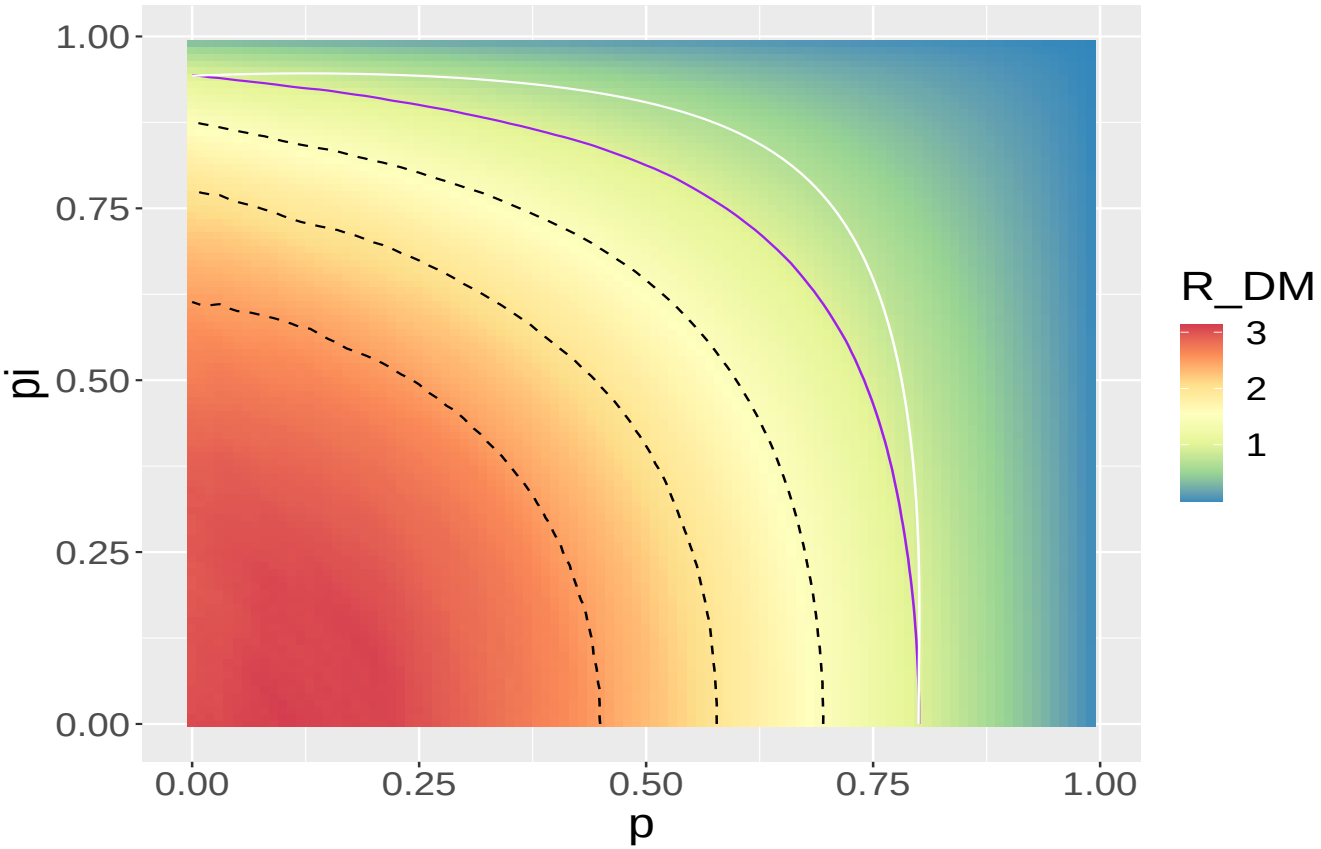
If the two effects in the combined model acted independently we would have
$(1-r_{MD}) = (1-r_M)(1-r_D)$

Problems in comparing different type of reproduction numbers ...

Next slide we plot critical combinations of (p,π) for which R_{MD} equals 1, and corresponding values for which $(1-r_M)(1-r_D)R_0$ equals 1

Critical (π, p)-curves for which $R_{DM} = 1$ and $(1 - r_M)(1 - r_D)R_0 = 1$

Purple curve: $R_{DM} = 1$, White curve: $(1 - r_M)(1 - r_D)R_0 = 1$



The combined model has better effect than if they acted independently!

Conclusions and extensions

Main conclusions:

– The models for Manual, Digital and combined CT could be approximated by different Branching processes

– The reproduction numbers are not for the original individuals, so harder to interpret and compare

– For the M and D model individual reproduction numbers can be derived (and are more sensible)

– The MD model has better effect than if the two CT acted independently: Manual CT shortens infectious periods also for Digital and vice versa

Ongoing work:

Add delay between being diagnosed and successful manual CT, and

Add social network with higher infection rates

Price to pay: no iterative CT

Limiting Branching process is continuous type

Thanks for your attention!

References

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