COVID-19-Outbreak Response combining E-health, Serolomics, Modelling, Artificial Intelligence and Implementation Research

WP III – Task 1	**Use mathematical modelling for estimating completeness of reporting and effectiveness of contact tracing and other interventions for the COVID-19 (RIVM)**
Deliverable D3.1	**Report**
Title of Deliverable:	**Report on model analysis of effectiveness of contact tracing for reducing case numbers (RIVM) (M36)**
Author:	**RIVM**

Authors:

Mirjam E. Kretzschmar[1,2], Mart L. Stein[1], Yannick Helms[1]

Affiliations:

[1]Centre for Infectious Disease Control (Cib), National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands.

[2]Julius Centre for Health Sciences and Primary Care, Utrecht University, Utrecht, The Netherlands.

Report on model analysis of effectiveness of contact tracing for reducing case numbers

1.   Background

Contact tracing (CT) is a core intervention in the global public health response to the SARS-CoV-2 (COVID-19) pandemic and other infectious diseases. The primary aims of CT are to identify and reach contacts of individuals with a confirmed COVID-19 infection (i.e. index cases), in order to notify them of their exposure-risk and inform them of what measures may be needed to prevent further spread of the pathogen, such as testing and quarantine. If contacts subsequently also test positive for COVID-19, they are requested to isolate for the remaining duration of their infectious period, and the CT-process is repeated, and so forth. In addition, the (epidemiological) data collected through CT are important for knowledge generation about - and surveillance of the virus.

Traditionally, CT is facilitated by public health professionals (PHPs), who work for public health services (PHS). The execution of CT may differ between countries, but typically consists of several stages:

- First, after a positive test result is communicated to PHS, a PHP interviews the index case, usually by phone, to collect epidemiologically relevant (health) data and identify individuals who have been in close physical proximity to the index case, in the *contact identification* stage
- Second, in the *contact notification stage*, a PHP notifies and informs the index case's contacts
- Third, in the *contact monitoring* stage, contacts are monitored by PHPs (e.g. through a phone call every x-number of days) to oversee their health, and to advise on – or organize adequate measures, if necessary.
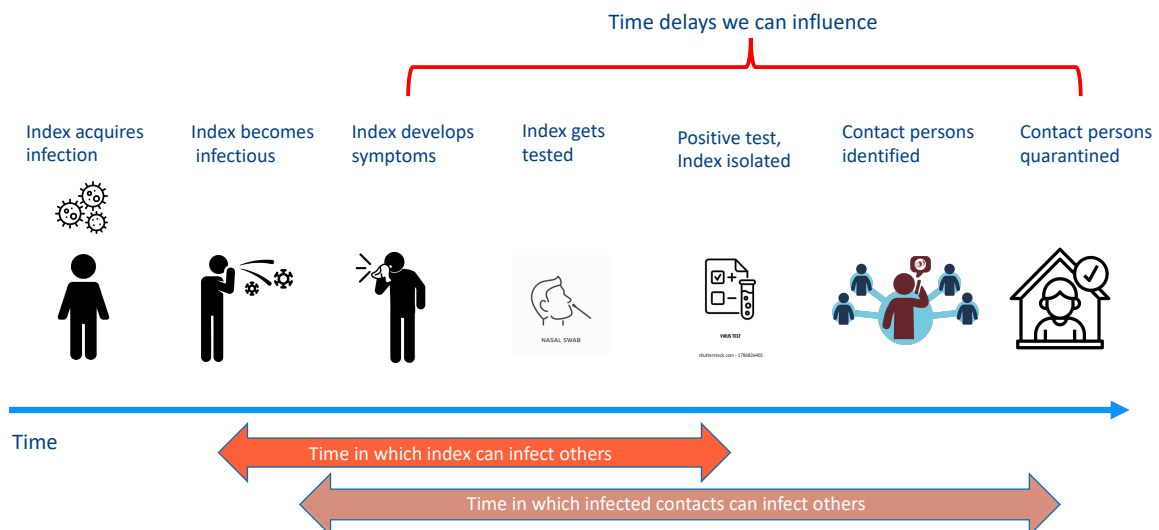

Figure 1: Steps in the contact tracing process.

However, under pandemic circumstances, with a relatively high – and increasing daily caseload, PHS may not have sufficient human resources at their disposal to effectively facilitate CT. As a consequence, PHS may have to prioritize which index cases and contacts they target, and/or stop the execution of

parts of the CT-process. This potentially makes CT less comprehensive (in the sense that less index cases and contacts are reached and informed) and/or slower, allowing more infections to remain undetected and spread further through the population.

To evaluate the effectiveness of contact tracing for COVID-19 using mathematical modelling, we needed to formalize the process of contact tracing and distinguish and quantify the steps of the process. We then aimed to assess whether and how contact tracing can stop epidemic spreading or how much it can contribute to slow down epidemic growth.

2.   Modelling the contact tracing process

Contact tracing is a process that contains several key steps that have to be taken by various actors involved in the process (Figure 1). The chain of events starts with an index person, who acquires infection. Some time passes until the index case becomes infectious for others (latent period) and/or symptoms of infection occur (incubation period). The latent period can be shorter than the incubation period, which means that contact persons can be infected before the index case shows any symptoms. At symptom onset the index case may get tested and receive a positive test result sometime later. With a positive test result the diagnosis is established and contact tracing can start. It will take some time until contact persons are identified and notified, after which they go into quarantine or isolation to avoid further transmission of the pathogen. For some pathogens, treatment or vaccination of the contact persons is the aim.
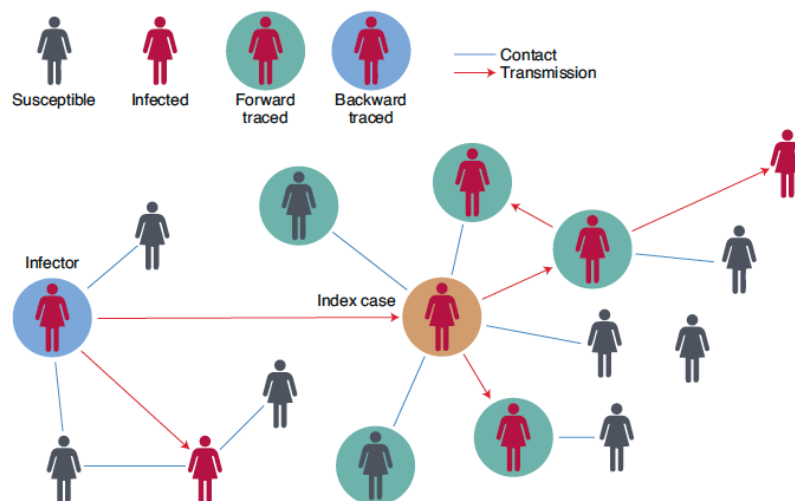

Figure 2: Contact tracing individuals interacting on a graph (Müller & Kretzschmar 2021b). In a simplified model, individuals are represented as either susceptible (black) or infected (red) and the edges between them represent contact without transmission (blue) or directed transmission of the disease (red). Contacts can be either forward traced (green circles), backward traced (blue circle) or both, and this choice can affect the efficacy of the approach.

In tracing contacts, one can distinguish forward and backward tracing (see figure 2). Forward tracing refers to tracing those contacts, who have been infected by the index case, while backward tracing refers to finding the source of infection of the index case. In reality, the two are not always distinguishable, because we do not always know the direction of transmission. However, for an analysis using mathematical models, the distinction is important. Tracing the source of the infection

of an index case is in general less effective, because more time has passed since the source person was infected and became infectious. Tracing this contact may therefore come too late to prevent onward transmission. It is different, if tracing the source leads to discovery of a larger transmission cluster, which can then be stopped. In an outbreak where super-spreaders play a role, such source tracing may be effective. Considering the various steps in the process, it is clear that the effectiveness of contact tracing depends on behavioural factors and on the characteristics of the infectious disease, in particular, on infectivity of the index case, onset of symptoms, the duration of latent period, incubation and infectious periods, and the type of contact needed for transmission.

In the CORESMA project we focussed on CT for COVID-19 infections. In the early phase of the pandemic, before physical distancing measures were implemented and long before vaccines became available, contact tracing was the most important measure available to public health professionals. There was hope that the spread of the new virus SARS-CoV2 could potentially be stopped by tracing infected contacts and isolating them. It was in this time period that the proposal for the CORESMA project was written and therefore contact tracing took a prominent place in the proposal. The importance of contact tracing for COVID-19 control changed in the course of the explosive spread of the pandemic worldwide, and we needed to extend the workplan of work package 3 to also consider other interventions. In this report, we describe the work performed on the effectiveness of contact tracing and some related work that discusses the role of contact tracing for other infectious diseases and within larger intervention strategies.

3.   Impact of delays on effectiveness of contact tracing

In our first study (Kretzschmar et al. 2020) we performed a systematic analysis of the various steps required in the process of testing and diagnosing an index case as well as tracing and isolating possible secondary cases of the index case (Figure 3). We then used a stochastic transmission model which makes a distinction between close contacts (e.g. household members) and casual contacts to assess which steps and (possible) delays are crucial in determining the effectiveness of CT for COVID-19. We evaluated how delays and the level of contact tracing coverage influence the effective reproduction number, and how fast CT needs to be to keep the reproduction number below 1. We also analyzed what proportion of onward transmission can be prevented for short delays and high contact tracing coverage. Assuming that around 40% of transmission occurs before symptom onset, we found that keeping the time between symptom onset and testing and isolation of an index case short (<3 days) is imperative for a successful CT. This implies that the process leading from symptom onset to receiving a positive test should be minimized by providing sufficient and easily accessible testing facilities. In addition, reducing contact-tracing delays also helps to keep the reproduction number below 1.

The mathematical model was adapted from an earlier model designed to assess the impact of contact tracing and vaccination in a hypothetical smallpox outbreak (Kretzschmar et al. 2004). We modified the model to include knowledge on the incubation period distribution and infectivity profile of SARS-CoV2, contact data as collected before the SARS-CoV2 pandemic and during the first lockdown in the Netherlands, and information about contact tracing strategies as communicated to us by public health professionals.

We considered a baseline scenario in which a certain amount of background measures were assumed to be in place, such that the effective reproduction number is reduced to a value of 1.2. Then various contact tracing strategies were implemented, and conventional contact tracing (defined by duration of delays, see Table 1) was compared to more rapid contact tracing, possibly achieved by the use of contact tracing apps. In the best possible case, using app-based contact tracing on a large scale, we assumed that delays between testing of the index case and informing and isolating infected contacts

could be reduced to less than 1 day. In that case, the effective reproduction number can be reduced to well below 1, which implies that the spread of the virus can be controlled (Table 1 and Figure 4). We computed by what percentage the reproduction number is reduced by various contact tracing strategies (CTS) and found that mobile app-based strategies are more effective than conventional contact tracing due to the reduction of the delay between positive test of the index case and isolation of infected contacts (Figure 5A). These results are largely independent of the value of the basic reproduction number without CTS.
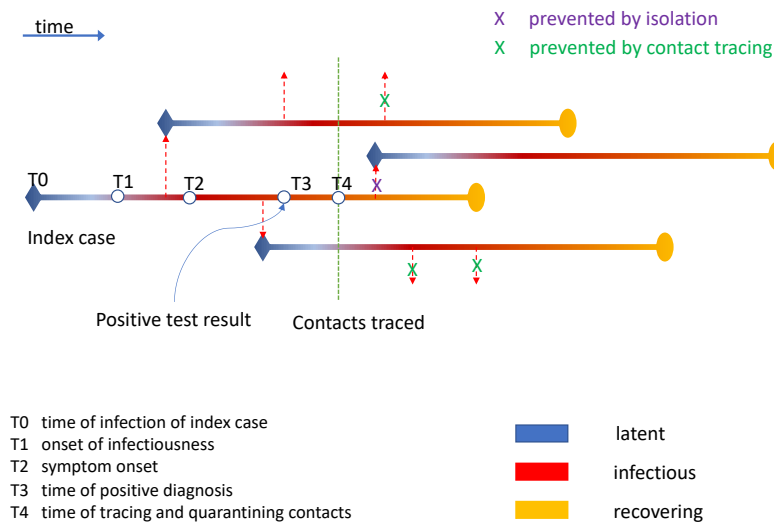

Figure 3: Steps in the contact tracing process (Kretzschmar et al. 2020).

We also tested the robustness of these results by implementing individual reproduction numbers, which took into account heterogeneity between individuals in how many secondary cases are produced. We assessed the distributions of number of secondary cases per index case for the above-described scenarios. We found that use of mobile contact tracing apps could reduce the mean individual reproduction numbers to below 1, but outliers of larger reproduction numbers remained (Figure 5B).

Table 1: Comparison Conventional CT and Mobile app CT

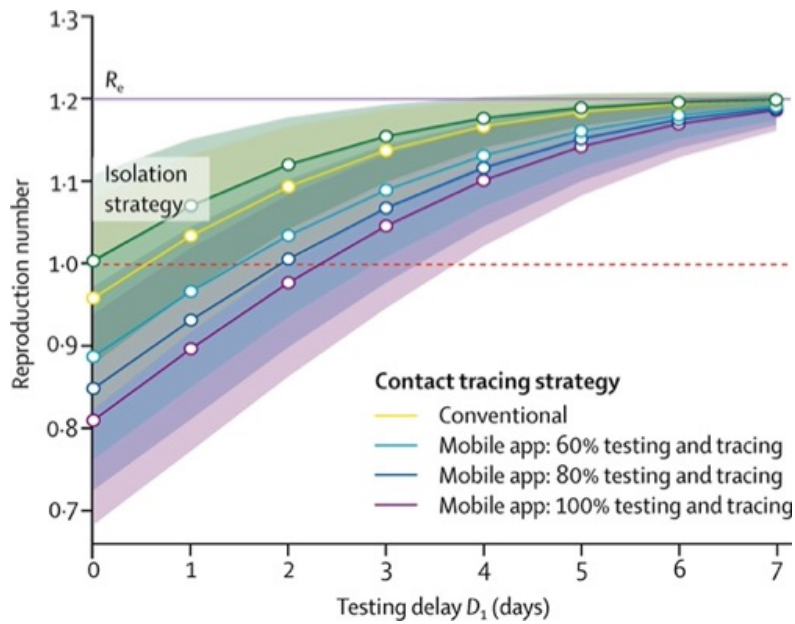|	Conventional CT	Mobile app CT
Testing coverage	80%	20%, 40%, 60%, 80%, 100%
Testing delay (D_1), assuming immediate isolation when testing positive	4 days	0 day
Time to trace close contacts (D_2)	3 days	0 day
Time to trace other contacts, assuming testing and isolation of those who test positive	3 days	0 day
Tracing coverage close contacts	80%	20%, 40%, 60%, 80%, 100%
Tracing coverage casual contacts	50%	20%, 40%, 60%, 80%, 100%
Time traced back	7 days	7 days

Figure 4: Comparison of a conventional and mobile app CTS. For parameter values, see table 1. We assumed that testing coverage is 80% for the conventional CTS and 60%, 80%, and 100% for the mobile app CTS. For mobile app CTS it is assumed that the tracing coverage equals the testing rate, i.e. it is 60%, 80%, and 100%, respectively. Expected reproduction numbers are shown as a function of testing delay D1.
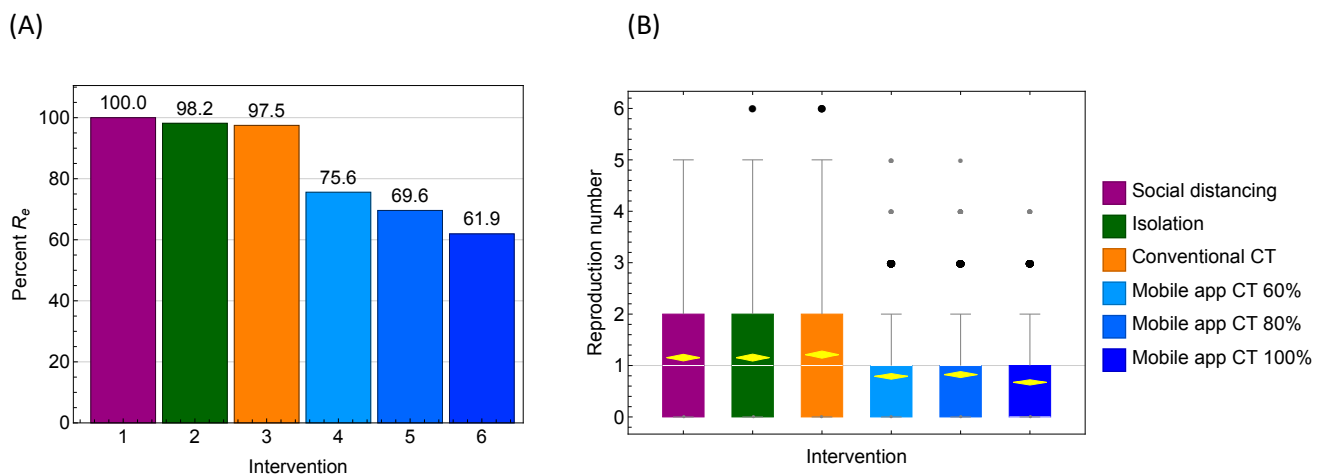
(A)   (B)

Figure 5: The reduction of the effective reproduction number for various CTS. (A) The reproduction number with CTS, Rcts, is shown as a percentage of the reproduction number where only social distancing is implemented (Re). For the isolation scenario and conventional tracing scenario we assumed that there is a delay of 4 days between symptom onset and isolation of the index case. For the mobile app CTS, testing delay was assumed to be 0 days. Testing coverage was assumed to be 80% in the isolation and conventional CT scenarios; app use prevalence was assumed to be 60%, 80%, and 100% in the mobile app CTS. (B) Distributions of individual reproduction numbers for 1000 individuals and the same scenarios as in (A).

Our analyses highlighted that a contact tracing strategy (CTS) can only contribute to control of COVID-19 if it can be organized in a way that time delays in the process from symptom onset to

isolation of the index case and his/her contacts are very short. In the best case, CTS can prevent around 80% of onward infections, but if delays are more than a few days, the impact of CTS on epidemic control becomes small. The process of conventional contact tracing should be reviewed and streamlined, while mobile app technology in the future may offer a tool for gaining speed in the process. Reducing delay in testing subjects for SARS-CoV-2 should be a key objective of CT.

4.   Contact tracing and physical distancing measures

In a related study (Kretzschmar et al. 2021) we evaluated whether and under which conditions containment of SARSCoV-2 is possible by contact tracing and isolation in settings with various levels of social distancing. In particular, we analysed in more detail by how much household and non-household contacts need to be reduced by physical distancing measures in addition to contact tracing to reduce the overall effective reproduction number to below 1. As our model distinguished between household and non-household contacts, differential effects on these contacts could be investigated. Social distancing may affect the numbers of the two types of contacts differently, for example while work and school contacts are reduced, household contacts may remain unchanged. The model allows for an explicit calculation of the basic and effective reproduction numbers, and of exponential growth rates and doubling times. Our findings indicated that if the proportion of asymptomatic infections in the model is larger than 30%, contact tracing and isolation cannot achieve containment for a basic reproduction number R_0 of 2.5. Achieving containment by social distancing requires a reduction of numbers of non-household contacts by around 90%. If containment is not possible, at least a reduction of epidemic growth rate and an increase in doubling time may be possible. We showed for various parameter combinations how growth rates can be reduced and doubling times increased by contact tracing. Depending on the realized level of contact reduction, tracing and isolation of only household contacts, or of household and non-household contacts are necessary to reduce the effective reproduction number to below 1. In a situation with social distancing, contact tracing can act synergistically to tip the scale toward containment. These measures can therefore be a tool for controlling COVID-19 epidemics as part of an exit strategy from lock-down measures or for preventing secondary waves of COVID-19. Detailed results are shown in figures 6 and 7.
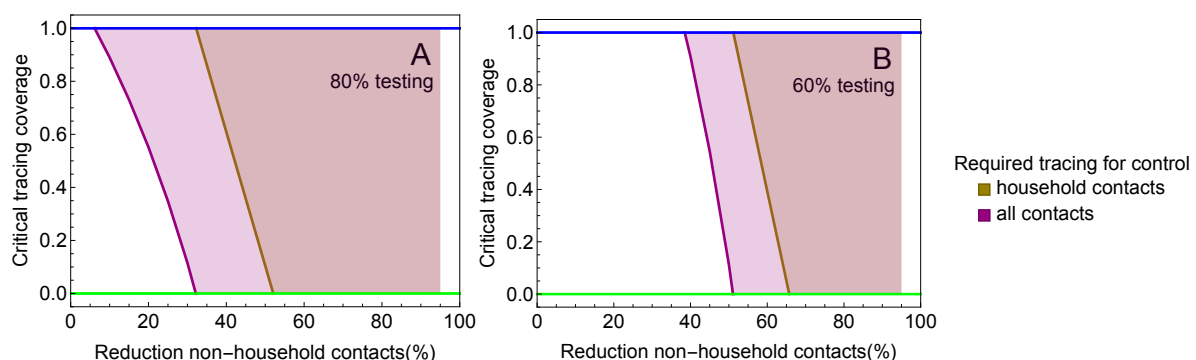

Figure 6: The critical tracing coverage in a population with social distancing and R_0 = 2.5. In the brown shaded area tracing of household contacts is sufficient, in the purple area a certain level of non-household contacts have to be traced in addition to 100% of household contacts. (A) 80% testing coverage; (B) 60% testing coverage.
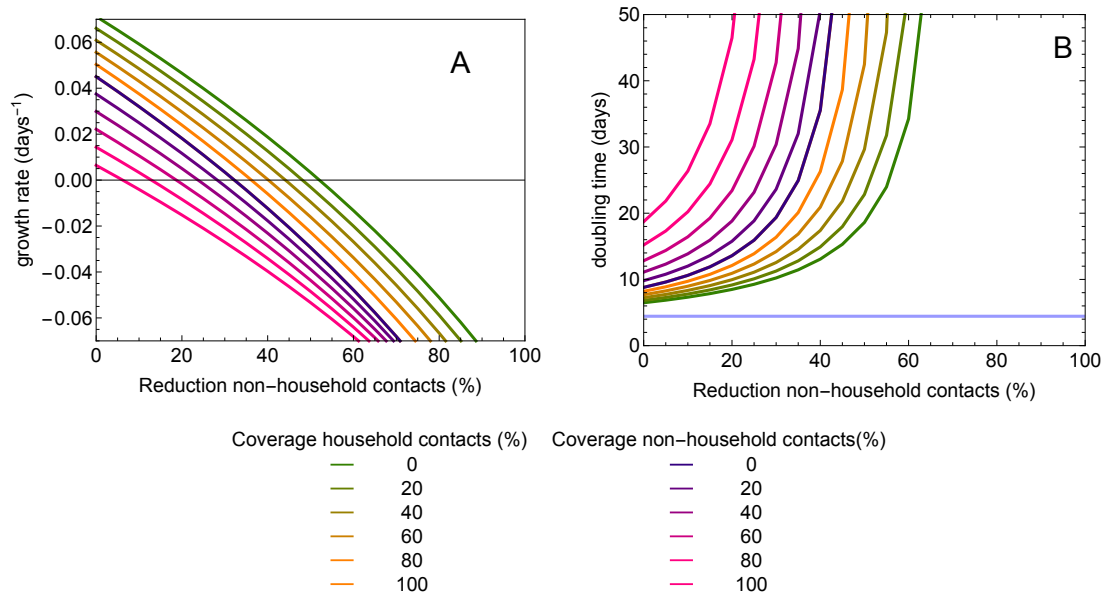
Figure 7: The exponential growth rate (A) and epidemic doubling time (B) as a function of the level of social distancing and coverage of contact tracing. Testing coverage is set to 80%. The colors represent different coverage levels of contact tracing. For the lines colored from green to yellow only household contacts are traced and isolated; for the lines colored from blue to magenta, 100% of household contacts are traced and an additional fraction of non-household contacts are traced and isolated.

In conclusion, our results show that in populations where social distancing is implemented, isolation and contact tracing can play an essential role in gaining control of the COVID-19 epidemic. On their own, none of these strategies are able to contain COVID-19 for realistic parameter settings, but in a combined strategy they can just tip the balance toward containment. These insights provide guidance for policy makers, who will have to decide when and how to implement or release severe lock-down or social distancing measures, and whether additional contact tracing and isolation is then a feasible alternative to keep a resurging epidemic at bay.

5.   Use of digital tools for contact tracing

As stated above, for effective contact tracing of SARS-CoV2, it is important to improve the speed of the process and reduce delays as far as possible. One possible way to achieve that is to make use of digital tools, be it contact tracing apps or other digital solutions. As contact tracing apps using Bluetooth or GPS functionalities were fraught with privacy issues and therefore were not downloaded and used by a sufficient proportion of the population (Jenniskens et al. 2021 and 2022; Ter Haar et al. 2024), we also investigated the applicability of other types of digital tools. In particular, we performed qualitative and quantitative studies among public health professionals in the Netherlands, to assess their attitudes towards using digital tools for contact tracing, where index patients and their contacts are asked to perform some of the tasks of the CT process. Results of these studies have been published (Helms et al. 2022; Helms et al. 2024), and were described in details in Deliverable 3.3.

Unfortunately, it has not been possible yet to obtain actual data from SORMAS of the contact tracing process, so it was not possible to use this type of data for parameterizing our model. We are still working on a data set obtained by public health services in Germany (see Heinsohn et al. 2022 for a description of the data), which we plan to use for model parameterization and for evaluation the

possible impact of contact tracing in a particular situation. However, getting data sharing agreements in place has taken a very long time and has delayed the data analysis such that the modelling could not be performed within the project duration of CORESMA.

6. Estimating parameters on contact tracing from data

In collaboration with colleagues at the Technical University of Munich, we worked on an analysis of contact tracing in a tree-like contact graph. The model was used to derive a method for estimating the proportion of infected contacts found by tracing from contact tracing data (Okolie et al. 2023). In particular, we adopted a maximum-likelihood framework to estimate parameters of a stochastic susceptible–infected–recovered (SIR) model with contact tracing on a rooted random tree. Given the number of traced persons per index case, our estimator allows to determine the degree distribution of the random tree as well as the tracing probability. As usually not all infected contact persons are found via contact tracing, this estimation gives an indication of the coverage of contact tracing. To keep things simple and stable, we developed an approximation suited for realistic situations (contract tracing probability small, or the probability for the detection of index cases small).

In this approximation, the only epidemiological parameter entering the estimator is the basic reproduction number R_0. The estimator was tested in a simulation study and was furthermore applied to COVID-19 contact tracing data that we took from the literature from a study in conducted India (Figure 8). For the empirical COVID-19 data, we compared different degree distributions and performed a sensitivity analysis. We found that particularly a power-law and a negative binomial degree distribution fitted the data well and that the tracing probability was rather large (Figure 9). The sensitivity analysis showed no strong dependency of the estimates on the reproduction number.
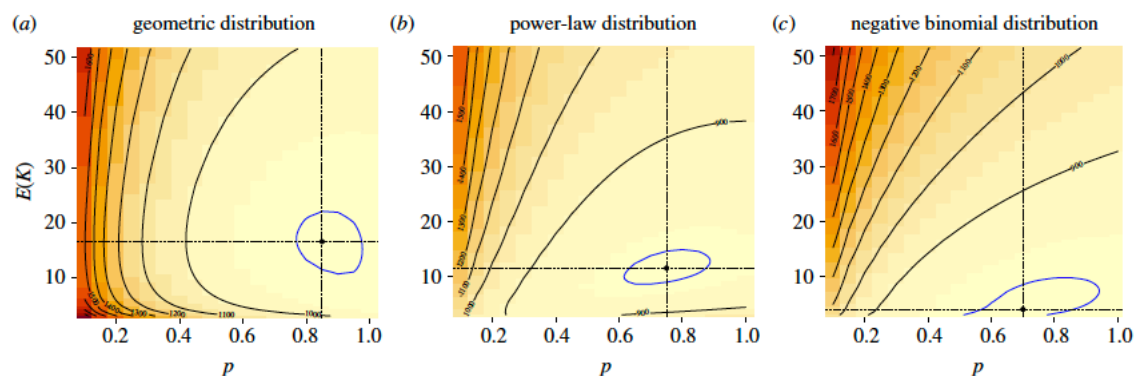

Figure 8: These contour plots show the estimates for parameter p describing the fraction of infected contacts found, and E(K), which is the mean number of contacts per index case. The estimates are shown for three different assumed distributions of number of contacts. The negative binomial distribution was the best fitting model for the given data set.

This modelling study and findings highlight the importance of selecting appropriate models for estimating tracing probabilities and local contact structures in real-world scenarios. These estimates demonstrated the effectiveness of our graph-based method in capturing key epidemic parameters within heterogeneous and age-structured contact networks. The estimated degree ranges for the negative binomial and power-law distributions fell within plausible ranges found in the literature, supporting the validity of our approach in comparison to other studies that have examined contact tracing data. Furthermore, sensitivity analysis on the estimated parameters w.r.t. R_0 for the power-

law and negative binomial distributions showed limited sensitivity to the choice of R_0. These results provide valuable insights into estimating key epidemiological and intervention parameters with greater confidence, enabling more effective public health strategies and interventions. All in all, our research contributes to the ongoing development of improved parameter estimation techniques in graph-based models for infectious disease dynamics. By utilizing a graph-based approach and building upon the methods of previous studies, we have demonstrated the value of incorporating contact graph structures, such as trees, for a more accurate representation of contact patterns and infectious disease dynamics. The results of our analysis highlight the need to consider heterogeneity in individual-level contact networks when designing and evaluating contact tracing strategies.
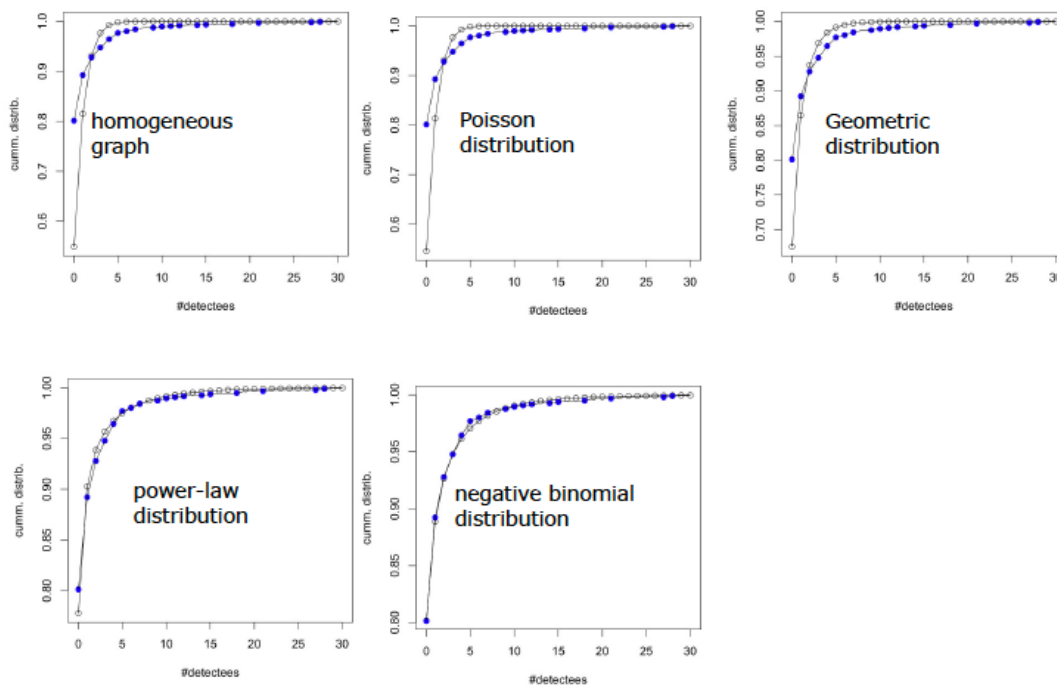

Figure 9: Cumulative distribution from data (blue dots) compared to cumulative theoretical distributions from the model (black circles) for the number of contact persons found per index case. The panels describe different assumptions about the shape of the distribution of numbers of contacts per individual in the contact graph.

7. Modelling contact tracing for other infectious diseases

Our work on modelling CT for COVID-19 built on earlier work for contact tracing for smallpox (Kretzschmar et al. 2004) and more broadly on the literature on modelling contact tracing, which has been growing over the last decades. To discuss models for contact tracing in the context of the challenges of COVID-19, we wrote a perspective paper, in which we discussed the various questions and challenges that arise in modelling contact tracing, and modelling CT for COVID-19 in particular (Müller & Kretzschmar 2021a).

First, different approaches for modelling contact tracing were discussed, namely

1. Simulation models that directly simulate individuals in large populations;
2. Pair approximation models that are extensions of mean field models incorporating information about correlations of pairs of individuals;

3. Stochastic and deterministic models that are based on a rigorous analysis of a simple branching process modelling CT.

Each of these approaches have advantages and disadvantages. While simulation models (mostly individual based simulation models) are most suitable to include realistic details of the CT process and population heterogeneity, they require very detailed data for parameterization, which is often not available. Also, working with individual based models is time consuming, because many simulation runs have to be performed to assess the variability and robustness of results. Pair approximation models offer the possibility to derive analytic results to some extent, by making assumptions on the higher order correlations between pair of individuals. Including more population structure and heterogeneity into these models is however difficult and quickly leads to very large systems of equations. The third type of models analyzing branching processes are very useful for understanding early phases of an outbreak or small outbreaks, in which there are no saturation effects. They are only valid during the exponential growth phase of an epidemic.

Challenges arising in modelling contact tracing can be classified into intrinsic challenges that are due to the complex nature of the dynamical process, and challenges due to the practical realization and data availability. Concerning the former, we conclude that the contact tracing process is difficult to model, because it is shaped by the contact networks in a population, which can be very heterogeneous, clustered, or otherwise inhomogeneous. Also, contact tracing is in essence a spreading process which follows the spreading process of the infection in the contact network, so it also depends strongly on characteristics of the infectious disease in question, e.g., on the generation time distribution, but also detection and transmission probabilities. Local network structure and correlations play a role, and therefore contact tracing cannot be modelled by a conventional SIR modelling framework.

Concerning the practical implementation, new opportunities and challenges have arisen due to the possibility of using digital tools for contact tracing, but also through the increasing availability of genetic sequence data, which may allow reconstruction of transmission routes in outbreaks and can help assessing the effectiveness of contact tracing and assist the interpretation of data collected by contact tracing. While simulation models can help with designing and evaluation contact tracing strategies for public health, more analytic models are also needed for better understanding of the impact of correlations and heterogeneities (e.g. superspreaders) on the effectiveness of contact tracing.

Based on our perspective paper, we were invited to write a commentary in Nature Physics (Müller & Kretzschmar, 2021b) on a modelling study that looked into the effectiveness of backward and forward tracing (Kojaku et al. 2021).

8.   Contact tracing as part of larger intervention packages

As mentioned above, during the COVID-19 pandemic, contact tracing was only one of many intervention measures that were implemented in various combined strategies (such as school closures, physical distancing measures, mask wearing). As the importance of contact tracing declined with increasing case numbers, more and more attention switched to the effectiveness of other measures. One problem with contact tracing was that capacities of public health services were limited and therefore they could not manage tracing of all contacts. With increasing case numbers, the process of contact tracing was scaled down and became less effective. Besides exploring the possible use of digital tools for contact tracing, we also performed modelling studies in which contact tracing was only one of several intervention options to evaluate which combination of strategies would be most advantageous.

In Pham et al (2021) contact tracing was one of the measures modelled using an individual based model describing spread of COVID-19 in a hospital setting among patients and health care workers. One of the conclusions was that regular screening and contact tracing of health care workers are effective interventions but critically depend on the sensitivity of the diagnostic test used.

In 2020 we participated in an international programme organized by the Isaac Newton Institute for Mathematical Sciences (Cambridge, UK, https://www.newton.ac.uk) on "Infectious Dynamics of Pandemics: Mathematical and statistical challenges in understanding the dynamics of infectious disease pandemics", where we presented our work on contact tracing to an international audience. Based on the programme, a working group was formed to discuss and review challenges for modelling interventions for future pandemics. Based on our experiences as modellers during the COVID-19 pandemic, we summarized what we have learned and which challenges still need to be overcome for better use of modelling interventions during future pandemics (Kretzschmar et al. 2022). There is a complex relationship between data collection, parameter estimation and model fitting, and design of interventions (Figure 10), which needs to be optimized for better public health policy support.
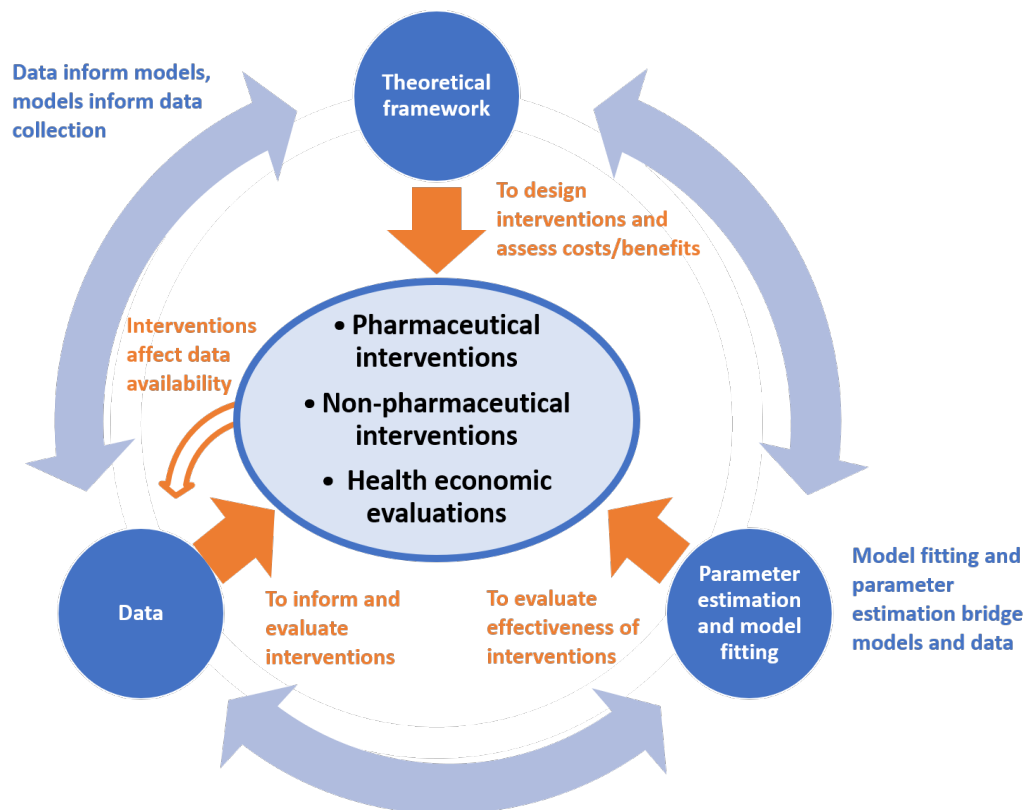

Figure 10: Relationships between interventions and methodological aspects.

In the context of comparing interventions, one of the main advantages of contact tracing and cluster investigation is that they are directed specifically to individuals who are more likely to have been exposed to the infection. However, capturing the specific contact network and the test, trace, and isolation (TTI) process over such a network constitutes a key modelling challenge for mathematical epidemiology (Müller and Kretzschmar, 2021a), particularly because realistic networks and clustering due to social settings (e.g., households and workplaces) are difficult to measure and describe

mathematically (see also Marion et al. 2022), but strongly affect the effectiveness of TTI (House and Keeling, 2010). Different tracing policies (e.g., forward tracing of the secondary cases or backward tracing of the potential infector of a confirmed case) require different modelling considerations (Müller et al. 2000; Kojaku et al. 2021), although in practice it is often impossible to identify the direction of the infection between two confirmed cases. Backward/forward tracing often becomes indistinguishable from outbreak investigation, which focuses on transmission in particular environments rather than between specific individuals, bringing in additional complexities in terms of modelling possibly overlapping clustered networks and superspreading events. TTI serves a dual role as a transmission surveillance and control tool, finding cases among harder-to-reach groups, and informing interventions which break transmission chains. The balance between these roles can vary greatly.

TTI typically requires an extensive infrastructure able to identify infected cases and swiftly search and isolate as many of their contacts as possible. In the case of fast epidemics, this translates into important limitations, for instance in terms of the maximal number of individuals that can be reached and isolated every day and unavoidable delays along the process, which strongly influence the effectiveness of the intervention (Kretzschmar et al. 2020; Contreras et al. 2021; Scarabel et al. 2021). Modelling the real impact of these limitations is often extremely challenging, but at the same time fundamental to evaluate the effectiveness of TTI and identify what aspects can be improved. In LMIC, the lack of resources such as diagnostic tests and isolation facilities adds additional limitations to the effectiveness of TTI. Recently smartphone apps for digital contact tracing have been developed, which are aimed at mitigating these limitations, while introducing further challenges connected with a realistic modelling of the app uptake and mechanisms (Ferretti et al. 2020). The effectiveness of TTI needs to be balanced with the societal impact of quarantine, which depends on its duration and effectiveness in preventing onward transmission, hence models should not only quantify the transmission potential prevented by isolation, but also the expected isolation burden of both infected and healthy individuals (Ashcroft et al. 2021; Kucharski et al. 2020).

Overall, we can conclude that work on contact tracing for COVID-19 in the CORESMA project has contributed to the efforts of the scientific community to better understand the effectiveness of CT, to advise policy makers on the use of (digital) CT also in combination with other interventions, and to help prepare us for future pandemics.

9.   References

Ashcroft P, Lehtinen S, Angst DC, Low N, Bonhoeffer S. Quantifying the impact of quarantine duration on COVID-19 transmission. Elife. 2021 Feb 5;10:e63704.

Contreras S, Dehning J, Loidolt M, Zierenberg J, Spitzner FP, Urrea-Quintero JH, Mohr SB, Wilczek M, Wibral M, Priesemann V. The challenges of containing SARS-CoV-2 via test-trace-and-isolate. Nat Commun 12: 378.

Ferretti L, Wymant C, Kendall M, Zhao L, Nurtay A, Abeler-Dörner L, Parker M, Bonsall D, Fraser C. Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. Science. 2020 May 8;368(6491):eabb6936.

Heinsohn T, Lange B, Vanella P, Rodiah I, Glöckner S, Joachim A, Becker D, Brändle T, Dhein S, Ehehalt S, Fries M. Infection and transmission risks of COVID-19 in schools and their contribution to population infections in Germany: A retrospective observational study using nationwide and regional health and education agency notification data. Plos Medicine. 2022 Dec 20;19(12):e1003913.

Helms YB, Stein ML, Hamdiui N, van der Meer A, Baron R, Eilers R, Crutzen R, Kretzschmar ME, Timen A. Dutch public health professionals' perspectives and needs regarding citizen involvement in COVID-19 contact tracing through digital support tools: an exploratory qualitative study. BMC Health Services Research. 2022 Dec;22(1):1-7.

Helms YB, Stein ML, Hamdiui N, van der Meer A Ferreira JA, Crutzen R, Timen A, Kretzschmar ME. Determinants of Dutch public health professionals' intention to use digital contact tracing support tools: a cross-sectional online questionnaire study. PLoS Digital Health 2024; in press.

House T, Keeling MJ. The impact of contact tracing in clustered populations. PLoS Computational Biology. 2010 Mar 26;6(3):e1000721.

Jenniskens K, Bootsma MC, Damen JA, Oerbekke MS, Vernooij RW, Spijker R, Moons KG, Kretzschmar ME, Hooft L. Effectiveness of contact tracing apps for SARS-CoV-2: a rapid systematic review. BMJ Open. 2021 Jul 1;11(7):e050519.

Jenniskens K, Bootsma MC, Damen JA, Ghannad M, Oerbekke MS, Vernooij RW, Spijker R, Moons KG, Kretzschmar ME, Hooft L. Effectiveness of contact tracing apps for SARS-CoV-2: an updated systematic review. F1000 Research. 2022 May 12;11:515.

Kojaku S, Hébert-Dufresne L, Mones E, Lehmann S, Ahn YY. The effectiveness of backward contact tracing in networks. Nature Physics. 2021 May;17(5):652-8.

Kretzschmar M, van den Hof S, Wallinga J, van Wijngaarden J. Ring vaccination and smallpox control. Emerg Infect Dis 2004; 10(5): 832-41.

Kretzschmar ME, Rozhnova G, Bootsma MC, van Boven M, van de Wijgert JH, Bonten MJ. Impact of delays on effectiveness of contact tracing strategies for COVID-19: a modelling study. The Lancet Public Health. 2020 Aug 1;5(8):e452-9.

Kretzschmar ME, Rozhnova G, Van Boven M. Isolation and contact tracing can tip the scale to containment of COVID-19 in populations with social distancing. Frontiers in Physics. 2021 Feb 10;8:677.

Kretzschmar ME, Ashby B, Fearon E, Overton CE, Panovska-Griffiths J, Pellis L, Quaife M, Rozhnova G, Scarabel F, Stage HB, Swallow B. Challenges for modelling interventions for future pandemics. Epidemics. 2022 Mar 1;38:100546.

Kucharski AJ, Klepac P, Conlan AJ, Kissler SM, Tang ML, Fry H, Gog JR, Edmunds WJ, Emery JC, Medley G, Munday JD. Effectiveness of isolation, testing, contact tracing, and physical distancing on reducing transmission of SARS-CoV-2 in different settings: a mathematical modelling study. The Lancet Infectious Diseases. 2020 Oct 1;20(10):1151-60.

Marion G, Hadley L, Isham V, Mollison D, Panovska-Griffiths J, Pellis L, Tomba GS, Scarabel F, Swallow B, Trapman P, Villela D. Modelling: understanding pandemics and how to control them. Epidemics. 2022 Jun 1;39:100588.

Müller J, Kretzschmar M, Dietz K. Contact tracing in stochastic and deterministic epidemic models. Mathematical Biosciences. 2000 Mar 1;164(1):39-64.

Müller J, Kretzschmar M. Contact tracing–old models and new challenges. Infectious Disease Modelling. 2021a Jan 1;6:222-31.

Müller J, Kretzschmar M. Forward thinking on backward tracing. Nature Physics. 2021b May;17(5):555-6.

Okolie A, Müller J, Kretzschmar M. Parameter estimation for contact tracing in graph-based models. Journal of the Royal Society Interface. 2023 Nov 22;20(208):20230409.

Pham TM, Tahir H, van de Wijgert JH, Van der Roest BR, Ellerbroek P, Bonten MJ, Bootsma MC, Kretzschmar ME. Interventions to control nosocomial transmission of SARS-CoV-2: a modelling study. BMC medicine. 2021 Dec;19(1):1-6.

Scarabel F, Pellis L, Ogden NH, Wu J. A renewal equation model to assess roles and limitations of contact tracing for disease outbreak control. Royal Society Open Science. 2021 Apr 7;8(4):202091.

Ter Haar W, Bodriesz J, Venekamp RP, Schuit E, van den Hof S, Ebbers W, Kretzschmar M, Kluytmans J, Moons C, Schim van der Loeff M, Matser A, van de Wijgert JH. The epidemiological impact of digital and manual contact tracing on the SARS-CoV-2 epidemic in the Netherlands: empirical evidence. PLoS Digital Health 2024; in press.