

Assessing the efficacy of contact tracing apps to help mitigate the COVID-19 pandemic: an agent-based approach

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Résumé – Pendant la pandémie COVID-19, de nombreuses stratégies ont été testées par différents gouvernements pour atténuer et contrôler la dynamique épidémique et ses impacts, notamment sanitaires, sociaux et économiques. Dans cet article, nous évaluons la performance des applications de recherche de contacts sur la dynamique épidémique en comparant plusieurs scénarios réalistes appliqués à une société artificielle. En utilisant la modélisation basée sur les agents et l'exploration numérique, nous soulignons les possibilités et les limites des applications de *contact tracing* et l'importance de les combiner avec d'autres mesures de contrôle, en particulier l'isolement et le dépistage.

Abstract – During the COVID-19 pandemic, many strategies were tested by different governments to mitigate and control the epidemic dynamic and its impacts, namely sanitary, social and economic. In this paper we evaluate the performance of contact tracing applications on epidemic dynamic by comparing several realistic scenarios applied to an artificial society. Using agent-based modelling and numeric exploration, we highlight the possibilities and limits of contact tracing apps and the importance of combining them with other control measures, especially isolation and testing.

1 Introduction

As soon as the COVID-19 pandemic rose, contact tracing applications were identified as important tools to mitigate and control the course of the pandemic spread. Designed to break a patient chain of transmission by identifying close contacts, these applications have been developed, implemented and tested in various countries. However, despite their apparent logic and evident contribution to rapid identification and breaking of the chains of transmission of the virus, especially when compared with traditional investigative work, it is still not very clear today whether contact tracing applications really make a difference. One of the main difficulties, when assessing their effective impact on virus propagation, relies indeed on the conjunction of multiple actions (social distance, masks, hygiene, confinement...).

We propose here an alternative approach based on the computational exploration of artificial societies. The main idea is to generate from scratch a synthetic population and then introduce COVID-19, with processes and parameters calibrated from empirical data and knowledge. Once this virtual epidemic world is created, contact tracing is added and different scenarios are compared.

2 Contact tracing : how and why ?

Contact tracing relies on a simple principle : a symptomatic patient is identified and reported to the relevant health authority for a specific country, which then launches an investigation to try to find the contacts that this person has had during the last days, with the aim of warning them and offering them a test before they infect other people. Classic interview and investigation based contact tracing can be very effective to discover potentially infected people that are known to the initially identified person : friends, family, work relations. It will be less efficient to discover people this person has spent time with in an enclosed space, but without knowing them : in the transports, in shops, restaurants, concerts. For those settings a mobile app that can somehow detect other wielders of the app could help accomplish this investigative work.

The question we will seek more precisely to answer regarding such an app is the following : what would be its impact on the epidemic in terms of controlling the disease - especially concerning two specific outcomes, epidemic peak on the one hand and limitation of the population to be isolated on the other hand ?

3 Related works

3.1 Contact tracing

Numerous East-Asian countries have led the world in the efficiency of their fight against the COVID-19 epidemics, possibly because of their earlier confrontations with other respiratory diseases like swine flu, SARS-CoV-1 or H1N1 flu, or the African Ebola crisis that motivated Taiwan to build an efficient contact tracing system as early as 2017 [8]. It is therefore no surprise that contact tracing has been evaluated very early in the COVID-19, in China or the UK. [6] proposed a mathematical model to test how effective this tactic could be depending on different epidemics parameters. Although some values for these were later to be proven false as understanding of the disease progressed – they overestimated the transmission by fomites and underestimated asymptomatic transmission – their conclusion were fairly pessimistic as for the use of tracing as the sole measure for controlling the epidemics : 80% of symptomatic individual had to be quickly traced to obtain control.

3.2 Mathematical model of contact tracing apps

From this necessity to trace infected individual appeared quickly the necessity of assisting classic contact inquiries with a digital app. This software assistance would allow a recording of the people an infected individual had crossed in the previous days including those unknown to her/him, whose presence they shared for example in bars, restaurants or public transport. In one of the first and most well-known studies [4] investigated the possibilities of such a supplemental tool. Two conclusions emerge from the exploration of their analytical model : first, for a 3-day delay in notification assumed for manual contact tracing, no parameter combination leads to bringing R_0 below 1 ; second, immediate notification through a contact-tracing mobile phone app could be sufficient to stop the epidemic if used by a sufficiently high proportion of the population, who would accept an eventual quarantine. The effect of recursion in contact tracing, while being an important difference between automatic and manual tracing, could not be investigated because of the intrinsic limitations of the mathematical models. No other containment measures were investigated either.

3.3 Agent-based models of contact tracing apps

Mathematical models of infectious diseases are very widespread but, despite their increasing complexity, are not the most natural tools when the distribution of individual behaviors in the studied population is a key notion to predict the correct outcomes for a given input. They can include complex demographic components by using age-stratified matrices for example, and they can model a distribution of compliance to edicted rules among a given population, but linking these two notions is not easy – to model that for example people aged 19-29 are both more resilient to the COVID-19 and a bit less likely to follow

social distancing rules. And when even more individual characteristics modelling are needed, using agents to model the individual is more direct and efficient.

[5] describe many Agent-based models used to explore the efficiency of COVID fighting strategies, but we will focus here on two that explored more specifically contact tracing apps. [1] and [10] are both very interesting, data-intensive, ABM of the question. They use non spatialised network based representation of the agents society and a mathematical model of the evolution of the disease in an individual. [1] models three counties in the state of Washington, while [10] models the whole population of Austria. They are therefore of course dependant on the quality of the data they use, and the computational burden linked to this dimension imposes some simplifying assumptions. Their aim is to guide decision making on specific territories and they belong to the KIDS end of the spectrum of complex systems simulation [3].

Our approach is more on the KISS side of the spectrum : we want to find out the important parameters and their interactions, and to test a large combination of them. We therefore adopted an agile development cycle, with a agent-based model nimble enough for us to run 50 000 simulations a night, perform a statistical analysis in the morning, and implement bug fixes, new functionalities and simulation scenarios in the afternoon. Our approach is less data intensive and calibrated, but we believe it allows exploring the parameters and their interactions in greater depth. For example we explored the recursion aspects allowed by digital contact tracing, which was not done in previously cited works.

4 The contact tracing model by COVprehesion

In order to investigate more precisely these issues, we developed a contact tracing model within the COVprehesion initiative [2]. COVprehesion – a portmanteau of COVID and comprehension, is an initiative born in March 2020 to help the general public understand the epidemics and the measures adopted to fight it. Its motto is : one question - one model.

4.1 Mobility model

We developed an agent-based model of a simplified environment populated with a limited number of mobile individuals. The days are divided into four 6-hour segments. The first three sections are occupied by daily mobility and close social interactions : the model is calibrated for an average 10 per day and per person, after [9]. Most trips are made near home, but 20% of them are longer distances. The last part of the day is spent at home, which is shared by an average of three people. In total, 2000 people occupy this small virtual territory.

4.2 SEIR Model

In addition, we introduce a SEIR epidemic model with two possible categories of Infection : symptomatic and asymptomatic, the latter being more difficult to identify by simple medical diagnosis due to the absence of symptoms.

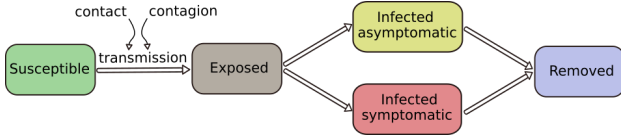


FIGURE 1 – graphic representation of the epidemic path of individuals in the SEIR model developed

At initialization, all individuals are healthy (Susceptible). A small number of Infected individuals is then injected into this initial population and the spread of the virus is simulated from the behaviors of the individuals modeled. Changes of state take place as follows and use the reference values set by the Institut Pasteur [7]

- *Susceptible* → *Exposed* : a *Susceptible* individual will become *Exposed*, in contact with an *Infected* individual, according to a probability that depends on the value of R_0 chosen and the category to which this infected individual belongs (see next point). The formula used to calculate this probability is as follows : $P(S \rightarrow E) = 1/R_0 * c * d$, with c the number of average contacts per day (fixed at around 10) and d the duration of the contagious period.
- *Exposed* → *Infected* : an individual will remain in the *Exposed* state during his incubation period (fixed here at 5 days), during which he will gradually become contagious, until becoming *Infected asymptomatic* (3 chances out of 10) or *Infected symptomatic* (7 chances out of 10). The contagiousness of a symptomatic individual is estimated from the R_0 (see previous point) and is considered to be twice that of an asymptomatic individual.
- *Infected* → *Removed* : after 14 days, an *Infected* individual is considered *Removed* and is not contagious anymore in the model.

4.3 App contact model

At every time step, an agent A equipped with the contact tracing app records all the agents also equipped in its immediate surroundings, along with the date of the contact. If A is later tested positive, and if it accepts to take measures accordingly (as described in 4.4), it will notify all the agents in its recorded contacts list down to a given date – 5 days ago in the scenarios below. At the next time step, depending on the scenarios, the notified agents will either start directly the countermeasures such as self-quarantine, or get tested first. They then find themselves in the same position as the agent A. The contact network is therefore explored width-first, at a speed of all the nodes at a distance of 1 at each time step.

4.4 Scenarios

On this basis, four distinct scenarios are proposed, in a comparative perspective. We present here the main lines, their precise details will be exposed later :

- S1 “Let it go” : we do nothing, the epidemic is going on without any interference ;
- S2 “Simple isolation” : symptomatic carriers are identified (tested) and isolated with their families (understood here as people who share the same roof) ;
- S3 “Tracing and systematic isolation” : symptomatic carriers are systematically tested and those who are positive are isolated while their contacts are isolated without being tested ;
- S4 “Tracing and selective isolation” : symptomatic carriers are systematically tested and those who are positive are isolated, while their contacts (and their contacts) are tested and then isolated if the test is positive.

5 Systematic comparison of scenarios performances

In order to compare the performance of the different scenarios, we have simplified the problem by fixing the following common initial conditions :

- the population size is 2000 people ;
- 80% of trips are made near home and 20% of them are made at longer distances ;
- the number of initially contagious people is equal to 10 (i.e. 0.5% of the population) ;
- the R_0 set at initialization takes on three different values : 1, 2 and 3 ;
- the duration of the incubation phase is 5 days ;
- the duration of the contagious phase after the incubation phase is set at 14 days ;
- the proportion of asymptomatic carriers is fixed at 30% ;
- the tests are available in less than 6 hours ; the tests are 95% reliable ;
- people who test positive systematically notify their contacts via the app ;
- people who test positive systematically go into isolation for 21 days and respect it scrupulously ;
- each simulation is repeated 100 times, in order to take into account the stochastic nature of the model, i.e. the presence of randomness.

Scenarios	R0	Epidemic peak		Population isolated		Non-contagious population isolated		Population tested		Total number of tests carried out
		(% total population)	(% total population)	(% total population)	(% total population)	(% total population)	(% total population)	(% total population)	(% total population)	
S1 Let it go	1	0.65	0.15							
	2	22.13	41.21							
	3	48.3	5.26							
S2 Simple isolation	1	0.75	0.15	1.58	0.65	56.67	6.83	0.4	0.1	8
	2	0.95	0.25	1.65	0.5	48.08	5.58	0.4	0.1	9
	3	1.25	0.35	1.85	0.55	43.36	3.62	0.45	0.15	10
S3 Tracing and systematic isolation	1	0.7	0.15	50.13	57.06	98.51	1.92	0.45	0.15	9
	2	0.95	0.3	59.03	43.75	98.05	3.32	0.55	0.4	11
	3	1.3	22.95	66.55	24.34	97.44	28.62	0.75	26.05	16
S4 Tracing and selective isolation	1	0.65	0.15	0.55	0.25	0	0	1.5	1.8	33
	2	0.85	0.45	1	1.3	0	0	3.1	5.93	78.5
	3	38.48	49.06	61.43	64.51	0	0	65.25	72.45	1972.5

FIGURE 2 – Final comparison of the performances of the four scenarios S1, S2, S3 and S4 for the main indicators selected.

The detailed experiments are described on the COVprehen website, in French. Figure 2 is a table of the main information we can retrieve from these experiments. The values are estimated over 100 replications of each simulation. The inter-quartile range (IQR) gives an indication of the variability of the results around the median. In the end, when $R_0 = 2$, scenario S4 “Tracing and selective isolation” obtains the same results in terms of controlling the epidemic peak as scenario S2 “Simple isolation” (the observed difference in median is not statistically significant, according to the Mann-Whitney non-parametric U-test). On the other hand, the observed difference of around 0.65% (1.65% for S2 against 1% for S4) in terms of the median isolated population, between the scenarios S2 and S4, is statistically significant. This difference must therefore be evaluated in the context of a population much larger than our 2000 individuals modeled. Thus, applied to a population of 67 million and all other things being equal, the scenario S4 would lead - in the case of $R_0 = 2$ - to isolate 670 000 people, all contagious, in the model where scenario S2 would isolate more than one million (1 105 500), of which nearly half (530 640) would not be contagious. And this, even with a low coverage rate (less than 20%). This success is however only valid for $R_0 = 2$, the proportion of isolated population literally exploding in scenario S4 when $R_0 = 3$, unlike scenario S2 which shows great robustness in its performance.

6 Discussion

We have voluntarily placed ourselves in an ideal framework in order to set a reference basis as well as objectives to be achieved in terms of fight against the epidemic :

- RT-PCR tests are available in number and in less than 6 hours ;
- RT-PCR tests are 95% reliable ;
- people who test positive systematically notify their contacts via the app ;
- people for whom isolation is recommended strictly observe this instruction.

We used fairly optimistic hypotheses (fast available tests, total compliance to isolation) to give the contact tracing app a good chance to show its interest. We have tested that these input values give similar results when they vary for less than 10%, depending on the R_0 and the scenario. This exploration of sensitivity should be explored in further depth.

Our computer-based experiments suggest on the one hand that a tracing application, like contact tracing in general, is only efficient when the epidemics is relatively under control, with a limited $R(t)$ of less than 3, and on the other hand that it should be closely associated with screening strategies and very rigorous and effective isolation. It is at this price only that it would be likely to present an added value with regard to a more classic strategy of screening and isolation of symptomatic carriers and their families (a strategy which is moreover very parsimonious and effective in terms of isolation of the population), mainly

through its ability to isolate only contagious people. A relative gain on epidemic control when $R(t)$ is already not too high (for example thanks to other measures) is in line with other results from the literature. Finer contact tracing with testing allows for an interesting balance of fighting the epidemics without excessive force, hence improving its social and therefore political acceptance.

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