

Towards Deep Digital Contact Tracing: Opportunities and Challenges

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Abstract—During the COVID-19 pandemic, digital contact tracing using mobile devices has been widely explored, with many proposals from academia and industry highlighting the benefits and challenges. Most approaches use Bluetooth Low Energy (BLE) signals to learn and trace close contacts among users. However, tracing only these contacts can mask the risk of virus exposure in scenarios with low detection rates. To address this issue, we propose fostering users to exchange information beyond close contacts, particularly about prior ‘deep’ contacts that may have transmitted the virus. This presents new opportunities for controlling the spread of the virus but also poses challenges that require further investigation. We provide directions for addressing these challenges based on our recent work developing a technological solution using this approach.

Digital contact tracing (DCT) has received significant attention during the COVID-19 pandemic because of its potential to surpass traditional contact tracing methods [1]. Unlike manual contact tracing, which relies on individuals to recall their interactions, DCT utilizes mobile phone technology to record encounters among people. Users can easily participate by installing an app on their smartphone and exchanging information with other users, typically via Bluetooth Low Energy (BLE). The app can then register close contacts, which, in combination with positive COVID-19 test results, can be used to analyze the risk of virus exposure for app users. As a result, DCT has the potential to significantly improve the speed, accuracy, privacy, and scalability of contact tracing efforts in the fight against COVID-19 and other infectious diseases [2].

In contrast to the traditional procedure, which reactively investigates close contacts only after an infected case, DCT proactively collects all close contacts to

analyze their risk for each positive case. This helps to stop virus transmission much earlier than traditional contact tracing as it avoids typical delays of interviewing and notifying individuals. However, DCT must collect, store and manage more data than the traditional contact tracing scheme. So far, most of the effort in designing DCT solutions has focused on preserving user privacy, resulting mainly in two architectural approaches [3]. One approach involves *centralized* solutions, where users must share their contact data with a trusted central authority that can notify them if any risks are detected. However, this approach risks compromising individuals’ privacy, as the central authority may access sensitive information such as location, personal details, and social activity. The other approach involves *distributed* solutions that store contact history locally on the user’s device. This approach can help protect app users’ privacy by avoiding disclosing sensitive information. However, to assess the risk of virus exposure in a decentralized scheme, data from infected users shall be accessed to contrast with contact history stored inside the phone; while in centralized systems, data from infected users are always kept in the authority domain. While differ-

ent solutions have been proposed for centralized and distributed systems to protect privacy, limitations and risks cannot be entirely avoided.

Risk analysis beyond close contacts

While user privacy has been a major focus in developing digital contact tracing (DCT) solutions, the importance of risk analysis has not received as much attention. Currently, most DCT solutions only consider close contacts for risk assessment, similar to the traditional contact tracing process. This means that to determine the potential contagion risk, a positive test has to be associated with each close contact. However, the accuracy of this approach is significantly impacted when asymptomatic cases are present or when individuals are reluctant to be tested, leading to a low detection rate [4]. To address this issue, tracing could consider contacts beyond close ones. These contacts, which we refer to as *deep contacts*, are not detected as close contacts but can be identified by tracing a chain of previous contacts. A deep contact can be understood as an individual at the end of a chain of close contacts. By tracing deep contacts, it may be possible to identify potential infection paths that wouldn't be found by only considering direct contacts [5]. In particular, this enables the analysis of individuals' risk even when their close contacts are all asymptomatic and may not have been tested. Asymptomatic case detection can also be improved as they can be more aware of being infected by analyzing contagion paths that include deep contacts, encouraging getting diagnosed even without symptoms. Besides, since DCT impact is highest when the testing delay is low [6]; tracing deep contacts enables access to diagnoses even before a close contact is tested; hence, speeding up the risk assessment process. To ensure effective risk analysis in DCT, it becomes important to consider both close and deep contacts, especially when the detection rate is low.

Tracing deep contacts is done in traditional contact tracing and recently proposed DCT solutions, although recursively. In practice, close contacts of an infected case are expected to get tested, and if positive, a new tracing iteration is started to identify its close contacts. Even in scenarios where detection rates are high, tracing contagion paths toward all potentially infected persons can require several iterations, each of which introduces delays given to the need to test close contacts at each step. The slower the process, the more likely the spread of the virus. Tracing deep contacts opens new opportunities to analyze contagion risk and challenges in properly exploiting contact data collected by mobile devices.

A straightforward approach for tracing deep contacts would be storing close contacts from all users in a single database to establish contagion paths among users who have not acknowledged any close contact between them. This goes beyond what centralized architectures currently propose, which isolates close contacts from users instead of enabling any connection among them. This aims to protect user privacy, mainly regarding social activity, but also to make the system scalable as it may become too complex to store and process. Besides, DCT proposals based on ephemeral identifiers impose limitations on the capability of relating close contacts as close contacts from the same user may not be feasible to associate. As a result, a different strategy is required to trace deep contacts.

This paper introduces and discusses a novel DCT approach to enable close and deep contact tracing using mobile devices. This is achieved by extending the mobile app's capabilities to share relevant contacts via BLE towards users from which virus transmission is feasible. As a result, each device collects all relevant contacts that, given a positive test, can be used to assess the contagion risk better. In other words, each user shares with others all contacts from which a contagion path can be considered feasible, given the specific factors required for the virus to spread. These contacts include close ones, learned by detecting the presence of other users, and deep ones, learned instead by the information shared by other users during an encounter.

From early detection to prevention

Early notification of contagion risk is among the most relevant opportunities this approach can offer. Users may get risk notifications even before close contacts are tested positive. Indeed, the infection period for COVID-19 typically begins before any symptom is present. This means that eventually, an individual may be warned of potential risks. At the same time, their close contacts are also notified of the risk, which helps to isolate all the contacts in the chain that may be affected. In particular, this could enable being notified as soon as possible, likely before starting the infection period.

Besides speed, our proposal can also offer the capability to monitor the spread of the virus. Like radar, risk notifications could indicate the distance of contacts from the positive cases. This could help to take preventive measures to avoid infection as much as possible. Even if no risk is found, the amount of contacts from which infection is feasible also helps to adopt a preventive behavior. In practice, the fewer contacts are identified, the more protected the indi-

vidual is, as fewer chains of contagion are possible. Recently, a proactive contact tracing scheme has been proposed [7] in which *risk messages* that indicate the likelihood of contagion are exchanged among users during an encounter. These messages could consider results from deep contact tracing analysis.

While individual behavior modification based on app notifications is important, our proposal can provide real-time and granular data to central authorities for government planning and triage during a pandemic. By tracking direct and deep contacts, the app can provide a more comprehensive picture of potential contagion dynamics. This can result in more effective and targeted interventions, such as prioritizing testing and resources in areas with a high density of deep contacts or implementing localized lockdowns to prevent further spread. The deep contact approach thus can significantly enhance the value of contact tracing apps, transforming them from individual risk assessment tools into crucial resources for strategic pandemic response.

However, tracing deep contacts requires considering the contagion risk beyond close contacts, which needs to consider transmission factors such as infection periods. This could make our proposal extremely complex and expensive for mobile devices. Our main contribution relates to modeling deep contact tracing in a distributed fashion such that each device can assess the risk of contagion and decide on the relevant information to be shared at each encounter. In particular, our proposal aims to reduce data exchange and preserve privacy by storing all contact data locally. In the following sections, we consider a general contagion risk model and describe the algorithmic and technological requirements for mobile devices to implement it efficiently.

CONTAGION MODEL

In the context of tracing social interactions, an encounter between individuals can be characterized by several attributes, among which the participants' identities and the event's timing can be considered the minimum required. Additional factors could encompass the distance between the individuals, and the type of environment (indoor [11] or outdoor), among others [10]. For the sake of simplicity, we model encounters involving only two individuals, which can also cover the case of more individuals by considering multiple simultaneous encounters. With this approach, we can represent the history of social interactions within a community up to a given time, denoted as t , using an undirected multigraph where nodes represent

individuals and edges encounters. Note that since multiple encounters between the same individuals can occur at different time intervals, multiple edges can be associated with the same pair of nodes.

In Figure 1, we show the encounters between 6 individuals, f, g, h, i, j and k , by indicating a start time t_s and end time t_e for each encounter during an interval of 20 time units. The figure also includes two encounter graphs captured at different moments: $t = 18$ and $t = 20$, which we will use in this section to discuss how contagion risk can be modelled.

Contagion chain

Given an encounter graph, we can define a path among two individuals as a sequence of nodes connected by edges. Infection can spread through this path if associated encounters satisfy contagion time constraints, a notion we coin *contagion chain*. An elemental constraint is that an encounter's start time t_s precedes subsequent encounters' end time $t'_e \geq t_s$, ensuring the events' temporal order. Even both $f \rightarrow h \rightarrow i$ and $i \rightarrow h \rightarrow f$ can be considered paths on the encounter graph from Figure 1, only the former satisfies the temporal constraint. An important parameter of our model is T_c , the maximum time between when an individual becomes infected and stops being contagious. This period may depend on their vaccination history, previous infections, and other factors. For COVID-19, T_c is usually estimated as 14 days. In a contagion chain, the time between an encounter's end time and the next one's start time must be less than T_c . This ensures that if an individual is infected in the first timestamp, he is still contagious in the second timestamp, passing the infection to the subsequent individual in the chain. In infectious disease dynamics, the interval between when an individual is infected and becomes infectious is called *latent period*. In our model, this interval is incorporated as parameter T_l , whose value is typically 2 days for COVID-19, and plays an important role in the containment of the infection risk. Finally, in a contagion chain the time between an encounter's end time and the next one's start time must be equal or greater than T_l .

In Figure 1 (b), we show examples of contagion chains. Assuming $T_c = 5$, and for simplicity, $T_l = 0$, there exist a chain from g to i (blue) and one from g to j (green). Each encounter is itself a contagion chain of unit length. Besides, notice that there is no possible chain from f to i because the end time of the encounter between f and h is too far away from the start time of any encounters between h and i .

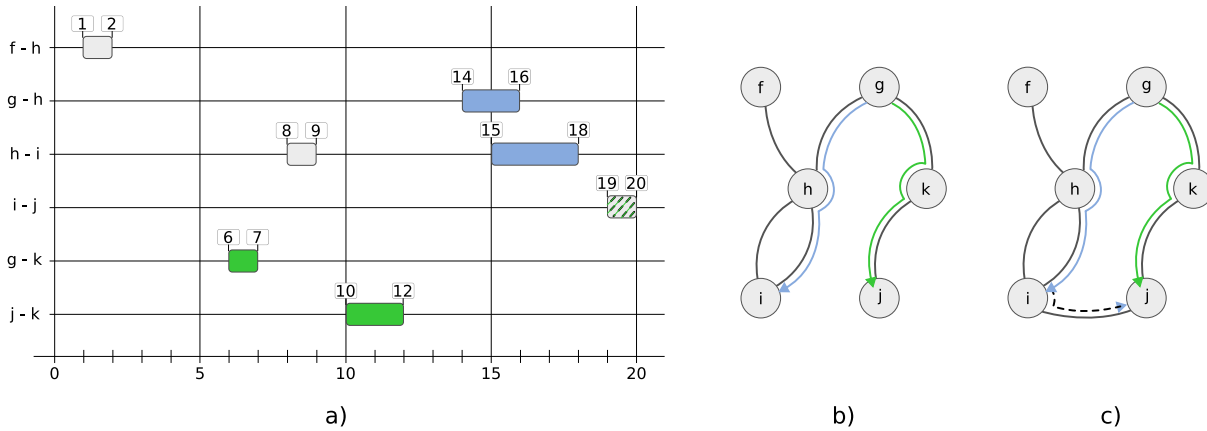


FIGURE 1. (a) Encounters between pairs of individuals during 20 time units, (b) encounter graph up to instant 18, (c) up to instant 20.

Contagion risk

We define two classes of contagion chains: *confirmed* and *active* chains. Both classes are valid at specific moments in time. A chain can become confirmed with the availability of new diagnoses. A chain can stop being active with the mere passage of time.

A *confirmed* chain begins with an infected individual and continues with a sequence of hosts that may be infected without knowing it. These hosts certainly could spread the infection. For a chain to be confirmed at instant t , it is enough that there is a positive diagnosis available at t for the individual at the beginning of the chain. The diagnostic must overlap temporally with the start time of the first encounter of the chain.

A chain is *active* when it can still be extended by incorporating new encounters, thus reaching new individuals. For a chain to be active at instant t , the time elapsed between the ending time of the chain's last encounter and t must be less than T_c .

Thus, we can establish that the last individual of an active and confirmed chain is at *risk of contagion*. Since the chain is confirmed, there is a particular possibility that the infection has reached the individual. If true, the individual is still infected and contagious because the chain is active. In turn, while the chain remains active, a new encounter would indicate the new participant is at risk of contagion. This way, the contagion risk spreads from a diagnosed individual to other increasingly distant individuals.

We assume the existence of a set of diagnoses containing all available positive diagnoses up to the instant t . Each diagnosis of the form (i, d_s, d_e) indicates the interval, from d_s to d_e , in which infected individual i is contagious, and satisfies $d_e - d_s \leq T_c$. Recalling the

encounters of Figure 1 (b): if there exists a diagnosis $(g, 10, 15)$, then h and i are at risk of contagion. Since the encounter between g and k is previous, the green chain does not involve an infection spread. However, at instant 20 (Figure 1 (c)), once the encounter between i and j begins, the chain from g is extended (in dots), putting j at risk.

The model presented so far is not intended to calculate the contagion risk effectively. It is impractical and insecure to depend on the availability of complete and centralized information on the encounters of all the individuals in a community. But, the centralization of diagnoses may be reasonable as it is information protected by a health authority. Indeed, while information is expected to be used for population well-being, centralizing encounters data threatens individual privacy. Such a database could become prohibitively large and a target of attack. A violation of its security could have severe consequences. However, the presented characterization allows us to define precisely what we understand by the risk of contagion and the information necessary to compute it. We will use this model to determine the scope of what we can compute in a more concise and distributed model while considering data volume, privacy, and security concerns.

A MODEL FOR DEEP CONTACTS

By analyzing the notion of contagion risk on an encounter graph, we can discover three key factors that allow us to design a distributed model for assessing the infection spread:

- 1) The contagion risk for a particular individual in a given time t depends on the contagion chains

reaching them.

- 2) A contagion chain is determined by the individuals on both ends and the time restrictions of the encounters of the chain; hence, data from other individuals of the chain are not necessary.
- 3) Contagion chains become irrelevant over time depending on whether individuals at the origin have a positive diagnosis.

We can exploit these factors to define a model where individuals only track information relevant to their risk.

The first step is to move to a more compact and unstructured representation. We replace the notion of *encounter* with that of *contact* between i and j , representing a chain of contagion from j to i . We leverage the explicit start timestamp of the first link and the ending timestamp of the last link in the chain. Also, we incorporate the length of the chain as the *depth* of the contact, distinguishing *close* from *deep* contacts, with depth equal to 1 and depth greater than 1, respectively.

An individual only has to be aware of their close and deep contacts to determine the possibility of infection. Thus, the notion of *contact* allows us to move from a centralized and structured global repository of information like the encounters graph to a local unstructured one for each individual. However, the amount of information required could scale significantly. Each final sub-chain in a chain of contagion is, by definition, a chain of contagion. Therefore, each participant in a chain reaching i defines a contact of i .

Recall the example of Figure 1 (b). For i , chain beginning at g is represented as the contact $(g, 14, 18, 2)$. The first encounter with h is represented as $(h, 8, 9, 1)$, and the second as $(h, 15, 18, 1)$.

Contact computation

The main idea of a distributed model is that an individual can compute their contacts by recording the close contact with any other individual and from the contacts that the individual had with third parties. In a scheme where i and j keep an account of their contacts and can communicate them to each other, the management of contacts of i comprises three activities:

- 1) To determine and register the occurrence of the encounter with j .
- 2) To determine and transmit relevant contacts to j .
- 3) To derive own (deep) contacts from the contacts provided by j .

The detection of encounters and the communication aspects are outside the description of this model since they depend on the implementation technology. We will present some of its details later. According to

the listed activities, the computation of contacts of i during their encounter with j is carried out as follows.

The encounter registration does not present major challenges once the technical aspects are resolved. After determining the start time t_s and ending time t_e of the encounter, and the identity of the participant j , i registers the close contact $(j, t_s, t_e, 1)$.

Regarding the information that must be transmitted, notice that notions of an active and confirmed chain of contagion extend directly to notions of active and confirmed contact. Thus, active and confirmed contacts of i determine their risk of being infected. During the encounter with j , all the active contacts of i , which satisfy the timing constraint imposed by the latent period, become active contacts of j . Therefore, i must transmit every active and confirmed contact (f, t'_s, t'_e, n) to j as long as $t_s - t'_e \geq T_l$.

However, just transmitting these contacts is insufficient. There is a period between an individual suspect being infected (e.g., due to the appearance of symptoms or having had an encounter with a confirmed case) and the test is performed, and the result is obtained. Fortunately, it is reasonable to assume that there is a limit to the time between an individual becoming infected and when the respective positive diagnosis is available. We encode this limit as a parameter of the model, named T_d . This parameter helps us to delimit the contacts with individuals who do not have a positive diagnosis but can still receive it, representing a risk if it happens. For the case of COVID-19, we can estimate T_d as 6 days, considering 5 days for the appearance of symptoms plus one day for the test [8], [9]. For instance, while i and j encounter at t_s , there may be an ongoing analysis that determines in the future a diagnosis (h, d_s, d_e) for some previous contact (h, t''_s, t''_e, m) of i , with $d_s \leq t''_s$ and $d_e \geq t''_e$. If $t_s - t''_e \leq T_d$, contact information about h must be transmitted to j even if their diagnosis is unavailable.

With respect to how to derive deep contacts from the received information, when i receives a contact (k, t'''_s, t'''_e, l) from j during the encounter ending at t_e , they only need to appropriately update timing and depth components, registering $(k, t'''_s, t_e, l + 1)$ as their contact.

Let's examine the encounter between i and j according to Figure 1 (c). Assuming $T_c = 5$, $T_d = 4$ and a positive diagnosis $(g, 10, 15)$, at instant 19 i transmit to j contacts $(g, 14, 18, 2)$ since it is active and confirmed, and $(h, 15, 18, 1)$ since it is active and $19 - 15 \leq T_d$. However, contact $(h, 6, 7, 1)$ is not transmitted because it is inactive. In response, j registers contacts $(g, 14, 20, 3)$ and $(h, 15, 20, 2)$ respectively.

Finally, recall that the determination of *relevant*

contacts, i.e., those contacts that must be transmitted, only depends on the availability of diagnosis and time restrictions. Thus, individuals can manage their contacts over time by registering encounters with others, getting relevant contacts from them, and deleting irrelevant ones. Moreover, at any instant t , an individual will have received all active and confirmed contacts at t , either having received them as already confirmed or as contacts who obtained their confirmation after the reception. Therefore, the risk of contagion can be assessed using an individual's own contacts in the same way as can be determined from the complete encounters graph.

Equivalent contacts

There may exist situations where an individual will receive multiple *similar* contacts, matching the participant at the origin and the start time. Such situations can originate from multiple paths between a pair of individuals in the encounters graph and lead to considerable data circulation. Moreover, circulating data could grow indefinitely in some cases of cyclic paths.

It should be noted that the circular flow of contacts is not a problem of the model but an intrinsic characteristic of the circulation of an infection. It is perfectly plausible that an infection passes through an individual and continues a path that, at some point, returns to the same individual. In such cases, if enough time has passed, this poses a real risk to the individual, who may become re-infected.

Fortunately, from the point of view of the contagion risk, similar contacts are equivalent. From the point of view of relevance for its transmission, the most recent contact subsumes any other. Although we haven't considered it, a shorter chain implies a greater risk. Considering these aspects, individuals can merge multiple similar contacts into a unique contact integrating the most recent ending time and the shallower depth.

Obsolete contacts

Recall that a chain of contagion could be extended endlessly by new encounters as long as it remains active. This represents the possibility of infection continuing as long as those in close or deep contact with an infected individual continue having encounters with third parties. Consequently, active confirmed contacts will continue to be transmitted from individual to individual, increasing confirmed contacts circulating among the community. However, at the same time, we can speculate that the longer a confirmed chain of contagion becomes, the more likely other contacts representing the same path of infection will be confirmed. Thus, it is reasonable to establish the hypothesis that a

confirmed contact represents a risk as long as it does not become *obsolete*, i.e., its depth or the time passed since its start time does not exceed certain limits. Such limits are incorporated as model parameters, whose value should be determined by expert knowledge or by simulating the infection dynamics. During encounters, individuals avoid transmitting obsolete contacts, reducing the circulation of confirmed contacts, but maintaining an appropriate notion of infection risk.

Extensions

Duration and other characteristics of encounters In general, exposure to a certain minimum amount of a pathogen is necessary to become infected, which translates into being in contact for a certain amount of time with an infected individual. This minimum period can be incorporated as a model parameter T_m , commonly established as 15 minutes in the case of COVID-19. Thus, an individual should register contacts from an encounter only if it last longer than T_m .

Also, the encounters could be characterized more qualitatively, including the physical distance between individuals and whether it occurs indoors or outdoors. Defining a criterion for registering close contacts using such characteristics would recursively limit the circulation of deep contacts.

Negative test results Diagnosis sets could be extended to include negative test results. Such information can be used to prevent transmission of active contacts that certainly do not pose a contagion risk.

More expressive risk functions When defining the notion of contagion risk, it seems arbitrary that very deep contacts carry the same risk as close contacts. The most apparent improvement direction is moving from a binary notion to a risk scoring, considering the contact depth to weigh the risk.

In the same spirit, the number of occurrences of confirmed contacts could be incorporated. It must be taken into account that, basically, the risk is linearly proportional to the number of confirmed close contacts. However, the risk provided by deep contacts could overlap and therefore, their contribution should be carefully evaluated.

The risk function could also take a more qualitative approach. For instance, information on confirmed contacts could be arranged in some form of *heatmap*, based on their distance and number of occurrences, to analyze closeness to the pathogen. Information on non-diagnosed contacts could be added to the mix, allowing us to estimate the social bubble of individuals. Individuals could use such metrics, even in real-time, to

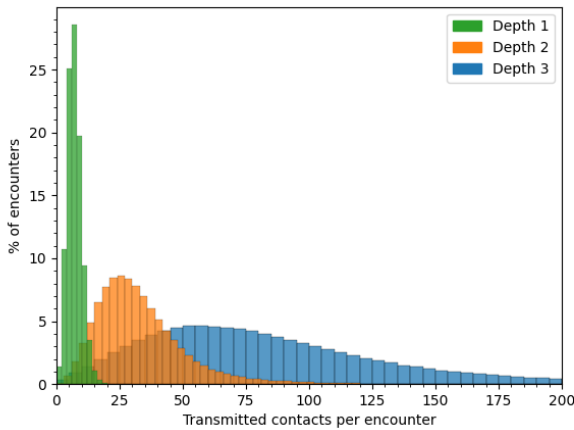


FIGURE 2. Simulation results of the contacts transmitted per encounter

understand their social dynamics and take preventive measures based on their perception of their risk and risk to third parties [12].

ANALYSIS

Estimation of transmitted data

We developed an analysis of the amount of data to be transmitted in each encounter based on the simulation of the infection dynamics in a synthetic community. As transmitted data depends on diagnoses, we replicated the probabilistic infection model of [12], which considers the probability of transmission relative to the individual's infection day and the heterogeneity in contagiousness amongst individuals. The simulated scenarios render a population density similar to that of Córdoba City (Argentina) and its periphery during 6 months, with a number of daily encounters similar to that measured experimentally in Argentina for public social interactions. We considered a positive diagnosis rate of 0.25 and an adoption rate, namely, the proportion of individuals effectively using our tracing mechanism, of 0.40. The model parameters were set as 14 days for the infection period, 2 days for the latent period, and 6 days for diagnosis time.

We analyzed the cases in which the maximum depth of the contacts to be transmitted were 1, 2, and 3. The limits for obsolescence by contact's start time were established at 12, 18, and 24 days accordingly. The histogram of the number of transmitted contacts per encounter is presented in Figure 2. The first two cases, those that *a priori* seem suitable to be used in real-life implementations, show a contained amount of

contacts feasible to be transmitted.

Proof of concept

A proof-of-concept for analyzing the technological feasibility of the proposed approach was developed. We implemented a mobile app for BLE data exchange among near users. We relied on a back-end running in the cloud for storing the diagnosis database. This mobile app was originally aimed at investigating encounter detection performance and accuracy using BLE and different machine learning models [13]. This previous activity motivated this paper's discussions about the role of mobile apps: whether they should limit to performing proximity detection or profit of the encounter to share relevant contact data (e.g., deep contacts) with near users. In this context, we extended the initial BLE protocol to carry information about close and deep contact.

Selection of technologies BLE technology is among the most appropriate technology for DCT [14]. Several works have concluded that proximity sensing using BLE is feasible even if open challenges still exist [16], [17]. It supports the advertisement of packets with payloads up to 255 bytes, with the possibility of packet chaining in case of the need to broadcast data exceeding this size. Application data transmitted in advertising mode travels in the payload of the so-called PDU (Protocol Data Unit) segment within the BLE frame. Two modes are available for this: Legacy and Extended. In Legacy, the space available for the payload is up to 31 bytes, and it is transmitted only on the primary advertising channels. Even though the reduced size, this message is visible to any BLE scanner using BLE v4.0 onwards. On the other hand, in the Extended mode, the available space is up to 255 bytes, which is more suitable for deep contact sharing but requires BLE v5.0 onwards.

Exploitation of technologies We developed the first application version to publish BLE packets using Android SDK (Level 23). We prioritized compatibility with the largest fleet of devices possible, so the app advertises in BLE's Legacy mode. Each BLE packet incorporates a 16-byte UUID (Universal Unique Identifier) into its PDU payload, ensuring the uniqueness of each device identification. We leverage half of the UUID to encode the user ID, leaving 23 bytes free in the payload to populate with more data. Advertisement of the user ID was enough since the goal of this first app was the determination of other devices' presence (i.e., *encounter detection*).

Later, we prototyped a second version of the mobile app for deep contact sharing, including an *advertiser* and a *scanner* modules. These modules are responsible for sending and receiving information about deep contacts. Advertiser and scanner modules run in parallel every certain predetermined time interval. A third component is responsible for calculating the risk of contagion using the stored information on user demand.

Contacts to be transmitted are computed once diagnosis information is received from a remote database. Relevant contacts are prioritized and encoded. Then, all available PDU payload space is used by the advertiser to share them with nearby devices, according to their priority order. The PDU payload carries both the user ID (8 bytes) and a sequence of encoded contacts, each of which includes the identity of the contact (8 bytes), the start time (4 bytes), the ending time expressed as duration (2 bytes), the depth (3 bits), the transmission power to infer distance (1 byte) and optional environment characteristics (5 bits). Thus, in Legacy mode, each packet allows only one contact to be sent, making the exchange of information very inefficient. We decided to move to Extended mode to send multiple contacts at once. This allows us to send up to 15 contacts per message every 100ms. In this mode, we can exchange hundreds of contacts during one-second intervals; hence, the cost in terms of time for data exchange is very low.

When the scanner receives a packet, it determines as a first step if collected data initiates a new encounter or if it belongs to an encounter in progress. This depends on the time elapsed since the last packet was received from the same ID. In the first case, a new close contact is registered by setting the start and ending time at the current instant. In the second case, the ending time of the ongoing contact is updated. Next, the advertised contacts are extracted, evaluated, and consolidated as deep contacts in the local database, updating timing information if necessary.

OPEN CHALLENGES

Privacy

Our contribution aims at extending risk analysis for DCT solutions, but we have not deepened on privacy preservation aspects. We acknowledge the concerns associated with using static identifiers for tracing individuals, particularly the potential for third-party tracking and the implications for the privacy of infected individuals. We claim that there are no technical impediments to using ephemeral identifiers; however, using temporal

identifiers might incur extra storage and processing effort since identifiers from the same individual cannot be distinguished. Furthermore, our approach can be adapted to identify encounters rather than individuals, enhancing privacy at the expense of larger contact identifiers. The use of static identifiers in our analysis is primarily for the purpose of our analysis of deep contact tracing, and privacy-preserving methods should be considered in the real-world implementation of deep contact tracing. The research and development of privacy-preserving enhancements are among the most relevant challenges in deep contact tracing.

Usability

Besides, app users may adopt different privacy profiles based on the data aiming to share with others at a given time. Even if the expectation is that users advertise their presence and contacts relevant for deep tracing, some users may decide to avoid sharing some data. Some may share only relevant contacts but hide their presence to protect their identity, while others could only expose their presence but keep other contact data private. As a result, different privacy profiles may coexist and interact during user encounters, leading to user negotiation schemes about what profile to use. Indeed, it is expected that users may tend to share similar data as shared with them. This opens new questions about potential negotiation protocols among users to agree on their roles at each encounter. Additionally, the effectiveness of our deep contact tracing system can be impacted by improper app use, like disabling Bluetooth or encountering a noisy channel that prevents successful data transmission. Such factors can significantly hinder coverage.

Evaluation

One of the open challenges of deep contact tracing (and DCT in general) is performance evaluation. Digital contact tracing performance strictly depends on the application adoption rate [15]. However, digital app adoption depends on convincing evidence regarding the approach's effectiveness, which is hard to obtain without broad acceptance from the community: a so-called causal loop. One means of approaching evaluation is to leverage agent-based simulation environments to assess resulting epidemic sizes [12]. The drawback is that these models abstract and simplify human behaviors, limiting the results' credibility. Indeed, these models could consider a multitude of influencing factors to model virus spread and exposure risks, such as mask-wearing, room size and ventilation, and changes in emission due to human activities like

singing, speaking, and shouting. Another alternative is to consider localized deployments (e.g., a school or a hospital) where deep digital contact tracing can be enforced and closely monitored, resulting in high tracing coverage. However, the reduced scope might also generate skepticism about the validity of the results in a broader context. In any case, creating an accurate and comprehensive simulation of the spread of infections is a highly complex task that interweaves multiple disciplines, such as epidemiology, human behavior, and computational modeling.

Storage

Storage in deep contact tracing will scale proportionally to the number of contacts. When memory resources are constrained, a contact pruning approach can be leveraged. However, defining a pruning criterion that minimizes the impact on the contagion risk analysis is not trivial. Given that each contact may result from one or more heterogeneous chained encounters, the factors contributing to risk may be present differently. For example, we may have a contact of length 1 (close contact) of 15 minutes duration in an outdoor environment and a contact of length 2 (deep contact), composed of 2 encounters of 60 minutes each, in indoor environments. The question arises regarding which contact should be kept if the information volume needs to be reduced. A different approach to the storage issue is to rely on a centralized entity where mobile devices could upload and store all their contact data. However, extra data exchange between devices and the database might impact energy efficiency and risk computation latency as deep contact data must be fetched via 4G/5G networks. In general, the storage challenge reduces to determine the optimal trade-off between memory requirements and available contact information.

Energy

Because deep contact tracing implementations must continuously run on end-users' smartphones, energy consumption must be seriously considered. This is crucial, provided that app adoption is to be promoted. One approach toward energy optimization is to impose a duty cycle to the aforementioned advertiser and scanner tasks, although at the expense of reduced contact detection and sharing efficiency. Another solution worth exploring is to reduce BLE's transmission power. However, the contact detection range will be reduced, requiring careful fine-tuning of the power levels. Again, achieving energy efficiency involves an in-depth trade-off study between contact detection and

sharing efficiency against risk assessment accuracy.

CONCLUSION

Since COVID-19, the use of mobile devices for contact tracing attracted the attention of the research community due to its capability to register close contacts automatically, without any user intervention. In this work, we proposed deep digital contact tracing as a means to collect and process not only close contacts but all contacts from which the virus may have been transmitted. This enables risk analysis even when infected close contacts have not been tested. We presented a model for contagion risk computation with multiple practical uses such as risk notifications and monitoring. Then, based on experimental experiences, we put forward concrete technical approaches to implement deep contact tracing in mobile devices. A series of open challenges comprising privacy, evaluation, storage, and energy motivates this emerging field of study.

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