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SMARTPHONE CONTACT TRACING TECHNOLOGY TO REDUCE THE SPREAD OF INFECTIOUS DISEASES: THE CASE OF COVID-19

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Abstract: Controlling and detecting the spread of diseases like COVID-19 is essential in controlling epidemics. The measures to decrease the spread is to detect infected people ad track their previous illnesses. Contact tracing helps to isolate anyone who may be infected, since the virus can be transmitted between people without even showing any symptoms. These previous contacts can be used with mobile devices such as smart watches or smartphones that track the location and contacts through the use of communication technologies like GPS, Wi-Fi, Bluetooth or other cellular networks. This paper evaluates the importance of these technologies and determines the spread of toxic diseases. In this paper, we uses an epidemic model to evaluate productiveness and the measures to be taken, depending on contact tracking technologies from smartphones. The result show us in order to be effective of COVID-19 disease, the contact tracking technology must be accurate, contacts must be tracked quickly. This requirements make smartphone-based contact tracing to turn down the spread of virus in this period.

Keywords-Mobile computing, social networks, digital epidemiology, epidemic models.

I. INTRODUCTION

The COVID-19 pandemic imposes a large impact to our society and the way of life. Many people died, and millions were infected due to this virus. Many of the countries takes several measures, like lockdowns, quarantines and social distancing to control this crisis. The important way to reduce the spread of COVID-19 is to trace the contacts of people who are infected by the virus. This task was done through GPS and mobile communications. In this paper, we focuses on how smartphone contact tracing helps to reduce the spread of the COVID-19 diseases. We first evaluate and compare different contact tracing technologies and the similar methods for collecting contacts. We then use a temporal network graphs to characterise the temporal contacts of the different tracing technologies. On the basis of these graphs, we build a model that includes the contacts and the tracing technology. Thus we can apply this model to a large populations in a fast and accurate way. GPS helps to analyse and map the movement of individuals. Here we provide latest technologies like communications and localisation technologies. The benefits of this paper are:

- Quick isolation of people who is in contact with the COVID-19 infected person is possible.
- Early detection of contacts may help to reduce the death rate due to the impact of COVID-19.
- We can prevent the rapid spread of virus by tracing the contact of COVID-19 infected Person.

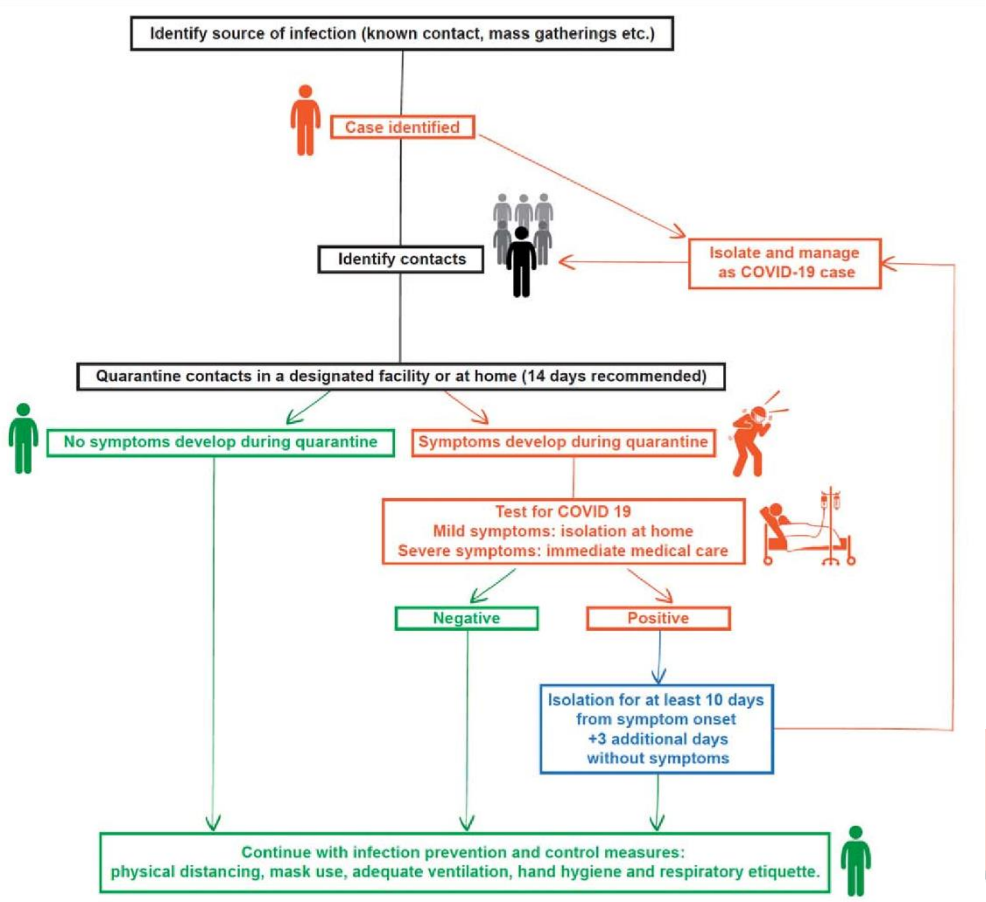


Figure 1. Chain of events for monitoring, tracing the contacts of COVID-19 confirmed cases

II. PROPOSED SYSTEM

i. CONTACT NETWORK AND TRACING

In this method, we create a model by contact network graphs. First we evaluate different technologies that is used for tracing the location of mobile phones. After that we create a network graph to describe these models and how these previous contacts may be tracked. Using a mobility trace method (NCCU trace), we can show that how different graphs used in epidemic models. For wide spreading diseases like COVID-19, personal interview provide very poor tracing of contacts and locations.

- **Mobile Tracing Technologies** :
  This method is used by latest technologies like localisations and communications. In our paper we evaluate the use of three different technologies to create a network of contacts.
  1. Wi-Fi: It is used to determine the MAC address of adjacent devices. Thus mobile nodes can store and scan information of these nearby devices, which can used to estimate distance by Received Signal Strength (RSSI).
  2. GPS: This is used to trace the location of the user. The precision of this solution is about 10 to 15 meters outdoors, in indoors the precision is very low. This makes a significant restriction although most of the infected contacts take place in indoors.

3. Bluetooth: Using this we can only trace the contacts with in a range of 1 to 2 meters, to determine close personal contacts.

Bluetooth and Wi-Fi technologies are used to exchange anonymous keys when a contact is detected. These results in two models to store and manage data, distributed and centralised. In centralised model, data is uploaded to the centralised server from the user's mobile. This technique is used by the health authorities to check and manage the contacts. In decentralised model, they stores the contact locally and allow the user to check if they are in contact with the virus infected person.

- **Characterising Contacts** :

One way of representing the communication between persons is through the network graphs. This is used for understanding the transmission of virus in population. We create a population of N nodes whose contacts are defined as a graph G(t), where the link between the nodes i and j represents the contact between i and j at a particular time t. In this model the contact between individuals in one day is calculated. That is, Gij (t) is 1 if the pair (i,j) of person in contact on day t, and 0 otherwise. For infection applications, the graph is symmetric which implies (Gij(t) = G(ji(t)), which means that the infection may pass in both directions. Ki(t) is known as the temporal degree of a individual i, is defined as the number of contact between a person to other person per unit time or days. We can obtain the average degree k from this temporal degree of a contact network over a time T as:

$$\mathrm{K} = \frac{1}{\mathrm{N}} \sum_{\mathrm{i=1}}^{\mathrm{N}} \left(\frac{1}{\mathrm{T}} \int_0^{\mathrm{T}} \mathrm{K_i(t)\,dt}\right) \qquad (1)$$

To evaluate the spread of infection, the number of contacts with the infected person is very useful. It can be calculates as:

$$\mathrm{K_i^*(t)} = \sum_{\mathrm{j=1}}^{\mathrm{N}} \mathrm{G_{ij}(t) I_j(t)} \qquad (2)$$

Where I_j(t) is 1 if the person j can infect others at time t, and otherwise 0.

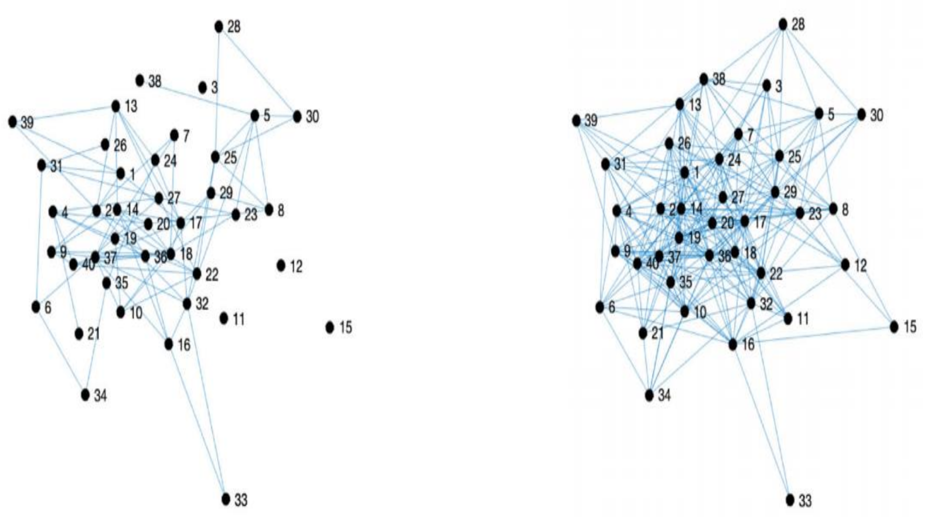
Using this contact network graph, we can track back the contacts to quarantine people who is more likely to be infected. In this we consider all contacts occurs in a time period 1. This idea is used to track back the recent contacts, we thus define a function $C_i(t, \Delta)$ that return 1 if it is true and 0 otherwise.

$$\mathrm{C_i(t, \Delta)} = \begin{cases} 1, & \sum_{j=1}^{N} \left(\max_{r \in [t-\Delta, t]} G_{i,j}(\tau) \right) D_j(t) > 0 \\ 0, & otherwise \end{cases} \qquad (3)$$

Where $D_j(t)$ gives 1 if a person j at time t is detected and traced, and 0 otherwise.

- **NCCU Trace Analysis:**

  To obtain a network of contacts, we use a NCCU trace which is obtained at the NCCU university campus. This trace was collected using Android app installed on smartphones of different students. The results of the trace was recorded over 15 days and stores the Wi-Fi access points, GPS data and Bluetooth devices in propinquity. The information such as time and position is recorded. Time is measured in seconds and position is measured in meters. Figure 2 shows the contact graph of first day which includes 40 individuals. We assumed that the pattern is similar for consecutive weeks. This fact is confirmed when we analyse the contact time series, which show more auto-correlation for the same weekdays.



(a) **(b)**

Figure 2. Contact network graph for 40 nodes during first day. (a) Real contacts, (b) Bluetooth contacts

ii. EPIDEMIC MODEL FOR EVALUATING CONTACT TRACING EFFICIENCY

In this we introduce a model called stochastic model which describes the contacts and tracing process of a person. This model is created using event-driven approach and consider each node separately. This stochastic model can transformed into a deterministic model, which is an extended of contact tracing. This model is very useful for the impact of various quarantine measures in huge populations.

- **The Stochastic Model:**

  We assume that individuals have six states: S, not infected; I, infected person; R, person who are recovered from the infection; QI, infected person that has been detected and then quarantined; QS, person having a chance of infecting being quarantined after being traced and QT, an infected person that has been detected and is being tracked. If the number of possible events is 8N, an event from S → I will make a change of state in this node for an individual. These events are represented by Table 1 and Table 2.

Table 1. Events of stochastic model.

Event	Rate	Description
$S \to I$	$(1 - q'\widehat{C_i}(t,\Delta))bK_i^*(t)$	Infected individuals that are not traced.
$S \to Q_S$	$q'\widehat{C_i}(t,\Delta)(1 - bK_i^*(t))$	Non-infected individual traced and quarantined.
$S \to Q_T$	$q'\widehat{C_i}(t,\Delta)bK_i^*(t)$	Infected individuals that are being traced and go directly to the tracing state.
$I \to Q_T$	δ	Detection of infected individuals, going to tracing.
$I \to R$	γ	Infected individual recovered from disease.
$Q_S \to S$	τ_Q	End of quarantine for susceptible individual.
$Q_I \to F$	τ'_Q	End of quarantine and infection.
$Q_T \to Q_I$	τ_T	End of tracing, goes to the rest of their quarantine.

Table 2. Notation table.

Symbol	Definition
N	Population
S, I, R	Susceptible, Infected and Recovered individuals states
Q_S	Susceptibles in quarantine by tracing
Q_I	Infected detected and quarantined.
Q_T	Infected detected and being traced.
Q_a	Accumulated individuals being quarantined by tracing.
R_0	Basic reproductive ratio ($R_0 = kb/\gamma$)
$K_i^*(t)$	Contacts per time unit with infected individuals, for node i.
$\widehat{C_i}(t,\Delta)$	Check if an individual has contacted with a traced one.
k	Average degree (i.e. average contacts per time unit and ind.).
b	Probability of transmitting the disease.
β	Transmission rate ($\beta = k \cdot b$)
γ	Recovery rate ($1/\gamma$ = days to recover)
δ	Detection rate of infected individuals
$1/\tau_Q$	Average quarantine time
$1/\tau'_Q$	Average quarantine time minus $1/\tau_T$
$1/\tau_T$	Average tracing time
q, q'	Fraction of traced contacts quarantined (normalised q')
q_i, q_s	Estimated fraction of traced contacts (deterministic model).
CFR	Case Fatality Rate.

When an individual is detected with virus, he/she must isolate immediately. Then their contact network is evaluated and then finds the persons who have been infected. In our model we consider two quarantine strategies, *Infected-Detected quarantine* and the *Tracing quarantine*. Infected-Detected quarantine is the commonly used quarantine measure, where the infected and detected persons are isolated and quarantine with a rate of δ (event I $\to Q_T$), and stay quarantine with an average time of $\frac{1}{\tau_Q}$ days. Before entering into final state of quarantine Q_I, these persons should stay for a short time $1/\tau_T$ in state Q_I, to trace their previous contacts. In tracing quarantine when a person is detected with virus, their contacts are traced using estimated contact network graph and some of people were quarantined.

- **Deterministic Model:**

The stochastic model can be converted into a deterministic model, in which the number of nodes depends the accuracy. As the number of nodes increased the accuracy also increases. In deterministic model there are six classes which is used to represent the count of persons in each state. We use the number of average contacts (k) of the network. We use two fractions of contacts of quarantined contacts, one is for infected (qi) and other is for capable ones (qs). Taking the values from Table1, the equation of this model is as follows:

$$S' = -(1 - q_i)\frac{KbIS}{N} - q_i\frac{KbIS}{N} - q_s\frac{K(1-b)IS}{N} + \tau_Q Q_S \quad (4)$$

$$I' = (1 - q)\frac{KbIS}{N} - \delta I - \gamma I \quad (5)$$

$$R' = \gamma I + \tau_Q Q_I \quad (6)$$

$$Q'_S = q_s \frac{K(1-b)IS}{N} - \tau_Q Q_S \quad (7)$$

$$Q'_I = \tau_T Q_T - \tau'_Q Q_I \quad (8)$$

$$Q'_T = \delta I + q_i \frac{KbIS}{N} - \tau_T Q_T \quad (9)$$

In all the above equations we omitted the value of time. As in the stochastic model which we mentioned above, we can obtain the accumulated number of persons that have been quarantined by a formula:

$$Q_a = q_i \frac{K(1-b)IS}{N} + q_s \frac{KbIS}{N} \quad (10)$$

Where $Q_a(t)$ is the total number of individuals quarantined up to time t.

iii. EVALUATION OF THE MODELS

This section evaluates the above models, their applicability and precisions. It also determine the dynamics of the COVID-19 with different quarantine measures. To evaluate both models, we use the estimated COVID-19 parameters shown in Table 3.

Table 3. Estimated COVID-19 parameters.

Parameter	Estimated value
R_0	3(1.5-6)
γ	1/15
β	0.52
τ_Q	1/14
δ	0.1(0.05-0.1)

In the following experiments, we determine the spread of the virus using NCCU trace. We assume that the initial outbreak at one day with five infected person is (I(0)=5),with no recovered persons (R(0)=0), and the time to trace a contact was set to one day ($1/\tau_T = 1$), which reflects in fast mobile tracking.

iv. EFFICIENCY OF QUARANTINE MEASURES AND TRACING TECHNOLOGIES

This section defines the effectiveness of each quarantine measures. It is also helps to evaluate the accuracy of different contact tracing technologies.

- **Efficiency Of Quarantine Measures**

  First, we evaluate the limit for controlling the outbreak depending on the proportion of capable individual S/N. We evaluate outbreak when some of the population gained immunity after they recovered from the virus. This becomes a key fact that helps in controlling and localising waves of infection since some of the people get immunity. The results are demonstrate in Figure 3, which implies that the blank lines correspond to the values for the NCCU trace scenario. If COVID-19 has an estimated average detection rate as 0.5 and reproductive ratio (R_0) as 3, we can see that the initial outbreak when S/N=1, then the virus cannot be controlled.

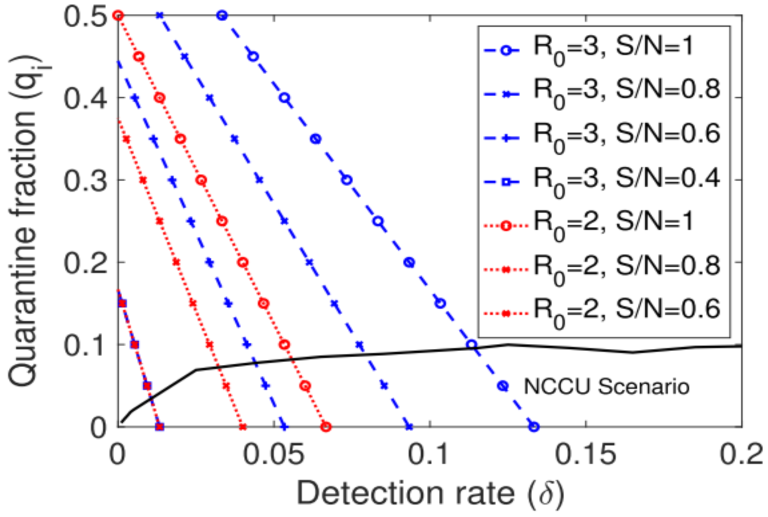
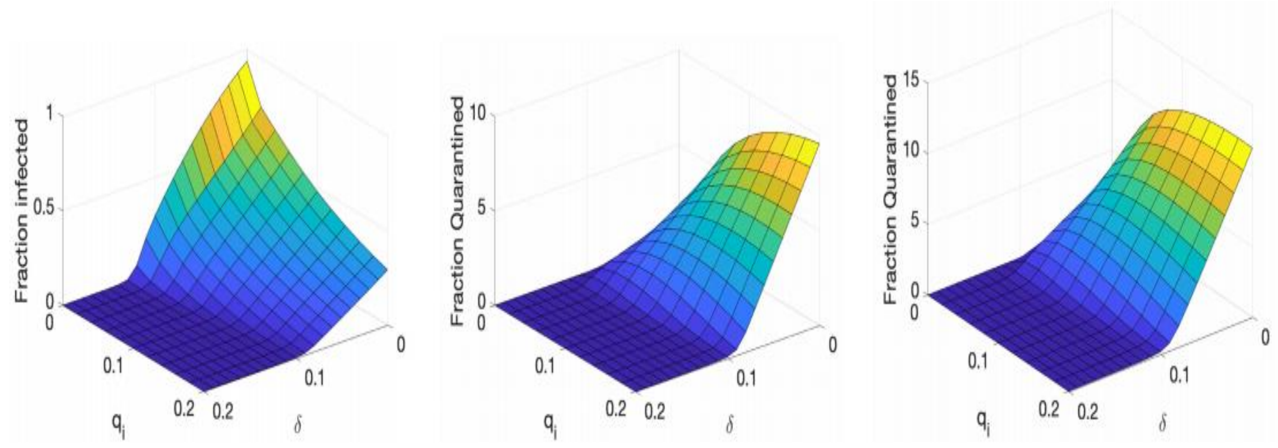


Figure 3. The control of infection for different ratio of population. The values above the dashed line shows a disease free equilibrium. The values below the black line corresponds to the values for the NCCU trace scenario.

We then evaluate the case that the infection has not been controlled and many people get infected. This evaluation is done using deterministic model. Using Bluetooth technology for tracing contacts, the same COVID-19 disease parameter is applied with 1 million population. The infected and quarantined results are expressed as a fraction of population (divided by N). Figure 4a shows the fraction of infected people depending on the rate of detection (δ), and the fraction of contacts of people in quarantine (q_i). We can distinct these values with a fraction of people who are quarantined, as shown in Figure 4b. Using GPS, we found that the fraction of quarantined people increases, as shown in Figure 4c.

- **Efficiency Of Contact Tracing Technology**

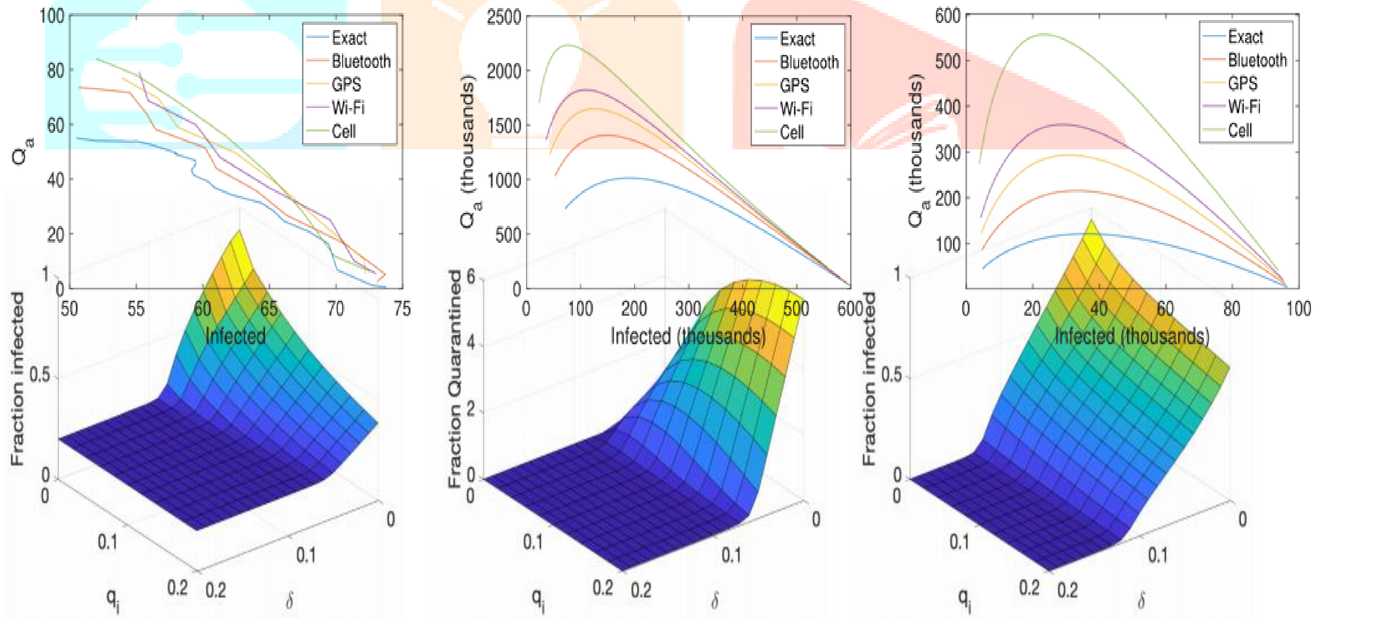
In this section, we evaluate quality of smartphone contact tracing technology. The first one is the precision of the speed and contact detection and the second is that, how it can reduce the control and spread of diseases. The main advantage of using smartphone contact tracing technology is its speed. When a person is detected with virus, tracing his/her contact should immediate. With usual contact investigation it takes many days to obtain the contact of infected person. Therefore, smartphone contact tracing plays an important role in case of COVID-19.



(a) (b) (c)

(d) (e) (f)

Figure 4. Effectiveness of quarantine measures: (a) Fraction of people infected using Bluetooth –based tracing technology (R (0) = 0), (b) Fraction of people quarantined using Bluetooth-based tracing technology (R (0) =0), (c) Fraction of people quarantined using GPS-based tracing technology (R (0) = 0), (d) Fraction of people infected using Bluetooth-based tracing technology (R (0) = 0.2N), (e) Fraction of people quarantined using Bluetooth-based tracing technology (R (0) = 0.2N).



(a) (b) (c)

Figure 5. Evaluation of the contact tracing technologies considering the number of infected persons versus quarantine effort (Q_a). (a) The NCCU tracing scenario using stochastic model, (b) Deterministic model for R (0) = 0, (c) Deterministic model for R (0) = 0.2N.

Using more precise tracing methods helps for greater selectivity of individuals who are more chance to be infected, thus reduces the number of quarantined people. Figure 5a, shows the importance of tracing technology, with more accurate technologies, the number of infected people and the number of quarantined people will decreases. Using values such as q_i and q_s, we can evaluate the importance of tracing technology over a mass population by deterministic model. Figure 5b gives a pattern similar to the result of stochastic model. Figure 4c shows the decrease in the number of quarantined people and newly infected individuals. This can be done with accurate tracing technologies such as Bluetooth. Summing up, smartphone contact tracing technologies shows a mass impact on the quarantine of individuals. This technology is very fast and also more precise in detecting real contacts.

III. CONCLUSION

In this paper, we focused on evaluating how smartphone contact tracing technologies can reduce the spread of COVID-19 virus. We introduced a stochastic model that can be transferred in to a deterministic model, while considering the importance of contact tracing techniques and quarantine measures. On the basis of these models, we define several scenarios for smartphone based contact tracing. Mobile technologies used for contact detecting provides mass impact on social and economic cost. Technology like Bluetooth, allow for huge selectivity when it comes to quarantining individuals. Contact tracing technologies provides faster and efficient access to trace the contacts of infected person. This technology will reduce the spread of COVID-19 virus and many of the people will gain immunity.

IV. REFERENCES

[1] K. Team, ''Contact transmission of COVID-19 in South Korea: Novel investigation techniques for tracing contacts,'' *Osong Public Health Res. Perspect.*, vol. 11, no. 1, pp. 60–63, Feb. 2020.

[2] K. Eames and M. Keeling, ''Contact tracing and disease control,'' *Proc. Biol. Sci. Roy. Soc.*, vol. 270, pp. 2565–2571, Jan. 2004.

[3] Singapore Government. (2020). *Tracetogether*. [Online]. Available: https ://www.tracetogether.gov.sg

[4] PePP-PT e.V. i.Gr. (2020). *Pan-European Privacy-Preserving Proximity Tracing (PEPP-PT)* [Online]. Available: https://www.pepp-pt.org

[5] (2020). *Safe Paths*. [Online]. Available: http://safepaths.mit.edu

[6] X. Zhang, G. Neglia, J. Kurose, and D. Towsley, ''Performance modeling of epidemic routing,'' *Comput. Netw.*, vol. 51, no. 10, pp. 2867–2891, Jul. 2007.

[7] J. Dede, A. Forster, E. Hernandez-Orallo, J. Herrera-Tapia, K. Kuladinithi, V. Kuppusamy, P. Manzoni, A. bin Muslim, A. Udugama, and Z. Vatandas, ''Simulating opportunistic networks: Survey and future directions,'' *IEEE Commun. Surveys Tuts.*, vol. 20, no. 2, pp. 1547–1573, 2nd Quart., 2018.

[8] E. Hernández-Orallo, M. Murillo-Arcila, C. T. Calafate, J. C. Cano, J. A. Conejero, and P. Manzoni, ''Analytical evaluation of the performance of contact-based messaging applications,'' *Comput. Netw.*, vol. 111, pp. 45–54, Dec. 2016.

[9] E. Hernandez-Orallo, M. D. S. Olmos, J.-C. Cano, C. T. Calafate, and P. Manzoni, ''CoCoWa: A collaborative contact-based watchdog for detecting selfish nodes,'' *IEEE Trans. Mobile Comput.*, vol. 14, no. 6, pp. 1162–1175, Jun. 2015.

[10] J. Hellewell, ''Feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts,'' *Lancet Global Health*, vol. 8, no. 4, pp. e488–e496, Apr. 2020.

[11] E, Hernandez-Orallo et al, "Evaluating how smartphone contact tracing technology can reduce the spread of infectious diseases", Vol 8,2020.

[12] A. Lima, V. Pejovic, L. Rossi, M. Musolesi, and M. Gonzalez, ''Progmosis: Evaluating risky individual behavior during epidemics using mobile network data,'' 2015, *arXiv:1504.01316*. [Online]. Available: https://arxiv.org/abs/1504.01316

[13] S. Rubrichi, Z. Smoreda, and M. Musolesi, ''A comparison of spatial-based targeted disease mitigation strategies using mobile phone data,'' *EPJ Data Sci.*, vol. 7, no. 1, p. 17, Dec. 2018.

[14] M. Salathé, M. Kazandjieva, J. W. Lee, P. Levis, M. W. Feldman, and J. H. Jones, ''A high-resolution human contact network for infectious disease transmission,'' *Proc. Nat. Acad. Sci. USA*, vol. 107, no. 51, pp. 22020–22025, 2010.

[15] R. Mastrandrea and A. Barrat, ''How to estimate epidemic risk from incomplete contact diaries data?'' *PLOS Comput. Biol.*, vol. 12, no. 6, pp. 1–19, Jun. 2016.

[16] C. Fraser, S. Riley, R. M. Anderson, and N. M. Ferguson, ''Factors that make an infectious disease outbreak controllable,'' *Proc. Nat. Acad. Sci. USA*, vol. 101, no. 16, pp. 6146–6151, Apr. 2004.

[17] J. Müller, M. Kretzschmar, and K. Dietz, ''Contact tracing in stochastic and deterministic epidemic models,'' *Math. Biosci.*, vol. 164, no. 1, pp. 39–64, Mar. 2000..

[18] K. Farrahi, R. Emonet, and M. Cebrian, ''Epidemic contact tracing via communication traces,'' *PLoS ONE*, vol. 9, no. 5, May 2014, Art. no. e95133.

[19] M. J. Keeling and P. Rohani, *Model. Infectious Diseases Humans Animals*. Princenton, NJ, USA: Princenton University Press, 2008.