Contact Tracing in Healthcare Digital Ecosystems for Infectious Disease Control and Quarantine Management

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Abstract — **Highly infectious diseases such as SARS (Severe Acute Respiratory Syndrome), Avian Influenza (Bird Flu), Small Pox, and currently Swine Flu, to name but a few, pose a significant threat to the global population. Detection and prevention of infectious diseases is notoriously complex and problematic due to the ever increasing number of international travellers. In addition, the risk of being infected with an infectious disease in densely populated urban areas tends to be much higher compared to rural areas. When an outbreak occurs, the detection of source of infection (or index case), clusters of cases and transmission routes in a rapid manner is crucial in preventing the infectious disease from further spreading. Contact tracing has proven to be helpful for these detections. Traditionally, contact tracing is a field work of the medical personnel with little assistance of IT (Information Technology), if any. During the worldwide outbreak of SARS in 2003, HCIS (Health Care Information Systems) were built to facilitate contact tracing. However, contact tracing, and thus the detection process, is not a fully automatic process in these systems. In this paper, with SARS as a case study, we realize detection as an automatic process by applying algorithms and data mining techniques in the patients' activities and social interaction together with characteristics of the infectious disease.**

Index Terms—**Contact Tracing, Healthcare Digital Ecosystem, Infectious Disease Control, SARS, Infection Tree.**

I. INTRODUCTION

Digital ecosystems have emerged as a new conceptualization of complex, interdependent, loosely-coupled and demand-driven interactive environments [1]. In the health domain, digital health ecosystems are conceived of as dynamic environments in which hospitals, medical centres, practitioners, medical researchers and others are linked in order to exchange medical records in a demand-driven manner, such as in the case of an epidemic. In this paper we focus on one such case that motivates the development of medical record digital ecosystems.

During the worldwide outbreak of SARS in 2003, the infected regions or countries had tried all measures to prevent the infectious disease from further spreading. As reviews after the outbreak showed, IT systems have been effective measures in combating SARS [2],[3].

However, soon after the outbreak of SARS, the relevant medical institutions in the infected areas found their existing IT systems to be inadequate in coping with the outbreak of SARS, mainly because these systems do not facilitate contact tracing. In this respect, new systems had to be built or existing systems had to be improved in these infected areas. For example, in Hong Kong, a new system, eSARS, was built [2],[4]; in Singapore, the existing HCIS was improved [5];

and in Taiwan, a new database was added to the existing system [6]. These three systems include two major components:

1. Management of cases: This component enables the management work for all the cases during an outbreak of the infectious disease. For example, quarantining, monitoring, contacting of the probable cases and/or suspected cases can be managed; treatment course for the confirmed case can also be managed.

2. Implementation of contact tracing: With the data available in the first component, contact tracing [7] is implemented in the second component. Contact tracing has two main purposes:

1. To get the infected persons to be treated as quickly as possible.
2. To find out the clusters of cases from which sources of infection and transmission routes within the clusters and of the overall outbreak can be deduced.

During the outbreak of an infectious disease, medical personnel try their best to find out, as quickly as possible, the source of infection and the transmission routes in the clusters and of the whole outbreak which in turn enables them to take appropriate actions on the infectious disease. So, contact tracing is crucial in preventing the infectious disease from spreading further.

When the transmission routes in a cluster are identified, an infection tree [8] (or cluster tree) of a cluster can be constructed; when the transmission routes between the clusters are identified, a merged infection tree can be constructed from the individual infection trees. This merged infection tree, as an overall picture of the outbreak, may enable medical personnel to find weaknesses and/or loopholes of the medical administrative work during the outbreak [9], [10],[11]. The generations [12] of the infectious disease which can be deduced from the height of the merged infection tree may reveal some characteristics of the disease, such as the persistence or duration of the disease, which may be a valuable reference in predicting the behaviours of the infectious disease in its next outbreak.

Traditionally, contact tracing for an outbreak of an infectious disease is usually performed in following steps:

1. Medical personnel interview the confirmed cases and ask them where they have been and whom they have met and/or lived with before and after their onset dates.
2. Medical personnel visit or contact the persons pointed out by the confirmed cases to see whether they have symptoms related to the infectious disease. If they have, medical personnel immediately ask them to go to

hospital for testing. If they are confirmed cases of the disease, they are treated immediately. In this respect, medical personnel can be sure that the transmission route is from the previous case to the new case.

3. Medical personnel carry out Step 1 and Step 2 for the new cases.
4. When Step 1 – Step 3 are carried out iteratively during the outbreak, infection trees (or cluster trees) and the merged infection tree of the outbreak are identified [8].

A weakness of the traditional contact tracing is that it greatly relies on whether the confirmed cases can remember whom they met in the places where they have gone. If they can't remember, can't be sure or even are not willing to point out the persons they met in the places they went, then it is difficult for contact tracing to fulfil its purpose.

In general it is easier for a person to point out where he/she has gone rather than to point out whom he/she has met in a particular period of time. The latter may even be impossible in some cases.

To overcome this difficulty, we make use of knowledge of the characteristics of an infectious disease to help contact tracing. In this paper, with SARS as a case study, we propose an approach to find out clusters of cases, the individual infection trees and the merged infection tree, mainly based on visiting records of the cases.

The reason why visiting records can be applied to the contact tracing of SARS is due to the characteristics of SARS [13],[14]. As SARS research has shown, SARS is an airborne, person-to-person infectious disease. Namely, when a person is within an environment in which a SARS case is present or has stayed, this person is likely to be infected whether or not he/she is aware of the presence of a source of infection. So, the visiting (whereabouts) of a SARS case before its incubation period can possibly tell where he/she got infected.

In order to find clusters of cases and transmission routes of SARS, contact tracing algorithms based on the infectious period and the incubation period of SARS are designed. As a high level description of our approach, we treat finding the clusters of cases, transmission routes and hence the infection tree of SARS as a process of data mining; that is, with the algorithms applied to the visiting records (raw data), the clusters of cases and the infection trees can be mined automatically.

In section II we briefly review related work of SARS contact tracing. A brief idea of the algorithms and characteristics of SARS are described in section III. Our algorithm for detecting clusters of cases is discussed in section IV; our algorithm for detecting the infection tree of a cluster is given in section V; and our algorithm for constructing a merged infection tree of an outbreak is described in section VI. We make concluding remarks in section VII.

II. RELATED WORK

Although the systems reported in [2],[3],[4],[5] have released medical personnel from the tedious management work of SARS cases, contact tracing was more or less implemented based on the traditional steps listed in section I.

Knowing the characteristics of SARS of being airborne and person-to-person, Chan et al. [15] have introduced social network analysis (SNA) [16] in their contact tracing. They construct the geographical locations (whereabouts) of confirmed cases into social networks to detect transmission routes. With the introduction of social network analysis, [15] has revealed more transmission routes between cases.

However, none of the above-mentioned systems and approach have utilized the characteristics of SARS such as incubation period and infectious period to automate the finding of clusters of cases, transmission routes and hence infection trees.

III. METHODOLOGY AND BACKGROUND INFORMATION

The proposed approach utilizes the visiting records of confirmed cases before and after their onset date of symptoms. These records are collected and input in the system. For finding clusters of cases and the infection tree of an infectious disease during its outbreak, we have designed three main algorithms: Algorithm 1 – for detecting clusters of cases. Algorithm 2 – for detecting the infection tree of a cluster; by this algorithm the source of infection (index case) and the transmission routes in a cluster can be identified. Algorithm 3 – for constructing the merged infection tree of an outbreak. First, algorithm 1 is executed to find clusters of cases. A cluster of cases is a group of cases who have visited the same place. Second, for each cluster, algorithm 2 is used to find the infection tree of this cluster. Finally, algorithm 3 is used to combine the individual infection trees into a merged infection tree.

Characteristics of SARS

Researchers show that SARS has following characteristics:

1. Transmission mode: As stated in [13],[14], SARS can be transmitted through droplets in the air, in a person-to-person manner. Mainly, a person can become infected with SARS by having close contact with very ill SARS patients. They may also become infected through contact with infectious respiratory droplets in the air or on contaminated surfaces.

2. Incubation period, onset date and confirmed date: When a person becomes infected with SARS, he/she will start to show SARS symptoms some days after infection. The duration between the infection and the date of onset of symptoms is the incubation period of SARS. Once a person has the onset of symptoms, he/she can be a source of infection.

However, non-SARS infected patients can also have symptoms resembling those of SARS. When medical personnel accept a patient with symptoms like those of SARS, they carry out a diagnostic laboratory test to confirm whether this patient is real case of SARS. If the test is positive, the patient is treated as a SARS patient. Due to the need for diagnostic laboratory testing, for a given case of SARS there is usually a time gap between the date of onset of symptoms (onset date) and the date of confirmation (confirmed date).

SARS has a quite clear and short incubation period. Although there are many papers about the investigation of the incubation period of SARS [17],[18],[19], we adopt the description of its incubation period in [20], which is in the range of 1 – 10 days, and a mean of around 5 days.

3. Infectious period: The infectious period concerns the transmission efficiency of an infectious disease. As stated in [21], "Maximum virus excretion from the respiratory tract occurs on about day 10 of illness (that is, 10 days after the onset date) and then declines to 0% by day 23." Therefore, SARS shows an up-and-down tendency in its transmission efficiency from the onset date.

From the characteristics of SARS described above, we know that the visiting (whereabouts), the incubation period and the infectious period of confirmed cases are the main factors for the infection of SARS. Therefore, our algorithms 1 – 3 are designed based on these three factors.

IV. DETECTING A CLUSTER OF CASES

Detecting a cluster of cases requires detailed information about the places the patient has visited before being identified as a confirmed case. Algorithm 1 is used to detect clusters of cases from an outbreak.

FOR all visiting records of the confirmed cases
  Detect the common visiting places of the records;
ENDFOR
FOR each common visiting place
  Group the cases who had visited the place;
ENDFOR
FOR each group of cases
  Draw it as a cluster of cases;
ENDFOR

Algorithm 1 – Algorithm for detecting clusters of cases

V. DETECTING AN INFECTION TREE OF A CLUSTER

Algorithm 2 uses two sub-algorithms as follows:

Algorithm 2a – algorithm for detecting the most relevant date of infection between two cases (note: when there are several dates of contact between an earlier confirmed case and a newly confirmed case, this algorithm is applied to determine the most relevant date of infection for the new case's infection).

Algorithm 2b – algorithm for detecting the most likely source of infection for a case (note: when a newly confirmed case has had contact with several earlier confirmed cases, this algorithm is applied to determine which earlier confirmed case will be the most likely source of infection for this newly confirmed case).

For the purpose of clarification we use the abbreviations shown in Table 1.

Algorithm 2a - Detecting the most relevant date of infection between two cases

Suppose two persons A and B are confirmed cases, and their onset dates were 1 May and 20 May respectively. Since A's onset date is earlier than B's, we call A an ancestor of B

Table 1 Terms and abbreviations used in this paper

Term	Abbreviation
Date of Start of Incubation Period of Patient J	S_J
Date of Mean of Incubation Period of Patient J	M_J
Date of Max Transmission Efficiency of Patient J	T_J
Date of End of Infectious Period of Patient J	E_J
The nth Meeting Date between Patient J with Patient K where J is the likely source of infection of K	${}_{JK}m_n$
${}_{JK}m_n$'s deviation from T_J	${}_{JK}\alpha_n$
${}_{JK}m_n$'s deviation from M_K	${}_{JK}\beta_n$
${}_{JK}m_n$'s deviation sum (${}_{JK}\alpha_n + {}_{JK}\beta_n$)	${}_{JK}\delta_n$
The most relevant date for Patient K's infection with respect to Patient J	${}_{J}r_K$

in this infectious disease. Suppose their visiting records indicate that they met on 25 April, 12 May and 16 May. Since A was a confirmed case earlier than B and they met, it is natural to think that A might have infected B. Now, we have the question: from these three meeting dates, can we determine which date was the most relevant for B's infection if B was really infected by his/her ancestor, A? The details of A and B together with the incubation periods and infectious periods are represented in Fig. 1.

From Fig. 1 we can see that S_A = 21 Apr, M_A = 26 Apr, T_A = 11 May, E_A = 24 May, S_B = 10 May, and M_B = 15 May. Now, we can analyze which of these three meeting dates: ${}_{AB}m_1$ = 25 April, ${}_{AB}m_2$ = 12 May and ${}_{AB}m_3$ = 16 May were most relevant to B's infection if A did infect B. First of all, store these three meeting dates in a list, say list_1. For ${}_{AB}m_1$ = 25 April, it was outside B's start date of incubation period (S_B = 10 May), therefore, ${}_{AB}m_1$ didn't have much significance for B's infection. We can discard it from list_1. However, the meeting dates 12 May and 16 May were within B's incubation period (10 May – 20 May), so we need to derive which date was more relevant to B's infection.

For ${}_{AB}m_2$ = 12 May, find its deviation from A's date T (T_A) and from B's date M (M_B), then sum up these two deviations as ${}_{AB}\delta_2$.

$$\,_{AB}\alpha_2 = |T_A - {}_{AB}m_2| = |11 - 12| = 1$$

$$\,_{AB}\beta_2 = |M_B - {}_{AB}m_2| = |15 - 12| = 3$$

$$\,_{AB}\delta_2 = {}_{AB}\alpha_2 + {}_{AB}\beta_2 = 4$$

For ${}_{AB}m_3$ = 16 May, repeat the same procedure as for ${}_{AB}m_2$ in the following,

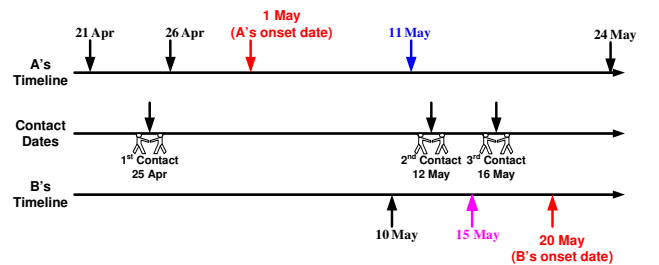$$\,_{AB}\alpha_3 = |T_A - {}_{AB}m_3| = |11 - 16| = 5$$

Fig. 1 Timelines of A and B

$$_{AB}\beta_3 = |M_B - {_{AB}m_3}| = |15-16| = 1$$
$$_{AB}\delta_3 = {_{AB}\alpha_3} + {_{AB}\beta_3} = 6$$

Store the deviation sums $_{AB}\delta_2$ and $_{AB}\delta_3$ in a list, say list_2. In this example, there are only two elements: $\{\delta_1, \delta_2\}$ in list_2, however in general there may be k elements: $\{\delta_1 \dots \delta_k\}$ in list_2. Now find the minimum from list_2. Then the meeting date corresponding to the minimum is selected as the most relevant date for infection. Therefore, in this example, the most relevant date for B's infection with respect to A, $_A r_B$ is:

$$_A r_B = \operatorname{argmin}_{j=1}^{k}(\delta_j) = 1$$

In this example $k = 2$, and 1 (element at index 1 of list_2) is returned for $\operatorname{argmin}_{j=1}^{k}(\delta_j)$, then $_{AB}\delta_2 \rightarrow {_{AB}m_2}$ (12 May) is the most relevant date for B's infection with respect to A.

The algorithm for detecting the most relevant date of infection between two cases can be described as follows:

IF A and B are two confirmed cases and A is B's ancestor
THEN
    Determine the meeting dates between A and B and store the meeting dates in list_1;
    IF list_1 is empty **THEN**
        Return "there is no most relevant date for B's infection with respect to A";
    ELSE
        IF there are meeting date(s) outside B's incubation period in list_1 **THEN**
            Remove these meeting date(s) from list_1;
        ENDIF
        IF list_1 is empty **THEN**
            Return "there is no most relevant date for B's infection with respect to A";
        ELSE
            FOR each meeting date in list_1
                Find its deviation sum (δ_i) and store it in list_2;
            ENDFOR
            Find the minimum of list_2;
            Return the meeting date corresponding to the minimum as "the most relevant date for B's infection with respect to A";
        ENDIF
    ENDIF
ENDIF

Algorithm 2a – Algorithm for detecting the most relevant date of infection between two cases

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Algorithm 2b - Detecting the most likely source of infection for a case

In Algorithm 2a there is only one ancestor involved. Now we look at the more general case of multiple ancestors. Suppose that A, B and C were confirmed cases and their onset dates were 1 May, 3 May and 24 May respectively. Now, C has two ancestors. Suppose that C met A on 17 May and B on 15 May. Since these two meeting dates were within C's incubation period, we need to determine which one, A or B, was the most likely source of C's infection. The details between A, B and C together with the incubation periods and
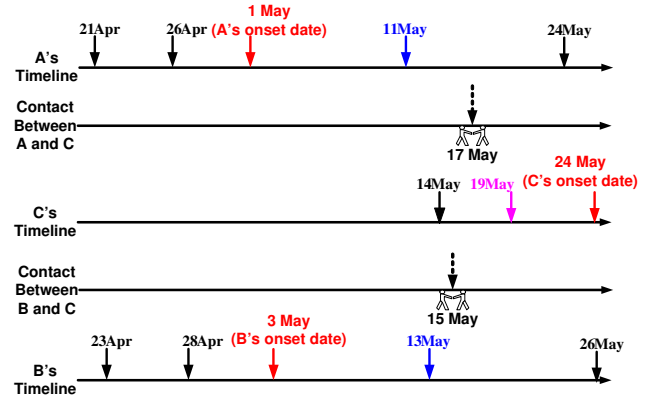

Fig. 2 Timelines of A, B and C

Table 2 Deviation sums of two meeting dates

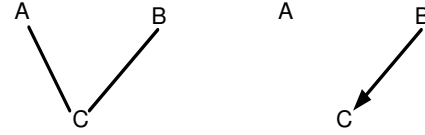|	α_1	β_1	δ_1
A-C	$_{AC}\alpha_1 = |11\text{-}17| = 6$	$_{AC}\beta_1 = |19\text{-}17| = 2$	$_{AC}\delta_1 = 8$
B-C	$_{BC}\alpha_1 = |13\text{-}15| = 2$	$_{BC}\beta_1 = |19\text{-}15| = 4$	$_{BC}\delta_1 = 6$

Fig. 3 The most likely source of infection for patient C: patient B

infectious periods are represented in Fig. 2.

By using the same procedure as in Algorithm 2a for the meeting dates 17 May (A-C) and 15 May (B-C), we can find the deviation sums as shown in Table 2.

As the deviation sum of the B-C meeting date is smaller, we can suppose that B was the most likely source of C's infection, as shown in Fig. 3. As a note on Fig. 3, in terms of social network analysis [16], the graphs on the left and right are the meeting graph and the infection graph of A, B and C respectively.

In the above example, if A and/or B had more than one meeting date with C then we firstly use Algorithm 2a to determine "the most relevant date for C's infection" from these meeting dates, and following that we use the determined dates in Algorithm 2b. Also, in the above example, C only had two ancestors. In fact, Algorithm 2b is also applicable if C had more than two ancestors. Now we can give the details of Algorithm 2b as follows:

IF a confirmed case j has two or more ancestors **THEN**
    Determine which ancestor j met and store that ancestor in list_1;
    IF list_1 is empty **THEN**
        Return "these ancestors are not the most likely source of infection for j's infection";
    ELSE
        FOR each ancestor in list_1
            Carry out Algorithm 2a to determine "the most relevant date for j's infection" and store the returned meeting date in list_2;
        ENDFOR
        IF list_2 is empty **THEN**
            Return "these ancestors are not the most likely source of infection for j's infection";

```
        ELSE
            FOR each meeting date in list_2
                Find its deviation sum with respect to j and store it
                in list_3;
            ENDFOR
            Find the minimum of list_3;
            Return the ancestor corresponding to the minimum as
            "the most likely source of infection for j's infection";
        ENDIF
    ENDIF
ENDIF
```

Algorithm 2b – Algorithm for detecting the most likely source of infection for a case

Table 3 Onset dates of confirmed cases

Person	Onset Date
A	2003-05-02
B	2003-05-12
C	2003-05-20
D	2003-05-26
E, F	2003-05-30
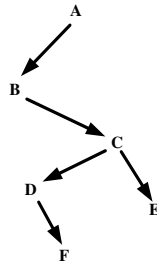
Fig. 4 Detected infection tree for the patients from Table 3

Now we are ready to describe Algorithm 2 as a whole. The onset dates of the confirmed cases of a cluster are listed in Table 3in ascending order.

First of all, from Table 3 we can see that A had the earliest onset date, so A was probably the index case of the cluster. In this cluster, B could only have been infected by A (i.e. if B's infection was contracted from within this cluster). That is, B was infected by his/her ancestor A. For C and D, apply Algorithm 2b to determine the most likely source of their infections. Suppose C was infected by B, and D was infected by C. Next, it came to E and F. Since their onset dates were the same, they could not have infected each other. So, the ancestors of E and F are the same: A, B, C and D. Apply Algorithm 2b to determine the most likely source of infection for E and F's infections. Suppose E was infected by C and F was infected by D. Finally, we can draw the infection tree for this cluster as in Fig. 4.

Now we can give the details of Algorithm 2 as follows:

```
Put the confirmed cases of a cluster into list_1 sorted by their
onset dates in ascending order;
FOR each node, except the first node, in list_1
    Carry out Algorithm 2b to determine the most likely
    source of its infection;
    Store this information into an adjacency matrix;
ENDFOR
Draw the infection tree from the adjacency matrix;
```

Algorithm 2 – Algorithm of detecting the infection tree of a cluster

VI. CONSTRUCTING THE MERGED INFECTION TREE

Once the infection trees of the clusters are found, Algorithm 3 is used to assemble the individual infection trees into a merged infection tree of an outbreak, as follows:

```
Put the root nodes of the individual infection trees in list_1
sorted by their onset dates in ascending order;
Set n to the number of nodes in list_1;
//iteration of child and parent relationship detection for the
nodes in list_1
FOR i = n – 1 to 1
    FOR j = i – 1 to 0
        IF node i is a child of the infection tree of node j THEN
            Record node i is a child of node j;
            break;
        ELSE IF j = 0 THEN
            Record node i does not have a parent node;
        ENDIF
    ENDFOR
ENDFOR
Draw the tree(s) according to the detected child and parent
relationship;
```

Algorithm 3 – Algorithm of constructing the infection tree of an outbreak

As an application of Algorithms 1–3, we have used the 2003 Hong Kong SARS outbreak [9],[23] as a real case study and analyzed it with our three algorithms. The index case (or index patient) of this outbreak, n1, was a professor from Guangzhou, China who went to Hong Kong to celebrate the wedding of his nephew. After a family dinner, he checked into the Metropole Hotel. During the night, the professor felt feverish. The next day, the professor felt so ill that he was admitted to the nearest hospital, Kwong Wah Hospital. In the hospital, he infected a nurse, n4.

Epidemiological investigation confirmed that n2 was the index case of St Paul's Hospital in which n2 infected three nurses while n3 was the index case of Prince of Wales Hospital (PWH) in which n3 infected three doctors and three nurses. In PWH, it then caused a SARS outbreak among the healthcare workers. Since then, SARS cases were prevalent in the community as the disease continued to propagate progressively on their down lines.

Further epidemiological investigation showed that the infection of both n2 and n3 took place in the Metropole Hotel while the professor was staying there, so the clusters were linked together.

We have taken data on the above cases and subjected them to our detection algorithms. Algorithm 1 revealed four clusters: {n1, n4}, {n1, n2, n3}, {n2, n5, n6, n7} and {n3, n8, n9, n10, n11, n12, n13}. Applying algorithms 2 and 3 produced a merged infection tree of these clusters. Our detection and visualization application displays the infection tree in graph form using the JUNG framework [22] as shown in Fig. 5. We found that the detected result from our algorithms is identical to the observed and documented situation during the initial stage of the Hong Kong SARS outbreak. This is an initial but strong confirmation of the validity of our algorithms for the detection of SARS infection trees, and thereby of the applicability and potential for use in contact tracing.
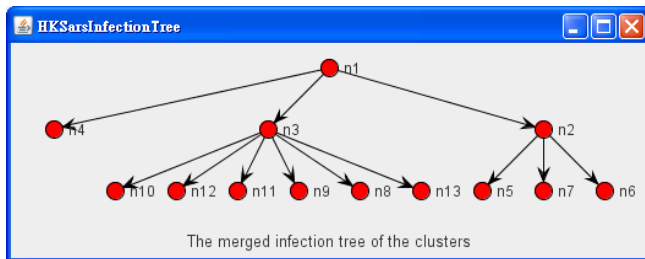
Fig. 5 Merged infection tree, 2003 Hong Kong SARS outbreak (initial stage)

VII. CONCLUSIONS

As an example of analysis of medical data that could become a valuable part of a digital health ecosystem, we have proposed a novel approach for contact tracing in finding clusters of cases, transmission routes and hence the infection tree of an infectious disease by incorporating its characteristics into algorithms. As a prototype to show our idea and due to the significant characteristics of SARS, infectious period and incubation period are adequate for our implementation in this paper. Our paper contributes a simple and systematic way to find the clusters of cases and the infection tree for SARS automatically. However, applying this novel approach to other infectious diseases, such as Tuberculosis, Dengue Fever, Swine Flu etc. may require further study of the characteristics of the infectious diseases in question. We hope that our paper can serve as a starting point and arouse attention of other researchers to do further research in this area, as a simple yet accurate and systematic way to find clusters of cases, transmission routes and the infection tree may save lives of people during the outbreak of an infectious disease.

The work described in this paper is part of our larger *Infectious Disease Control and Quarantine Management (IDCQM)* framework which has been developed with the help of *Macau Centre for Control of Communicable Disease and Surveillance of Diseases*. IDCQM includes modules for the extraction of detailed epidemiological history and patient's activities, identification of the source of an outbreak, identifying and visualizing clusters of infections, quarantine management, and GIS for locating clusters of infection. As future work we are planning to extend this novel approach for contact tracing to the infectious diseases that will be studied and implemented in IDCQM.

VIII. ACKNOWLEDGMENT

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