A note on community-detection (Kemeny) based testing for COVID-19

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Abstract—The Kemeny constant of a graph can be used to identify and analyse bridges between communities in a graph. Testing, tracking and tracing abilities have been identified as pivotal in helping countries to safely reopen activities after the first wave of the COVID-19 virus. Trajectories techniques aim at reconstructing past history of contacts, but can face practical limits in an exponential growth of either testing or overly conservative quarantining. We show how this application of graph theory can be conveniently used to efficiently intercept new virus outbreaks, when they are still in their early stage. Simulations provide promising results in early identification and blocking of possible ‘super-spreader’ links that transmit disease between different communities.

Index Terms—Markov chains, Covid-19, Kemeny constant

I. INTRODUCTION

A. Motivation

Amidst fears of a possible second wave of the COVID-19 disease, methodologies based around test, track, and trace (TTT) policies have been identified in many countries to lift confinement restrictions [19], [31], [36]. Some initial examples of contact tracing methods, that have been widely applied from the beginning of the epidemic, aimed at combining data from interviews, smartphones GPS and Bluetooth histories, credit cards and camera records. Examples of successful applications in China, Iceland, New Zealand, Singapore, South Korea and Taiwan, have been shown to contribute to mitigate the spread of the virus [1], but such manual contact tracing approaches are particularly time consuming, especially with large numbers of infected people. Besides, considering the long incubation period, and exponential growth in transmission, even short delays in actions may lead to the loss of control of the epidemic [11]. From this perspective, it has also been shown in [18] that reducing the delay in detecting a new case from 5 to 3 days leads to a 60-70% improvement in efficiency, in terms of reproduction number. Accordingly, an alternative more efficient solution for contact tracing includes the use of mobile phone applications with immediate notification. Considering a high penetration rate, and a high compliance of people in using this app, it could significantly help to stop the epidemic as shown in [11]. The benefits of efficient testing are clear. In addition to identifying infected individuals and tracing their contacts, fast diagnostic tests also allow estimation of the degree of spread of the virus in a region.

Accordingly, one proposal is to perform the tracing task by using Bluetooth connectivity to recognise when a prolonged proximity between two smartphones (and thus, their owners) occurs. For instance, the smartphone app that has been recommended by the Italian government stores a contact when a proximity of less or equal than two meters for at least 15 minutes is recorded. Thus, the tracing task is currently designed as a reactive process, as it is a reaction to a positive test. Consequently, unless the positive individual is tested in the very early stages of the infection, which may be unrealistic in practice in many cases since symptoms do not usually appear before 3-4 days, large numbers of naive tests and ineffective quarantines may be required for an effective 3T policy. It is therefore of interest to reshape the sampling process to be proactive and make sampling more efficient in the presence of limited testing capabilities. In this context, two related questions arise.

(i) Is it possible to identify the so-called super-spreaders? [31]

(ii) Is it possible to identify sub-communities in cities and those individuals that link these communities together? [37]

The second question is particularly important in the context of COVID-19 as the effect of the disease is highly compartmentalised; not only regionally, but also in terms of demographics, with older communities highly at risk, and younger children apparently in a low risk category, but still with the potential for acting as vectors. Indeed, the terrible effects of the disease in care homes for the elderly, and in communities such as the Satmar community, only reinforce the negative consequences of the disease jumping from one compartment to another. Our objectives are therefore to:

https://www.independent.co.uk/independentpremium/long-reads/ultra-orthodox-coronavirus-new-york-brooklyn-hasidic-antibodies-lockdown-a9537556.html

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B. State of the art

The issue of who should be tested is not new in epidemiology. This problem is very similar to the classic one of who should be vaccinated in a population. For instance, it is well established that random immunization requires immunizing a very large fraction of a population in order to abate contact-transmissible epidemics \[6\]. When time or resources are limited, better results can be achieved if smarter immunisation strategies are used; see, for instance the immunising random acquaintances of random nodes policy \[6\] which is known to be more successful than a fully random strategy in identifying the super-spreaders.

In principle, targeted immunization of the most highly connected individuals is also known to be more effective. However, since such vaccination policies actually require a global knowledge of the contact network, they are impractical in most cases \[6\]. In the COVID-19 context, the advantage of sample testing is confirmed in \[23\], the authors analyzed the effect of testing, isolation, tracing, physical distancing, and type of contacts (household and others) on the reproduction number. According to their simulations, focused testing strategies based on contact tracking help holding back the epidemic more efficiently than a widespread mass testing or self-isolation alone. From this perspective, it is clear that the contact tracing apps provide an unprecedented opportunity to infer the network over which an epidemic spreads, and to implement targeted immunization/testing policies \[19\].

Assuming that the tracing apps truly do provide a snap-shot of a city-wide network of contacts, then the problem becomes: what is meant by the most highly connected individuals? Such problems are highly topical in computer science, mathematics, and engineering, and a number of tools are available to us. In this short report we first consider the graph node degree (i.e., the number of daily contacts) as the most obvious option of who should be tested. A more refined indicator is Google’s PageRank indicator \[25\], as suggested in \[8\]. These indicators identify influential contacts in a graph, and do not necessarily identify communities or individuals that bridge communities, and so are not suitable for our purpose. Thus, we also consider an indicator based on the Kemeny constant \[7\] that appears particularly suitable for this task.

C. Organization

The report is organized as follows. Section II recalls some basic notions of Markov chains and graph theory, that will be the fundamental tools adopted in the subsequent analysis. Section III presents and discusses the main results obtained from our simulations. Finally, Section V concludes this manuscript and outlines our current research lines.

II. A PRIMER ON MARKOV CHAINS

Graph theory and Markov chains have been ubiquitously employed in many different fields of engineering and applied mathematics, including epidemiology \[21\], \[38\]. Here we only briefly recall some basic notions that will be later used in our analysis. In doing this, we shall repeat a discussion from \[7\], based on classic references \[22\], \[25\].

In this manuscript, we shall only consider discrete-time, finite-state, homogeneous Markov chains. In this situation, the Markov chain is a discrete time stochastic process \(x_k, k \in \mathbb{N}\) and characterised by the equation

\[
p(x_{k+1} = S_k | x_k = S_k, \ldots, x_0 = S_0) = p(x_{k+1} = S_{k+1} | x_k = S_k) \quad \forall k \geq 0,
\]

where \(p(E|F)\) denotes the conditional probability that event \(E\) occurs given that event \(F\) occurs.

A Markov chain with \(n\) states is completely described by the \(n \times n\) transition probability matrix \(\mathbb{P}\), whose entry \(\mathbb{P}_{ij}\) denotes the probability of passing from state \(S_i\) to state \(S_j\) in exactly one step. \(\mathbb{P}\) is a row-stochastic non-negative matrix, as the elements in each row are probabilities and they sum up to 1. Within Markov chain theory, there is a close relationship between the transition matrix \(\mathbb{P}\) and a corresponding graph. The graph consists of a set of nodes that are connected through edges. The graph associated with the matrix \(\mathbb{P}\) is a directed graph, whose nodes are given by the states \(S_i, i = 1, \ldots, n\), and there is a directed edge leading from \(S_i\) to \(S_j\) if and only if \(\mathbb{P}_{ij} \neq 0\). A graph is strongly connected if for each pair of nodes there is a sequence of directed edges leading from the first node to the second one. The matrix \(\mathbb{P}\) is irreducible if and only if its directed graph is strongly connected. Some important properties of irreducible transition matrices follow from the well-known Perron-Frobenius theorem \[25\]:

- The spectral radius of \(\mathbb{P}\) is 1; 1 also belongs to the spectrum of \(\mathbb{P}\), and has an algebraic multiplicity of 1;
- The left-hand Perron eigenvector \(\pi\) is the unique vector defined by \(\pi^T \mathbb{P} = \pi^T\), such that every single entry of \(\pi\) is strictly positive and \(\|\pi\| = 1\). Except for positive multiples of \(\pi\) there are no other non-negative left eigenvectors for \(\mathbb{P}\).

One of the main properties of irreducible Markov chains is that the \(i\)th component \(\pi_i\) of the vector \(\pi\) represents the
long-run fraction of time that the chain will be in state $S_i$. The row vector $\pi^T$ is also called the stationary distribution vector of the Markov chain.

In our application, a node of the graph is an individual with the contact tracing app installed in her/his smartphone. Two nodes are connected through an undirected edge if the app recognizes that two individuals have been in close contact for a sufficient time (i.e., sufficient enough for the spreading of the virus). If the app also records the amount of time, or the distance, between two individuals, then it would be possible to consider a weighted graph, where the weights could correspond to the probability of contagion (i.e., it would increase with the length of the contact, and decrease with the distance). So far, we do not consider this opportunity, as it is not clear whether this information will be truly made available or not. Also, note that the contact tracing apps give rise, in principle, to daily graphs which are not fully connected. This is due to the fact that some communities may be in fact isolated, and in general single individuals may not have significant contacts with other people during a day.

A. Mean first passage times and the Kemeny constant

A transition matrix $P$ with 1 as a simple eigenvalue gives rise to a singular matrix $I - P$ (where the identity matrix $I$ has appropriate dimensions), which is known to have a group inverse $(I - P)^\#$. The group inverse is the unique matrix such that $(I - P)(I - P)^# = (I - P)^#(I - P) = (I - P)$, and $(I - P)^#(I - P) = (I - P)^#$. More properties of group inverses and their applications to Markov chains can be found in [22]. The group inverse $(I - P)^#$ contains important information on the Markov chain and it will be often used in this paper. For this reason, it is convenient to denote this matrix as $Q^#$. The mean first passage time (MFPT) $m_{ij}$ from the state $S_i$ to the state $S_j$ denotes the expected number of steps to arrive at destination $S_j$ when the origin is $S_i$, and the expectation is averaged over all possible paths following a random walk from $S_i$ to $S_j$. If we denote by $q_{ij}$ the $ij$ entry of the matrix $Q^#$, then the mean first passage times can be computed according to [3].

$$m_{ij} = \frac{q_{ij}^# - q_{ij}^\#}{\pi_j} \quad i, j = 1, \ldots, n, i \neq j.$$  \hspace{1cm} (2)

We assume that $m_{ii} = 0$. The Kemeny constant is defined as

$$K = \sum_{j=1}^{n} m_{ij} \pi_j,$$  \hspace{1cm} (3)

where the right-hand side is independent of the choice of the origin state $S_i$ [22]. An interpretation of this result is that the expected time to get from an initial state $S_i$ to a destination state $S_j$ (selected randomly according to the stationary distribution $\pi$) does not depend on the starting point $S_i$ [9]. Therefore, the Kemeny constant is an intrinsic measure of a Markov chain, and if the transition matrix $P$ has eigenvalues $\lambda_1, \lambda_2, \ldots, \lambda_n$, then another way of computing $K$ is [27],

$$K = \sum_{j=2}^{n} \frac{1}{1 - \lambda_j}. \hspace{1cm} (4)$$

As can be seen from Equation (4), $K$ is only related to the particular matrix $P$ and it becomes very large if one or more eigenvalues of $P$ is close to 1.

Remark: The Kemeny constant admits many interpretations. First, it is related to the mean first passage times of the underlying Markov chain. But it is much more than this. It is also determined by the entire spectrum of the transition matrix. From a control theoretic perspective it resembles the sum of rise times along all the modes of the system. Thus, while the second eigenvalue of the transition matrix gives bound on the convergence rate of the underlying Markov chain, the Kemeny constant is akin to an average of rise times across all modes.

The Kemeny constant is usually computed using the group inverse (Equation (3)) or the knowledge of all the eigenvalues (Equation (4)). A more convenient computation, revealing the complexity of the calculation, can be developed as follows. Let $A$ be a $n \times n$ stochastic, irreducible transition matrix. We denote the eigenvalues of $A$ by $\lambda_1 = 1, \lambda_2, \ldots, \lambda_n$ and its characteristic polynomial is

$$p(s) = \det(sI - A) = (s - 1)(s - \lambda_2) \cdots (s - \lambda_n).$$

We define $\tilde{p}(s) = p(s)/(s - 1)$. The Kemeny constant of $A$ can be calculated using its characteristic polynomial:

$$K = \frac{1}{1 - \lambda_2} + \frac{1}{1 - \lambda_3} + \cdots + \frac{1}{1 - \lambda_n} = \frac{\tilde{p}'(1)}{\tilde{p}(1)}.$$  \hspace{1cm} (5)

Since $p(s) = (s - 1)\tilde{p}(s)$,

$$\tilde{p}(1) = \lim_{s \to 1} \frac{p(s)}{s - 1} = \lim_{s \to 1} \frac{p'(s)}{1} = p'(1),$$

and using the derivative of $\tilde{p}(s) = p(s)/(s - 1)$ we get

$$\tilde{p}'(1) = \lim_{s \to 1} \frac{p''(s)(s - 1) - p'(s)}{(s - 1)^2} = \lim_{s \to 1} \frac{p''(s)(s - 1) + p'(s) - p'(s)}{2(s - 1)} = \frac{1}{2}p''(1).$$  \hspace{1cm} (5)

Hence, the Kemeny constant of the matrix $A$ is

$$K = \frac{1}{2} p''(1).$$

Remark:

- A characteristic polynomial interpretation of $K$ is also given in [4]. However, this derivation uses the adjacency
matrix. To the best of our knowledge, our derivation is the first direct computation using the transition matrix.

- Calculation of the Kemeny constant is of the same computational complexity as that of calculating the determinant.
- The determinantal interpretation of $K$ suggests a deeper control theoretic interpretation of the Kemeny constant.

B. Clustering and the second eigenvector

Another interesting quantity is the second eigenvector. In general, it is well known that the eigenvectors of transition matrices for undirected graphs have good clustering properties, see for instance [37]. Comprehensive reviews of tools and techniques that can be used to identify communities are given in [12] and [33]. The LancichinettiFortunatoRadicchi benchmark is an algorithm that generates benchmark networks which have a priori known communities and are used to compare different community detection methods [10], [24]. Other data resources can be found in [35].

Detection of communities is an important topic in a wide range of fields of application, for example social, biological, or legislative networks. Among traditional methods, as described in [12], this includes: graph partitioning (dividing the nodes into groups of a particular size, with the minimum edges cut), hierarchical approaches (to reveal multilayer nature of the graph), partitional approaches (maximization or minimization of distances between nodes/centroids), and spectral clustering (applying the standard methods of clustering, but based on a transformation of the set of objects into a set of points in space) ([34], [28]). Modularity-based community detection is another popular class of community detection methods [30]. Modularity characterizes the strength of division of a network into communities, where a high value refers to good partitions. Therefore, to find an optimum clustering structure different optimization algorithms have been proposed, including greedy method, simulated annealing, and extremal optimization. Divisive or centrality-based community detection algorithms are based on the identification of the connections between communities and cutting them. To find the external edges [15] proposed an algorithm based on a measure of node importance centrality. Particularly, the betweenness centrality measures how often a node lies on the shortest path between two nodes in the graph. The algorithm is based on the cyclic calculation of centralities and removal of edges with the highest values.

In [7] it was shown that the sign pattern of an eigenvector associated with an eigenvalue close to 1 can be used to identify two different clusters. Since an irreducible transition matrix has only one eigenvalue equal to 1, such an eigenvector is called the second eigenvector (as it is associated with the eigenvalue of the second largest modulus). In our application, it may be indeed critical to develop the ability to use the network reconstructed by the contact tracing app to identify possibly hidden communities, as it is unfortunately well-known that an infected individual may quickly spread the virus within her/his community. In this manuscript we shall show that a single picture of a daily network may not be enough to clearly identify existing communities, but the second eigenvector of a cumulative graph that keeps record of contacts of the previous days as well, provides a more accurate information of the underlying structure of social communities.

C. PageRank and Betweenness Centrality

Our starting point is that we are interested in undirected and un-weighted graphs. In this case, if teleportation is not considered, then PageRank simply corresponds to the Perron eigenvector, and it is well-known that node degree and the Perron eigenvector are highly correlated [16]. In addition, our graph structures have some other important properties. In particular, if we denote by $A$ the symmetric $[0,1]$ adjacency matrix that has ones in positions $A_{i,j}$ and $A_{j,i}$ if individuals $i$ and $j$ are in close contact for a long enough time, then it can be noticed that the row-stochastic matrix $\mathbb{P}$ of our interest can be obtained as

$$\mathbb{P} = D^{-1}A,$$

where $D$ is the diagonal matrix, whose $D_{ii}$ entry corresponds to the degree of the $i$th node of $A$. Also, the eigenvalues of the row-stochastic (non-symmetric) matrix $\mathbb{P}$ are the same of the symmetric matrix $D^{-1/2}AD^{-1/2}$, and we remind the reader that eigenvalues of symmetric matrices are real. Thus: all eigenvalues and eigenvectors of $\mathbb{P}$ are real as well. This shall play an important role in the following discussion.

Another measure of centrality in graphs is represented by betweenness centrality. In its basic definition, it measures the number of shortest paths that pass through a node [13], [14]. In principle, it is known to show which nodes are acting as “bridges” between communities in graphs. For example, in Figure 1 all shortest paths connecting red and blue nodes will pass through the yellow node, which consequently has the maximum betweenness centrality value in the graph. However, in many networks, including the contact networks of our interest, the information (or here, the virus) does not flow along shortest paths, and will most likely take a random route [29]. Accordingly, a measure of betweenness...
The two indicators provide completely different results. In Kemeny constant (black). It is evident from the figure that highest degree (magenta) and the 10 individuals with highest degree were available, Figure 2 shows the 10 individuals with the highest degree from other communities. In the assumption that 10 tests meeting individuals from the same community than people were available, it is assumed that 240 individuals belong to 6 different communities (with 40 people within each community). Communities are created by giving a higher probability to both such communities, and if that node is removed, then the community tends to infinity (i.e., after removing that node, the graph is split into two non-connected sub-graphs, and it is impossible to find a path from one community to the other community, thus the walking time tends to infinity).

Remark: The Kemeny constant may be interpreted as the average time to take a random walk in the contagion graph, weighted according to likely destinations. As such it takes into account the stationary distribution, and the first mean passage times from a given starting location and all other destinations. As such, this constant represents a compromise between indicators that use only the stationary distribution (such as PageRank and node degrees), and those using path-based algorithms (such as the betweenness centrality indicators). Thus, the indicator should work in highly connected single-community graphs, and in more sparse graphs, associated with many unknown sub-communities.

III. Simulation results

A. Who should be tested: node degree vs. Kemeny constant
We use the Kemeny-based indicator as a proxy to determine individuals that should be tested. For this purpose, we associate with each node the value of the Kemeny constant that is obtained when that node is removed from the graph. The rationale of this choice is that nodes connecting two communities are associated with very high Kemeny constants, as walking times become much larger if such nodes are removed. In particular, if a single node connects two communities then it implies that only one person belongs to both such communities, and if that node is removed, then the Kemeny constant tends to infinity (i.e., after removing that node, the graph is split into two non-connected sub-graphs, and it is impossible to find a path from one community to the other community, thus the walking time tends to infinity).

Results are exemplified in Figure 2. In this example it is assumed that 240 individuals belong to 6 different communities (with 40 people within each community). Communities are created by giving a higher probability to meeting individuals from the same community than people from other communities. In the assumption that 10 tests were available, Figure 2 shows the 10 individuals with highest degree (magenta) and the 10 individuals with highest Kemeny constant (black). It is evident from the figure that the two indicators provide completely different results. In particular, the Kemeny constant identifies the individuals that meet people from different communities, independently from how many people they meet overall. While, in principle, benefits may be found for both solutions, we argue that this feature of the Kemeny constant may be particularly convenient as a better coverage of the graph is obtained (the same individual covers more than only one community), and also is convenient to intercept possible new virus outbreaks occurring in communities, when they are still in their early stages.

B. Impact of communities on indicators
Figures 3 and 4 compare how different indicators provide different outcomes depending on the existence or not of communities. In particular, Figure 3 refers to a case where people meet with the same probability people belonging to their community and to other communities (i.e., communities degenerate into a single large community). In this case, Figure 3 shows that both indicators based on node degrees and those based on random walks provide the same results. On the other hand, when the probability of meeting people of other communities is decreased, then communities reappear in the graph, and the two categories of indices clearly provide different results, see Figure 4.

C. Impact of tests on the dynamics of an epidemics
We now try to quantitatively evaluate the impact of using one specific indicator over another one (i.e., Kemeny indicators vs. Node degree) in terms of the spreading of the virus. For this purpose, we consider a very simple scenario where we assume that every day the individuals that rank in the top positions according to the different indicators are tested. If they are found infected, then they are quarantined for two consecutive weeks. Also, in this case, all their contacts of the same day are tested (and quarantined if positive). Note that in principle the procedure may be iterated in the past (i.e., the contacts of the previous days may be tested as well), but this is not considered here for simplicity. At the beginning of a simulation, two random individuals belonging to random communities are assumed to be infected. This simple case study may be associated with the spreading of the virus in a network of asymptomatic infected individuals, as we do not consider individuals who may autonomously decide to get tested (e.g., because they have developed symptoms), and only individuals detected by the test are quarantined.

Figure 5 shows the results of running 10 repetitions of the simulations for 30 days. The Kemeny constant gives an improvement by reducing the number of people infected, but does lead to an increased total number of days spent in quarantine by the population.

D. Identification of Communities
As mentioned in Section 1B, the second eigenvector (i.e., the eigenvector associated with the second eigenvalue of largest modulus) has clustering properties, and may be used to infer the presence of underlying communities. Of course, the knowledge of such communities may be conveniently used as further information to affect the choice of who should be tested. In fact, some communities may be easy to spot (e.g., care homes or families), but in other cases it may be less trivial to identify communities (people who go to the...
Fig. 2. The six existing communities can be clearly identified by visual inspection. Assuming that up to 10 individuals can be tested, the black circles show those that would be chosen according to their highest Kemeny value, while the nodes in magenta correspond to the nodes (i.e., individuals) with highest degree. Edges correspond to the random interactions on one day.

Fig. 3. If no communities exist, then all indicators appear to select the same nodes (i.e., those with highest degree) for testing.

Fig. 4. When communities arise, then it is easier to appreciate the different strategies pursued by indicators based on node degrees (left) and those based on random walks (right).

same church, or individuals who attend the same clubhouse).

Figure 6 shows the ability of the second eigenvector to identify the six existing communities. In principle, similar entries of the second eigenvector are expected to indicate people belonging to the same community. Also, it can be noticed that after a single day of observation of the contact graph, very noisy values are observed in the second eigenvector, and only after a consistent number of days of observations it is possible to clearly separate the existing communities.

IV. COMMENTS ON COMMUNITY DETECTION ALGORITHMS

A. Potential benefits of Kemeny based sampling

While this is the first use of the Kemeny constant in sampling problems that we are aware of, it is related to several other methods in the literature. In particular, the connection to the
Fig. 5. Impact of testing individuals using metrics based on the Node Degree (top) or Kemeny constant (bottom). The left-hand figures show the total number of people who were infected during a 30-day simulation. The right-hand figures show the cumulative number of days spent in quarantine for members of the population ($N = 240$). The boxplots show the distribution of 10 repetitions of the simulation process, to give insight into the level of variability between runs.

Fig. 6. Entries of the second eigenvector as a function of the number of days of observation.
random walk betweenness indicator is immediate. However, it is worth noting some important advantages of the Kemeny constant.

- First, is relatively simple to compute.
- Second, differently from the random walk betweenness, and other similar indicators that are computed on the basis of the adjacency matrix, the Kemeny constant is computed using the transition matrix. Accordingly, it can take into account weighted graphs, where the probability of infections can be properly modelled, assuming that the contact tracing app has the ability to keep track of the duration of contacts, and/or of the relative distance. This allows for asymmetric and variable transmission probabilities between different communities.
- Third, directionality can be important. Diseases can have asymmetric transmission paths between compartments. Furthermore, behavioural differences between communities, such as non-homogeneous wearing of face-masks, is also likely to lead to further asymmetries in transmission. Such asymmetries lead to directed graphs. While the Kemeny constant readily extends to such situations, it is not immediately evident how other similar indicators extend to this case in a computationally efficient manner.

B. Time-varying graphs

While the applicability of the Kemeny constant is clear when sufficient information about the social graph has been acquired in advance, if information about the social graph has not been acquired before lockdown, we will have no information to work with in the early stages. As the community leaves lockdown, the graph will change structure as particular activities are added and removed from the list of prohibitions, depending on the rules of lockdown. (e.g. office cliques are irrelevant when offices are closed, sports club cliques only become relevant when that sport is legalised again. However, other keyworker links like bus drivers, shop workers and taxi drivers will be constantly active, although with different levels of neighbourhoods). This effect is somewhat mitigated by our averaging methods, but is an important factor for further discussion.

C. Proactive intervention

Note that in the simple simulation in section III-C, while the nodes remained in the same community throughout, the graph representing their interactions was drawn randomly each day. This means that individual nodes do not remain in their role as potential bridge between communities for more than that day. An alternative model which drew a random graph structure at the start, then simulated random interactions on the edges might be a more realistic model, and furthermore would have more consistency between days, allowing us to benefit further from the precision of the Kemeny constant. In this scenario, nodes near bridges between communities would be likely to face repeated testing on multiple days. In real life this might face resistance, depending on the context. For example, while testing professionals, such as care workers repeatedly as part of their job would probably have high compliance, there may be others who would resist that. An alternative approach is to identify and intervene with bridge nodes proactively before infection. Such intervention could include quarantine measures, or more targeted education or police enforcement.

Comment 1: Our motivation is to make the community aware of a tool that can be used in the context of contact tracing. Since most currently proposed contact tracing apps do not enable a central picture of the connectivity graph, a natural question concerns the utility of any such approach. This is a valid concern. While not the concern of this present paper, we note here that distributed estimation of the Kemeny constant is in principle possible by initializing multiple random walks along the connectivity graph. Such strategies are considered in \([32]\) in the context of a distributed reinforcement algorithm, and can be enabled and secured using distributed ledger technology. We believe that such estimation strategies are realizable using the currently envisaged Apple and Google contact tracing API's. The study of such algorithms will be the subject of future publications.

Comment 2: As a final remark we note that the work presented here directly applies the ideas pioneered in \([2]\) by some of the authors of the present manuscript. In that paper the Kemeny constant, and its derivative, had been used to identify critical nodes and edges in networks, according to a node removal and renormalization approach. Since publication of that paper in 2011, many authors have applied the same idea in different application domains; see for example \([2]\) in Markov influence graphs.

V. CONCLUSIONS

We have presented a framework for using the Kemeny constant of a graph to identify and analyse bridges between sub-communities. The use of the Kemeny constant is computationally convenient, and also supports the study of weighted and directed graphs.

Applications of testing, tracking and tracing will be critical in helping countries to safely reopen activities after the first wave of the COVID-19 virus, but they will be faced with limitations on the number of tests they can apply each day, and the compliance of the population in respecting quarantine isolation measures. The theoretical and simulation results...
presented in this paper show how the application of graph theory and the Kemeny constant can be conveniently used to efficiently identify and block new virus outbreaks as early as possible by removing possible ‘super-spreader’ links that transmit disease between different communities.

The simulation models have deliberately been kept very simple, to illustrate the core concepts, but the work should be applicable to any simulation model which incorporates a graph or network representation of the population and their interactions. The work also has implications for the design of tracking processes and apps, to ensure that they can provide complete information on both the adjacency of nodes and the transition matrix. Further analysis will be needed to evaluate the efficacy of the approach when the knowledge of the network is incomplete (due e.g. to incomplete update of the tracking application).

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