Invited Paper: The Case for Small-Scale, Mobile-Enhanced COVID-19 Epidemiology

Fan Yi, Yaxiong Xie, and Kyle Jamieson
Department of Computer Science
Princeton University, Princeton, New Jersey 08540
Email: fanyi, yaxiongx, kylej@princeton.edu

***Abstract*—Our understanding of COVID-19 pandemic epidemiology has many gaps, with many challenges arising on a global scale. This paper looks at the problem at a smaller geographical scale, the extent of the campus of a large organization. Equipped with an asymptomatic testing program and rough location data from the campus wireless network, we make the case that epidemiological models may be informed from this new source of data, which offers fidelity at the temporal resolution of seconds and spatial resolution of a Wi-Fi cell size, in particular for the tasks of pinpointing clusters of cases and contexts of infection transmission. We sketch the design of a system that fuses the two foregoing information streams and explain how the result can be incorporated into standard epidemiological models of communicable disease, both for better parameter estimation in elementary models, as well as for providing spatial inputs into more sophisticated models. We conclude with logistical and privacy considerations we have encountered in an associated ongoing study, to inform similar efforts at other organizations.**

***Index Terms*—COVID-19, SARS-CoV-2, contact tracing, Wi-Fi, privacy, epidemiology.**

I. Introduction

While the ongoing COVID-19 pandemic has highlighted the importance of contact tracing, it has also exposed the challenges of performing epidemiological analysis and contact tracing for a virus that transmits asymptomatically and propagates in an airborne manner. Further exacerbating these challenges is the fact that in general, traditional contact tracing, which involves primarily human effort in identifying and communicating with the close contacts of a confirmed case, has suffered from low compliance rates in the US [1] and large budgets in, for example, the UK [2]. However, over the past year, two notable organizational trends have emerged in the US, Europe, and other countries, in particular.

First, in the past and particularly during the ongoing pandemic, people in the US have spent and will likely spend the majority of their time on a corporate or academic campus. As users roam about campus, their smart phones connect to a series of hotspots that comprise the campus Wi-Fi network. Once configured by a user, this securely-authenticated connection mechanism is automatic, and data concerning such connections is logged on the campus wireless network servers. With knowledge of each hotspot's deployed building and room location, this data captures users' rough room-level locations, as well as the corresponding window of time during which the user is connected to a certain hotspot. Data is therefore available for the location of the Wi-Fi hotspot, beginning and ending time of the user's association, and average signal strength between access point and mobile client during the association. There is good reason to believe that this room-level data may be of better use than simple "as the crow flies" distance between two mobile devices, as it may correlate better than simple distance with two users sharing or not sharing the same room air space. Therefore, a number of researchers [3]–[6] and at least one Wi-Fi infrastructure vendor [7] have proposed leveraging this Wi-Fi infrastructure for contact tracing.

Second, corporations and universities have begun to set up in-house or contracted asymptomatic COVID-19 testing programs, in order to open their campuses and workplaces more safely. Some pharmacies are offering these services as a product to corporations. This means that in addition to rough room-level location data, corporations and universities will and in some cases already do have asymptomatic testing results also available in house. This is expected to aid the operational process of reopening and managing the pandemic in the near and mid-term future, allowing greater numbers of people to return to campus and/or reducing the COVID-19 caseload, thus potentially saving lives.

This paper aims to make the case that the "join" of the two foregoing sources of data may serve as a new source of information for epidemiological models, particularly for those models that are attempting to pinpoint clusters to disease transmission, and those models attempting to understand SARS-CoV-2 transmission in various indoor spaces, with varying levels of ventilation and other safety measures.

Current medical consensus indicates that SARS-CoV-2 is transmitted through contact surfaces, droplets, and aerosols (airborne transmission), and that risk of transmission through the latter two modes, in particular, may increase with increased duration of close contact to a positive case. As SARS-CoV-2 spread requires contact between people, understanding the contact between members of the organization is important. Construction of a realistic contact network identifying the time, duration, and location of contact between individuals is therefore useful.

We propose mathematical and statistical modeling approaches to infer contact patterns from de-identified Wi-Fi network data and characterize the spread of SARS-CoV-2. Integrating contact and location information with weekly viral testing results from the organization can give a unique

perspective to identify locations where transmission is more frequent, as well as potential super-spreading events, which can, in turn, help prevent onward transmission.

The rest of this paper is structured as follows. Section II presents further details on our study design and information flow. Section III details several different ways the study data can inform some of the leading disease models in the literature. We explain our algorithm on identifying risky spaces, and how can it facilitates mitigating the disease transmission in Section IV. Section VII and Section V introduces the potential usage of Wi-Fi data in contact tracing systems, and the principles for improving subjects' privacy, respectively. We discuss other wireless technologies for contact tracing and proximity prevention in Section VI.

II. Study Design

While we describe the design of the system we have constructed at Princeton University, most other organizations with their own campuses have similar wireless networks, and many others have similar asymptomatic COVID testing programs.

A. Principal Actors

To allow other investigators to create similar studies, we begin with a list of the principal actors involved in our own study, and describe their roles in the research.

1) Health authority: Our study is conducted with the consultation and collaboration with the organizational health department, which has a primary interest in keeping the employees and students associated with the organization safe and healthy at work. In our organization, the health authority runs the organization's asymptomatic testing program with an on-site lab, whose results flow into the IT department servers. This affords easy access to data as well as improving privacy and data security considerations, as discussed in Section V.

2) Researchers: As the work is multidisciplinary by nature, it is essential to involve epidemiologists, computer scientists, and medical clinicians. It is also useful to consult with the organization's health authority and occupational safety authority for real-world context, which is vital to accurately interpret the data.

3) Information Technology department: In most organizations, the IT department runs the campus wireless network, whose servers contain the Wi-Fi association data that studies of this type require. In the case of our study, we have worked with the IT department to ensure certain privacy properties as discussed in Section V.

4) Research oversight bodies: As studies of this type work with human subjects, academic institutions generally have an Institutional Review Board (IRB) that approves research studies. While IRB review protects human subjects, it does not consider other institutional compliance issues, and so at Princeton, data access is governed at the functional unit level. This institutional review identifies conditions, articulated in a *Data Use Agreement*, that ensure that any data made available to researchers be used in a manner that is consistent with institutional policy and state and federal regulations.

5) Research subjects: While consent from study participants obtained on a case by case basis, obtaining a sense of "buy in" from the greater community at large is important to encourage participation. Explaining the benefits of the study to the community as well as to our knowledge of infectious disease helps in this regard, through the use of press releases and communications to the community at large.

B. Design Overview

In this section we describe the data sources our study uses, as well as the mechanisms our study uses to move data to the right locations within our organization to enable the analysis we describe in the remainder of the paper.

1) Campus wireless network data collection: Our campus wireless network uses a system provided by Aruba Networks, Inc., of which a subsystem called *AirWave* collects and correlates information from several components of the network, including hotspots, back-end "controller" servers, and authentication servers.

The data collected consists of a series of tuples containing the following data:

1) A unique user identifier in the organization;
2) the average signal strength (measured in dBm units) of the connection;
3) access point (AP) name, which uniquely identifies the AP the user connects to;
4) connect time: time of day and date the user connected;
5) disconnect time: time of day and date the user disconnected.

Information collected via the AirWave subsystem is stored in a securely-encrypted form in a secure virtual machine located on physical server machines owned by our IT department, and located at a data center nearby.

2) Asymptomatic COVID test data collection: Our study also uses the results of the on-campus testing for active infection via saliva sampling. This is an RT-PCR test administered by self-collection of a saliva sample in private and then submitted to our organization via drop boxes or delivery to an on-campus location.

3) Researcher access: The two foregoing data streams are de-identified as described in Section V, and filtered to include only participants who have voluntarily consented to the research. Then the data are presented to the researchers in de-identified form on a virtual machine accessible only to the researchers via the organization's single sign-on authentication mechanism, which employs two-factor authentication. At no time do the researchers have access to identifiable data, and under the terms of the Data Use Agreement, the researchers are explicitly prohibited from attempting to identify or contact any individual who might be included in the data.

III. Model Integration of Wi-Fi/COVID Test Data

In this section we consider multiple different ways of integrating Wi-Fi and asymptomatic COVID testing program data into various models of epidemiological disease spread, a key tool in the arsenal of techniques epidemiologists use to study

1) For each positive COVID test with study identifier x:
   a) Construct a list of study ids $\mathcal{N}_x$ in the same room as x for at least time T_{mct} within *transmission window* days W_t around x's positive test result date.
   b) For each $y \in \mathcal{N}_x$, query y's test results within a *incubation window* of time W_i after each encounter.
2) Estimate $\hat{c}$ as the fraction of positives in Step 1b.

Fig. 1. Estimation of the rate constant c in the SIR model, the rate at which susceptible individuals are infected after meeting infected individuals.

communicable diseases. We begin with the simplest models and consider progressively more complex models, comparing their advantages and limitations given the granularity and amount of data likely to be available to hand.

A. SIR Model Integration

The classic SIR model [8] describes the number of susceptible (S), infected (I), and recovered (R) individuals in a population, over time:

$$\begin{aligned} \dot{S} &= -cSI \\ \dot{I} &= cSI - wI \\ \dot{R} &= wI \end{aligned} \tag{1}$$

where rate constants c and w describe the rate at which susceptible individuals get the disease when meeting infected individuals, and infected individuals recover from the disease, respectively. This model assumes that recovered people are immune to the disease.

1) Estimation of SIR rate parameters: Even in this simple model, we may be able to estimate rates c and w in the following way, as shown in Figure 1. To estimate the rate at which susceptible individuals get the disease when meeting infected individuals ($\hat{c}$), we iterate over the study identifiers of positive COVID tests, and consider the close contacts of each within a *transmission window* of the respective positive COVID test, a period of time around the positive COVID test during which infection could plausibly take place. We then query COVID test results of that set of close contacts over a time window that reflects plausible incubation time of the disease (*incubation window*), and estimate $\hat{c}$ as the total fraction of positives over all these queries.

The foregoing $\hat{c}$ estimation algorithm relies on several time window parameters that are informed by the literature and public health advice, and hence may be updated as the current advice changes. We suggest a minimum contact time $T_{\mathrm{mct}} =$ 10 minutes based on US CDC guidelines as of publication.

The transmission window W_{t} should be set to three days before, through to one day after the positive COVID test result. The beginning edge of the transmission window in the past covers the potential for asymptomatic shedding and transmission prior to the positive test result, while the trailing edge of the transmission window accounts for the time between a positive test collection and the quarantine of the individual due to any laboratory processing and contact tracing delays. This window's settings are therefore informed by the organization's testing, tracing, and quarantine protocol: at Princeton individuals who test positive in the asymptomatic testing program are required to quarantine away from others on campus.

The incubation window W_{i} should be set to three days after, through to nine days after the encounter between the two individuals. These figures represent an incubation window that covers about 80% of all incubation times, and can be adjusted as medical knowledge improves or virus variants impact incubation time.

To estimate the rate at which infected individuals recover from the disease ($\hat{w}$), we can again select from the data all positive viral test results, and for each (again with study identifier x), query the next negative viral test result. By analyzing the distribution of these recovery times we expect to see a significant amount of noise in the upper quartiles of the distribution representing extended quarantine times and some amount of delay in administering a follow up viral test. The information contained in the lower quartiles of this distribution, however, trace an estimate of the distribution of recovery times, whose mean can be used to estimate w.

2) Spatial parameterization of the SIR model: An issue with SIR model is that it assumes healthy and infected persons are distributed homogeneously in space, which is not true in reality and the heterogeneous distribution has significant influence on a pandemic. Even for the simple SIR model, it may be possible to subdivide the model into multiple smaller models, each covering different regions of the campus being studied. While conceptually straightforward, each such division reduces the amount of data collected by the sub-model size, and so data fidelity may suffer if the subdivision is performed at a fine granularity: we take this issue up next.

B. SIR-DDFT Model Integration

Since the SIR model has no formal notion of space *a priori*, Vrugt *et al.* combine the SIR model with a dynamical density functional theory (DDFT) to model social distancing and isolation behavior. This SIR-DDFT model [9] models the time evolution of a density field with free energy F as follows:

$$\begin{aligned} \partial_t S &= \Gamma_S \vec{\nabla} \cdot \left(S \vec{\nabla} \tfrac{\delta F}{\delta S} \right) - cSI \\ \partial_t I &= \Gamma_I \vec{\nabla} \cdot \left(I \vec{\nabla} \tfrac{\delta F}{\delta S} \right) + cSI - wI \\ \partial_t R &= \Gamma_R \vec{\nabla} \cdot \left(R \vec{\nabla} \tfrac{\delta F}{\delta S} \right) + wI \end{aligned} \tag{2}$$

The model admits different mobilities Γ_S, Γ_I, and Γ_R to model the mobility of susceptible, infected, and recovered individuals, respectively. We propose to estimate the mobility coefficient via a query of the Wi-Fi hotspot association time series. Specifically, for each individual, we have the location information of the associated Wi-Fi hotsopts, and the corresponding time stamps. Within a mobility time window W_{mob}, the velocity of the user V is:

$$V = (L_S - L_E)/W_{\mathrm{mob}} \tag{3}$$

where L_S and L_E are the locations of the initially and lastly connected Wi-Fi hotspots, respectively, during the mobility time window W_{mob}. By considering the accuracy requirements of mobility and the collected Wi-Fi data granularity, we set the mobility time window $W_{mob} = 1$ minute. After we obtain individuals' mobility estimation, we further separate them into the three respective SIR-DDFT categories and averaged over all the individuals in each category.

In this model, the free energy F is given by

$$F = F_{id} + F_{exc} + F_{ext}. \tag{4}$$

The first term F_{id} is the ideal gas free energy, which can be calculated from the time evolution of a crowd density field [9]. We propose to estimate the density field via the location distribution of all users, where we use the associated APs' locations to approximate users' locations. The second term F_{exc} is called excess free energy, which captures the effect of interactions among people, it incorporates the effects of social distancing and self-isolation on crowd density, which can be seen as a repulsive potential between different persons. Social distancing corresponds to a repulsive potential between healthy persons, and self-isolation refers to a repulsive potential between infected persons and other persons. The last term is the external potential, it corresponds to externally imposed restrictions on crowd movements, including travel bans or the isolation of a region with high rates of infection. This term can be neglected in our campus scenario.

IV. Identifying Risky Spaces

Since the focus is on public spaces, we may be able to retrospectively identify "risky" spaces, and therefore facilitate mitigating transmission.

One possible algorithm for scoring the risk level of a particular space is as follows. First, enumerate all of the locations in our study by AP, *i.e.*, $\{l_1, l_2, \ldots, l_L\}$ if there are L APs in the entire campus. Then, we iterate first over all the positive viral test results and then over all the locations of the positive user existing within the transmission window period of time W_t (*cf.* Section III-A1: this basic structure of the algorithm is similar). With this list of AP locations where positive users have shown up, we construct a list of potentially exposed users with study IDs $\mathcal{N}_x$ in the same room as positive users for at least time T_{mct} within transmission window days W_t around positive users' positive test result date. We further query each potentially exposed users' test results within an incubation window of time W_i. If the viral test is positive, we identify this as a probable transmission event from one user to another, and then extract the location of that transmission event l_t ($t \in [1, L]$) and increment a *risk count* vector variable r_l. In this way a risk map can be constructed at the same granularity as the AP deployment in the campus Wi-Fi network that characterizes space risk; Figure 2 specifies this algorithm.

Our study may benefit society by increasing the understanding of the characteristics of high-risk environments that can inform pandemic responses in other areas, including other universities and similar workplace campuses. Much future analysis taking air flow, ventilation, and other safety mechanisms is possible to follow up this approach.

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   a) Construct a list of study ids $\mathcal{N}_x$ in the same room as x for at least time T_{mct} within *transmission window* days W_t around x's positive test result date.
   b) For each $y \in \mathcal{N}_x$:
      i) Query y's test results within a *incubation window* of time W_i after each encounter.
      ii) Increment risk count variable r_l if the viral test (whose location is l) is positive
2) Report the location risk distribution $\{r_1, \ldots, r_L\}$.

Fig. 2. Risk scoring of different locations based on the frequency of estimated probable transmission events in each space.

V. Privacy and Subject Protection

The proposed fusion of epidemiological modeling, location data, and asymptomatic testing program data is unique to our best knowledge, and so certain privacy issues arise.

The first and perhaps most notable hazard is the publication of individual location information. A reasonably foreseeable risk to the subject as a result of participation is the theoretical risk of breach of privacy of user location and COVID test result data. This risk is mitigated by the de-identification of all user data at the source of the data within the organization itself. Even if de-identified, there is another foreseeable risk because of the theoretical possibility of re-identifying users based on the data and real-world observation, for example. To mitigate this concern, data must be aggregated, and differential privacy techniques should be applied to any aggregated data before it is published in order ensure that statistically, individuals cannot be identified.

Beyond data publication itself, in an April 2020 webinar [10], Felten of Princeton's Center for Information Technology Policy identified several principles for improving subjects' privacy in the context of contact tracing apps, many of which overlap with our own proposed list for micro-epidemiology:

a) Principle: Use study identifiers, and recognize their limitations.: All individual identities are encrypted before use for the research purpose, with the encryption key stored at the data source (Office of Information Technology for wireless network data; University Health Services for COVID test result data). The study should ask for users informed consent to use these data, with all University netids, PUIDs, and subject names therein encrypted and anonymized,

b) Principle: Keep data in situ*:* In general, there is concern over the location of users' data and any sale of such data. To mitigate such concerns, we suggest keeping the data *in situ* to the greatest amount possible.

c) Principle: Informed consent: As part of the IRB process, studies like the present are required to gain informed consent from participants. As such, our organization has

instructed our IT department not provide to the research study data from individuals who decline to consent, or who have not viewed the consent form. Our IT department filters the data feed it provides to the study to include solely data from individuals who have consented.

d) Principle: Consider scoping data: both in space and time. In space: with the data redacted and scoped to include solely "public" locations ("public" locations defined to exclude all Residential College buildings, dormitories, and on-campus faculty/staff/student housing), In time: Use from a point in time beginning 90 days prior to today and continuing until the closure of the study.

e) Principle: Use study ids and recognize limitations: In our ongoing study, we de-identify user location and COVID test data that is stored on IT department servers in the following way.

Our IT department assigns each user a *study ID*, a unique identifier assigned for the purposes of the study that is separate from other identifiers such as email, employee identifier, name, *etc.* A separate *key file* the IT department holds in secure storage links study IDs to employee IDs, the purpose being the ability to delete the key file once the study concludes so that no one has access to personal identifiers. We have instructed our IT department to encrypt study IDs in the location data feed, and provide the research server with a full data feed but containing solely these encrypted study IDs. We have also instructed our IT department to work with University Health Services to map names to study IDs, then apply the same encryption function to the data subsequently stored on the research server.

The researchers will not publish any data tied to individuals, and will apply differential privacy techniques to aggregated data that is published, to ensure that that aggregated data cannot be tied to any individuals.

VI. Related Work

a) Contact tracing systems: Contact tracing is widely used to slow down the spread of COVID-19 [11]. Traditional contact tracing involves labor-intensive case investigation and thus is time-consuming and unscalable. Such methods have also suffered from low compliance rates in the US [1] and large budgets in, for example, the UK [2]. To make contract tracing practical, many technology-empowered cost-effective solutions have been proposed to automate this process.

Location-based contact tracing systems [12]–[15] track the social distance between citizens using GPS locations of mobile devices people carry. Tracking the exact location of citizens, however, raises serious concerns about the user privacy, significantly hindering its wide deployment. Proximity-based contact tracing solutions that directly estimate the proximity between citizens using Bluetooth Low Energy (BLE) beacons have been proposed by both the research community [6], [16]–[19] and commercial companies, like MSR [20], Google and Apple [21], [22], which preserves user privacy by hiding the absolute user location and thus is widely adopted by diverse organizations and governments of many countries [12], [13]. Our Wi-Fi data and COVID test data could help to streamline and increase the accuracy of existing contact tracing efforts.

b) Proximity prevention systems: A number of systems have been devised whose goal is to help people maintain social distancing measures that health authorities worldwide recommend or require. They vary in their design, using Wi-Fi probes [23], Bluetooth beacons [24]–[26], ultra wideband (UWB) probes [27], or a combination of Bluetooth beacons and UWB probes [27], [28] to estimate the proximity between mobile users. When close-contact, *i.e.*, distance smaller than six feet, is identified according to the proximity, the proximity prevention system signals an audible or tactile alert to one or more persons' wearable devices that they are too close.

c) Mathematical theory of epidemiology: Mathematical theory has been widely used to analyze the epidemiological disease spread, and containment. [29] has adopted a analytical model to explore the relationship between the level of infection, vaccination and community immunity. [30] leverages epidemiological models to explore estimates for the magnitude and timing of future COVID-19 cases, given different assumptions regarding the protective efficacy and duration of the adaptive immune response to SARS-CoV-2, as well as its interaction with vaccines and nonpharmaceutical interventions. The widely used susceptible-infected-recovered (SIR) model [8] can take externally imposed restrictions into account by varying the spreading rate and recovery rate. However, a drawback of this model is that it assumes healthy and infected people are homogeneously distributed in space. In facing of spatial diversities, some disease-spreading theories [31]–[35] extend the SIR model to reaction–diffusion equations. An issue with the reaction–diffusion equations is that they do not take crowd interactions into account, including the effect of social distancing and self-isolation. To make a more accurate estimation of the epidemiological disease spread, we apply our data on the SIR-DDFT model [9], which is a general form of the reaction–diffusion equations.

VII. Ongoing and Future Work

Currently, our project is recruiting subjects, to reach a dataset size sufficient for performing experiments and fitting the parameters of those models. Operationally, Wi-Fi and COVID test data may in future help to streamline and increase the accuracy of the contact tracing efforts of health authorities. Such efforts may assist the health authority and the organization's administration to understand the pandemic's evolution on their campus, thus to make more informed decisions on mitigation measures in future pandemics or outbreaks of the current pandemic.

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