

# Quarantine in Motion: A Graph Learning Framework to Reduce Disease Transmission Without Lockdown

Sofia Hurtado

*Electrical Computer Engineering  
University of Texas at Austin  
Austin, Texas  
slhurtad@utexas.edu*

Radu Marculescu

*Electrical Computer Engineering  
University of Texas at Austin  
Austin, Texas  
radum@utexas.edu*

Justin Drake

*Texas Advanced Computing Center  
University of Texas at Austin  
Austin, Texas  
jdrake@tacc.utexas.edu*

**Abstract**—Exposure notification applications are developed to increase the scale and speed of disease contact tracing. Indeed, by taking advantage of Bluetooth technology, they track the infected population’s mobility and then inform close contacts to get tested. In this paper, we ask whether these applications can extend from reactive to preemptive risk management tools? To this end, we propose a new framework that utilizes graph neural networks (GNN) and real-world Foursquare mobility data to predict high risk locations on an hourly basis. As a proof of concept, we then simulate a risk-informed Foursquare population of over 36,000 people in Austin TX after the peak of an outbreak. We find that even after 50% of the population has been infected with COVID-19, they can still maintain their mobility, while reducing the new infections by 13%. Consequently, these results are a first step towards achieving what we call Quarantine in Motion.

**Index Terms**—human mobility, contact networks, disease transmission, graph neural networks, epidemics

## I. INTRODUCTION

During the pandemic of 2020, SARS-CoV-2 quickly outran manual contact tracing leading to region-wide lockdowns [1]. As a result, tech companies digitized the process by incorporating Bluetooth technology with smart devices to inform people of recent exposure. Though these exposure notification applications aim to assist with disease tracking, targeted testing and guided isolation, their potential to cause privacy breaches and over-testing through inaccurate exposures lead to ongoing ethical debates [2].

Due to the nature of pathogens and human immune system, exposure to a virus does *not* guarantee contracting the disease. In fact, the epidemic community often describes infectious diseases as having an ‘iceberg’ effect where most exposed people will not test positive because their immune system acts swiftly or because the disease manifests asymptotically [3]. For this reason, we emphasize the difference between *exposure* and *transmission* to mean that an *exposure* happens when any person comes into close contact with the virus, while the resulting *transmission* happens only when the virus successfully propagates to another person.

Beyond Bluetooth miscalculations, failure to account for this nuance has led to overestimation of infection risk which, on a wide scale, could lead to testing shortages or increased pandemic fatigue [4]. Motivated by this state of affairs, we propose that exposure notification applications can learn how to detect likely *transmission* rather than proximal exposure to reduce false alarms that can exacerbate resource exhaustion.

In order to better identify the high-risk contacts, exposure notification applications need to estimate disease virality. However, estimating virality of an emerging infectious disease remains an open challenge. At the *micro-level* (tissue cells), epidemiologists use infectious dose 50 (ID50) to estimate the relationship between exposure and disease transmission. To investigate this metric, they test how many viral particles need to enter the tissue to mount the disease in at least 50% of the sample population [5], [6]. However, at the *meso-level* (person-to-person), we wonder whether we can combine disease tracking with deep learning to understand the relationship between *exposure* and *transmission*.

From a machine learning perspective, we can think of virality as an *activation function* which can be inherently learned during training. For this reason, we formulate this problem as a graph learning node regression problem to first estimate virality and then predict risk of *transmission*, given how many contagious individuals are dwelling at a location.

The COVID-19 pandemic presents an ongoing challenge to navigate personal mobility decisions, while considering both the collective and individual risk of exposure. The intersection of epidemics, model forecasting, and disease mitigation has been successful at testing non-pharmaceutical interventions at the macro-level (regions, countries, cities) [7]. However, with access to mobility data and machine learning techniques, we can now relay the knowledge of disease forecasting back to the individual—in other words, we can provide highly granular risk analysis that is actionable to an individual’s mobility.

In this work, we investigate whether a population fighting an infectious outbreak can smartly interleave their individual mobility in order to decrease the overall disease *transmission*. To this end, our contributions are as follows:

- We formulate the disease virality estimation as a node regression problem so we can infer the relationship between the viral *exposure* and the infection *transmission*.
- We propose a framework that performs highly granular (hourly) risk of *transmission* predictions at various Points of Interests (POIs).
- We provide a proof-of-concept of our ideas based on Foursquare data of Austin TX, by showing that a risk-informed population can reduce new infections by as much as 13%, even after the peak of an outbreak.

Taken together, our contributions can help move exposure notification applications from *reactive* to *preemptive* risk management tools. The remainder of this paper is organized as follows: Section II provides some relevant background, Section III describes the approach, followed by results in Section IV. Finally, we conclude the paper in Section V.

## II. BACKGROUND AND PRIOR WORK

In this section we present current challenges in exposure notification applications, and prior work in both COVID-19 risk analysis and graph learning in epidemics.

### A. Challenges in Exposure Notification Applications

Current limitations of Bluetooth technology pose a major challenge in estimating meaningful close contacts [8]. For example, a signal might propagate between two devices through a wall, however the users are not considered capable of transmitting a disease. Using the Google Apple Exposure Notification (GAEN) protocol, Wilson et. al investigate meaningful contacts by modeling uncertainty within Bluetooth attenuation and disease uptake after breathing in viral air [9]. Though useful to analyze the risk of micro interactions, we postulate whether we can use real mobility data to analyze risk of transmission at a POI rather than a single interaction.

In addition to proximity detection challenges, the nature of infectious diseases and mobility tracking elicits privacy concerns and reluctance in public uptake [10], [11]. Due to incubation periods, asymptomatic cases, and test delays, some form of identifier must be stored either centrally or transmitted between devices to retroactively identify close contacts.

Our contribution addresses both precision and privacy issues, as we only need an individual's log of POIs visited. Looking beyond current challenges, we emphasize the need to reduce overestimation of risk that can ultimately contribute to pandemic fatigue [12].

### B. Disease Risk Assessment

Researchers have thus far employed statistical modeling approaches to analyze the risk of contracting COVID-19. Chaande et al. follow county-level case count and utilize a binomial probability model to assess the percent likelihood that transmissions will occur within the region [13]. Rhambhatla et al. propose a Hawkes-based technique that incorporates human mobility with compartmentalized disease modeling in effort to assign risk scores to regions smaller than the county level (but still bigger than zip code level) [14]. Though both works

approach risk assessment from a policy maker's perspective (at the regional level per day), we push the granularity level down to help advise an individual's hour-to-hour mobility by predicting the hourly risk of transmission at various POIs.

Before diving into our approach, we review some spatiotemporal methods in graph learning and discuss their current use in COVID-19 applications.

### C. Graph Learning in Epidemics

Applications of graph learning focus on three major problems, namely, link prediction, node classification, and node regression [15]. Graph learning is powerful because it can incorporate dependencies between data to perform machine learning tasks [16]. More precisely, graph neural network (GNN) algorithms have variations of message passing convolutions where hidden layers share weights among graph neighborhoods [17], [18]. Researchers then combine graph learning with classical neural network layers like RNN [19] to exploit the temporal dependencies for spatial-temporal applications such as epidemic transmission [20], traffic [21], and human mobility forecasting [22]. In the context of Covid- 19, Fritz et al. utilize Facebook mobility data and a graph neural network to forecast COVID-19 cases within German regions [23].

We build on prior work in exposure notification applications, risk assessment, and graph learning to 1) implement node regression to predict risk of transmission at various POIs and 2) allow a population to avoid high-risk locations while navigating an infectious outbreak.

## III. APPROACH

In this section, we propose a proof-of-concept experiment to investigate whether 1) graph learning node regression can predict risk of transmission at various POIs on an hourly basis and whether 2) a risk-informed population of Foursquare devices can maintain their mobility while also reducing new infections. We overview our approach in Figure 1.

The preprocessing consists of using Foursquare mobility data to build a network of POIs and run an SEIR

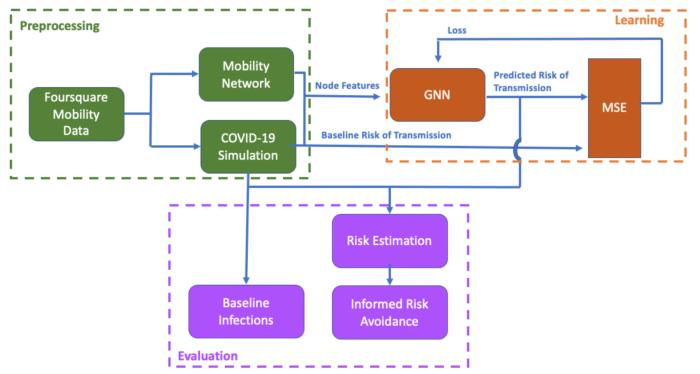


Fig. 1. Our approach starts with *i*) simulating an infectious outbreak and constructing a mobility network from Foursquare data, then *ii*) performing node regression to learn risk of transmission at Points of Interest (POIs) to then *iii*) compare efficacy of a risk-informed population to reduce new infections while maintaining their mobility.

(Susceptible-Exposed-Infectious-Recovered) COVID-19 simulation. As people get infected, we log the health statistics (i.e., number of infectious people, susceptible people, etc.) at each POI that serve as the dynamic node features. These features and network topology feed into the GNN module which then outputs the predicted risk of *transmission*. During training, the Mean Squared Error (MSE) between the predicted risk and the COVID-19 simulation is used as the loss function to update the GNN. After training completes, the GNN can predict transmission risk for the simulation days after the peak of infection occurs. We then rerun the COVID-19 simulation and let the Susceptible people avoid high risk POIs. To evaluate how many new infections are avoided by a risk informed population, we compare the mitigated infections against the baseline infections of the COVID-19 simulation. Next, we describe the network construction, disease model, risk estimation metric, and graph learning set up.

#### A. Network Construction

We construct the *network* as a composition of spatial and mobility graphs,  $G = (G_s, G_f)$  where  $G_s$  is the spatial network and  $G_f$  is the mobility (foot traffic) network. We define the spatial network  $G_s = (V, E_s)$  where  $V$  is a set of nodes that represent each POI,  $E_s$  is the set of edges that connect two POIs according to their physical proximity. To calculate the spatial edges  $E_s$ , we use the latitude and longitude value of each POI to connect  $k$  nearest neighbors. We define the mobility (foot traffic) network  $G_f = (V, E_f)$  where  $V$  is the same set of POIs, and  $E_f$  connects two POIs when an individual visits both locations. We weight  $E_f$  by the number of people that flow between two nodes. We note that by utilizing these two types of edges, we can capture both the spatial and mobility relationships between POIs (Figure 2).

In order to collect the node features that are used to infer the risk of transmission, we first simulate COVID-19 using the

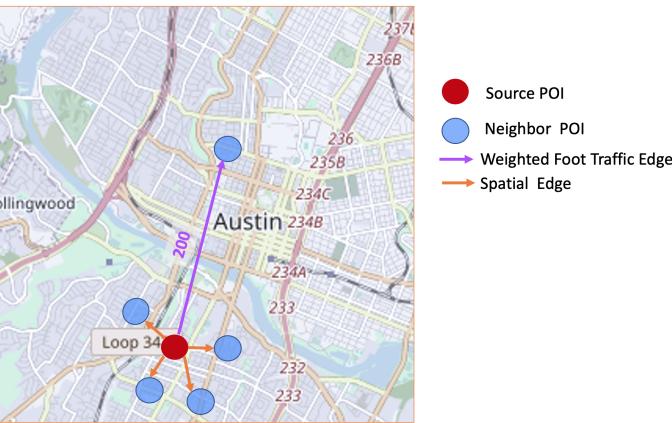


Fig. 2. Mobility network where a node (circle) represents a POI, the spatial edge (orange) connects  $k$  nearest proximal neighbors, and the foot traffic edge (purple) connects two POIs that share visitors weighted by the number of people that flow between them. In this example, 200 people travel from the source node (red) to the POI north of Austin's river.

Foursquare mobility dataset and SEIR compartmental model described in the next section.

#### B. SEIR model

To capture the difference between disease *exposure* and *transmission*, we apply the SEIR model at the individual level. Each person within the Foursquare population is initialized to either ‘Susceptible’ or ‘Infectious’ [24]. We seed the outbreak by choosing 10% of the Foursquare population that are present for 7 consecutive days and set them to ‘Infectious’. For each simulated day, people infect each other with a transmission probability  $\alpha_t$  defined in (equation 1). For every POI, let  $I_t$  represent the number of infectious people and let  $N_t$  represent the total number of people at time  $t$ . We insert a tunable parameter  $\beta$  to help model fit real COVID-19 case counts. This way the transmissibility probability  $\alpha_t$  is scaled by the ratio of infectious people within the POI:

$$\alpha_t = \frac{I_t}{N_t} \times \beta \quad (1)$$

The transition from Incubating-to-Infectious and Infectious-to-Recovered states is a time delay where we set  $\delta_{incubating} = 5\text{days}$  and  $\delta_{infectious} = 7\text{days}$  to match the average incubation and infection periods for COVID-19 alpha variant [25]. We then apply a random chance for each Susceptible person to evade transmission if they are dwelling within a POI that contains infectious people. We transition the Susceptible people to Incubating when their random chance is less than the transmissibility probability  $\alpha_t$  at the POI.

#### C. Risk Estimation

Given this set up, we define a POI’s risk metric at time  $t$  as the ratio between the number of Susceptible people that caught the virus (change to Incubating) after exposure to Infectious people within the POI (equation 2). For example, if two Susceptible people get exposed to one Infectious person within a POI at time  $t$ , however only one person subsequently contracts the virus at time  $(t + 1)$  then we say the risk of *transmission* is 50% (Figure 3).

$$Risk_t = \frac{Incubating(t+1)}{Susceptible(t+1)} \quad (2)$$

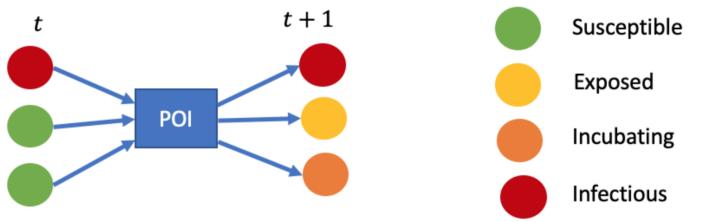


Fig. 3. Example to illustrate the risk of Susceptible people (green nodes) transitioning to Incubating (orange node) after an exposure to an Infectious person (red node) at a POI. The exposed (yellow node) person is there to emphasize that we are not estimating the risk of *exposure*, but rather the risk of *transmission* (Susceptible – to – Incubating).

Intuitively, from the perspective of a Susceptible person, the hourly risk metric is the probability that they will catch the virus at a particular POI. In the real world, we would not know the exact interaction responsible for an individual's transmission; however, in the SEIR compartmental model, we can keep track of how many people become infected after visiting a POI thus leading to an accurate risk evaluation. This risk metric will be learned and then predicted by the GNN.

After building a mobility network, simulating COVID-19, and collect transmission risk at POIs, we can now set up our node regression as described in the next section.

#### D. Graph Learning Setup

We formulate the graph learning problem as a node regression problem where we use a neural network for each node in the graph that inputs the collected features, performs convolution across the neighborhoods, and then outputs the predicted risk value (Figure 4). We utilize the deep graph learning library (DGL) [26] to implement the SAGE and Gated graph convolutional layers. The SAGE algorithm is a scalable convolutional layer that utilizes message passing along edges to aggregate (in our case, average) feature weights [27], whereas the Gated graph convolution handles sequential inputs by allowing past  $n$ -steps to update the current feature weights [17]. We compare both set-ups to test whether one or both can handle the highly sparse, dynamic, large scale feature learning for predicting hourly risk of transmission at various POIs.

We add a sigmoid layer to predict the risk of disease per each node (POI) between 0 and 1, where 1 means 100% of Susceptible people will turn to Incubating in the next hour following a visit to node  $i$ . We define the input features per node per hour  $X^t = [I_t, S_t, \delta_t, \alpha_t, \eta_t]$  as the number of Infectious people  $I_t$ , number of Susceptible people  $S_t$ , number of people that transition from Susceptible to Incubating  $\delta_t$ , the

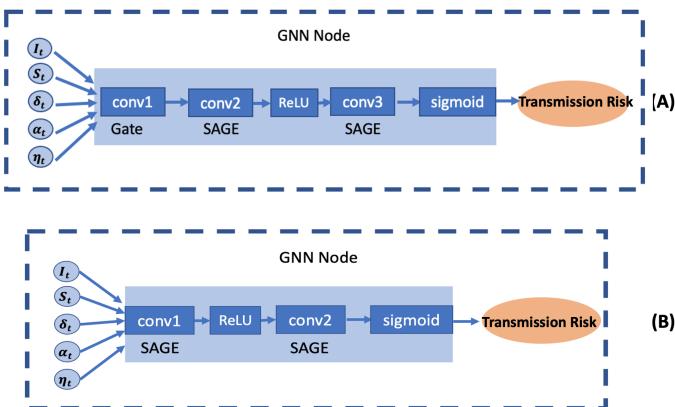


Fig. 4. GNN architectures to perform node regression. Architecture (A) Inputs the dynamic POI features into a gated graph convolutional layer and then feeds them forward into two SAGE layers with a ReLU activation function in between. Architecture (B) skips the gated graph convolution and instead feeds the features directly into the two SAGE layers. Both architectures have a sigmoid activation function to output the risk of transmission at the POI.

transmission probability  $\alpha_t$  (equation 1), and the percent of total population  $\eta_t$  that the POI is responsible for infecting. Of note, these features are collected in the COVID-19 simulation using the SEIR model described in the previous section.

Our approach can be summarized as building a Foursquare mobility network, simulating COVID-19 using SEIR to calculate the hourly risk of transmission and collect features to be used as graph learning inputs. We then utilize Gated graph convolution and SAGE convolution to perform node regression. We then train over the beginning and peak of the outbreak and predict the risk of transmission in the end stages of the outbreak (after more than 50% of the population has been infected). Finally, to evaluate the proof-of-concept experiment, we compare the new infections from the baseline SEIR simulation against the risk-informed population. We hypothesize that this risk informed mobility intervention will reduce new infections while maintaining population mobility (i.e. quarantine in motion).

## IV. RESULTS

We test the efficacy of our framework by first training the two different graph learning architectures on the same SEIR simulation run in the buildup of the outbreak and then infer the risk of transmission after the outbreak's peak. In this section we present the A) Foursquare mobility data, B) COVID-19 simulation, C) Mean Squared Error (MSE) metric to evaluate how well the graph learning architectures can predict risk of transmission; then D) we visualize the quality of predictions, and finally, E) put the risk-informed population to the test to mitigate new infections.

#### A. Foursquare Mobility Data

We use Foursquare mobility data [28] that contains an anonymized identification number for each device within the dataset over Austin. Our sample of the dataset captures 36,347 devices visiting 73,125 locations within Austin Texas in July 2020. Each data point has the device location and duration of visit at the hour level. Though we do not have the physical navigation information between locations, we assume that infectious diseases transmit more at the individual locations rather than in transit. We argue that this assumption is well justified in the context of Austin where there is more travel by vehicle (70%) than public transportation, bicycles, and pedestrians combined [29]. With this Foursquare dataset, we have access to individual trajectories and dwell times at POIs where, for example, we know how many devices go from location A to location B. With this path-like trajectory, we know the foot traffic between any two POIs which serve as the basis for the mobility network. Using the Foursquare dataset, the resulting network contains 73,125 nodes ( i.e., all the POIs captured) and 292500 spatial edges and 157,451 foot traffic edges for a total of 449,951 edges. After the mobility data is preprocessed into the network, we implement and tune the SEIR COVID-19 simulation.

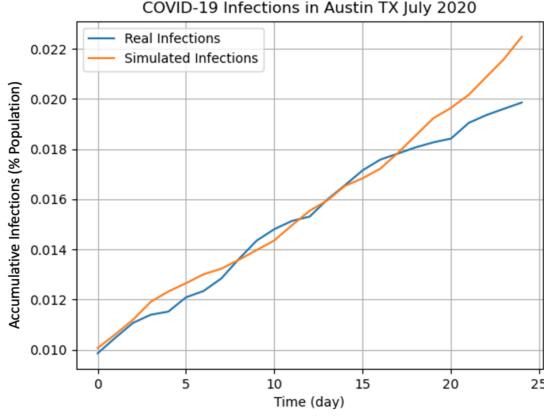


Fig. 5. Comparison between Austin's county-level COVID-19 infections in July 2020 versus the fitted SEIR simulated infections given Foursquare mobility data. Both infections are scaled to both Austin population (965,872) and Foursquare population (36,347).

### B. COVID-19 Simulation

Using the SEIR model and equation 1 defined in the approach, we find that  $\beta = 0.78$  as the best fit for Austin's real COVID-19 infection curve in July 2020 (Figure 5).

To get a feel for the difference in magnitude between exposures and transmission, we simulate an infection and then plot the number of infectious POIs vs time in Figure 6. The fluctuations within both signals have to do with varying hourly population density inside the various POIs. We can see that there is roughly a 5-to-1 relationship between venues with exposure and venues with transmissions at the peak of the outbreak (i.e., hour 300 where there are 500 venues containing infectious people, yet only 100 people where transmission occurred). Intuitively, if the population had access to a current exposure notification framework, there would be a 5x overestimation of risk according to the plot which could put a strain on testing resources.

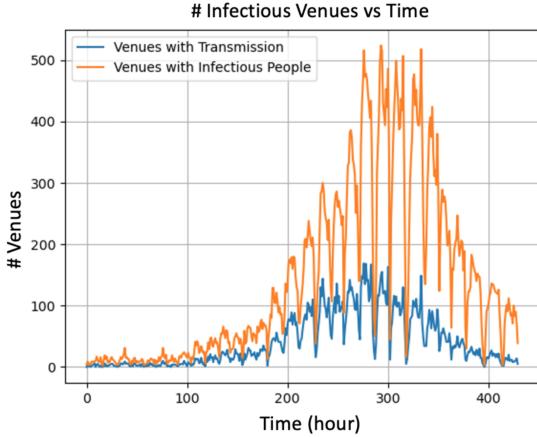


Fig. 6. Comparing the number of venues that have infectious people (orange) versus time against the number of venues that have actual transmissions (blue). Of note, there are over 73,000 total venues making this feature set very sparse to train the graph neural networks.

After simulating COVID-19 and collecting the node features, we train graph learning architectures and test the node regression predictions.

### C. Graph Learning

We utilize MSE as the evaluation metric for our graph learning architectures defined in equation 3 where  $n$  is the number of nodes in the mobility-spatial network,  $Y_i$  is the predicted risk of transmission, and  $\hat{Y}_i$  is the corresponding baseline risk pulled from the same SEIR simulation run:

$$MSE = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad (3)$$

Because the dynamic nature of a mobile infectious population, the number of infectious venues (Figure 6) fluctuates over time, thus resulting in very sparse features. This means that the training must take into account the sparsity of the dataset where, on average, each SEIR simulation has 0.002% of POIs containing infectious individuals and even less than that spread the disease. To account for sparsity, we train and test by using the MSE for non-zero POI nodes.

As seen in Figure 7, both architectures are similar in their MSEs, which for non-zero risk of transmission is consistently under 5%. Of note, we expect both MSEs fluctuate per hour due to the dynamics of the underlying mobility features.

### D. Prediction

To get a more granular feel for the difference between each learning architecture, we visualize the predictions at the POIs with the highest risk per hour shown in Figure 8. Of note, two different POIs are named HEB which is a popular grocery store franchise in Texas. In theory, a person who needs to shop for groceries and prefers HEB can compare the hourly risk of transmission and then choose which location to visit. We notice that both graph architectures A and B predict roughly

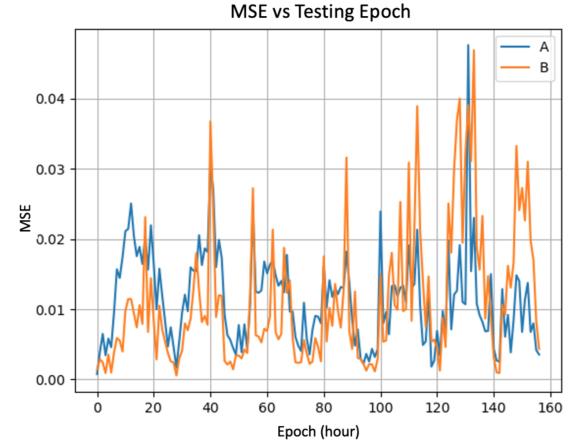


Fig. 7. Mean Square Error for graph learning architecture A (blue line) that includes Gated Graph convolution and architecture B that only uses SAGE convolution. The models are trained on 21 days of mobility and COVID-19 simulation data to predict the next 6 days of risk of transmission.

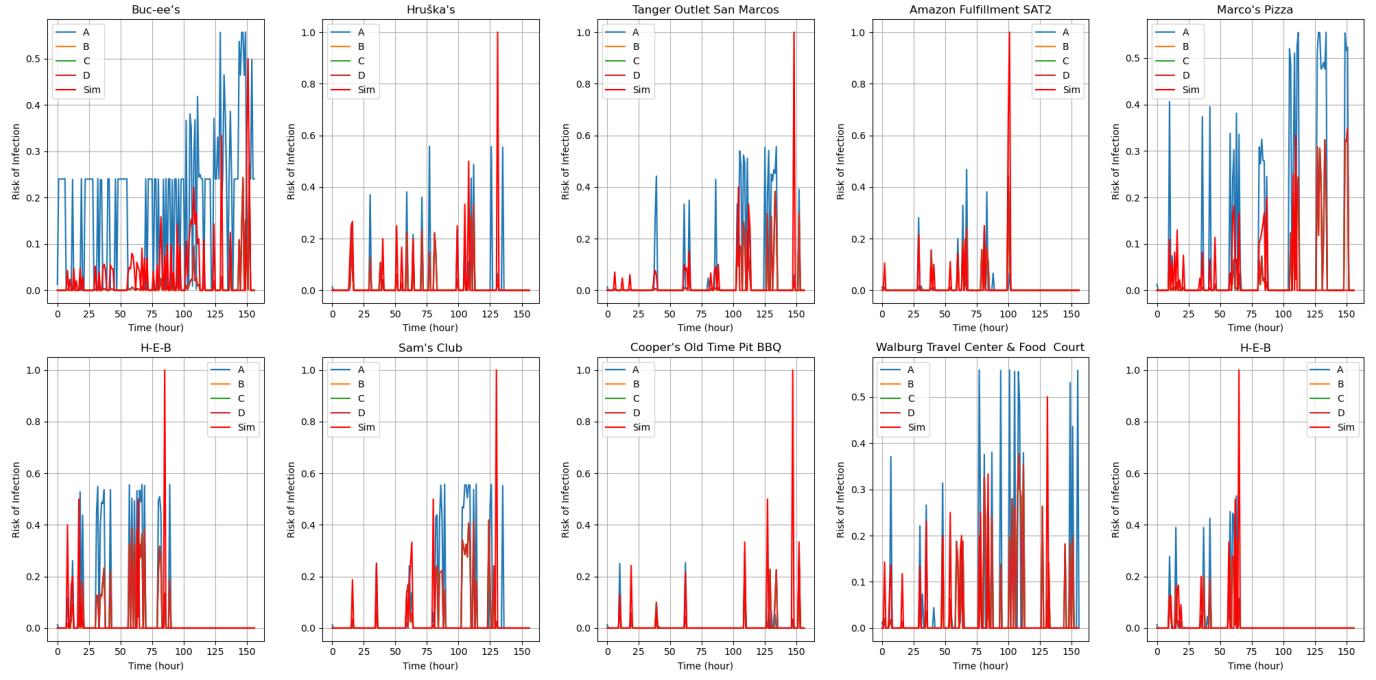


Fig. 8. After training the GNNs on health features from 21 days of the COVID-19 SEIR simulation, they then predict the risk of transmission at POIs for the next 7 days. Each plot represents a different POI where the GNN architectures A (Gated graph convolution) and B (SAGE convolution) output the risk of transmission per hour. The calculated risk of transmission from the baseline SEIR COVID-19 simulation is shown in red. Of note, the GNN architecture A overestimates the magnitude of risk, while B underestimates risk.

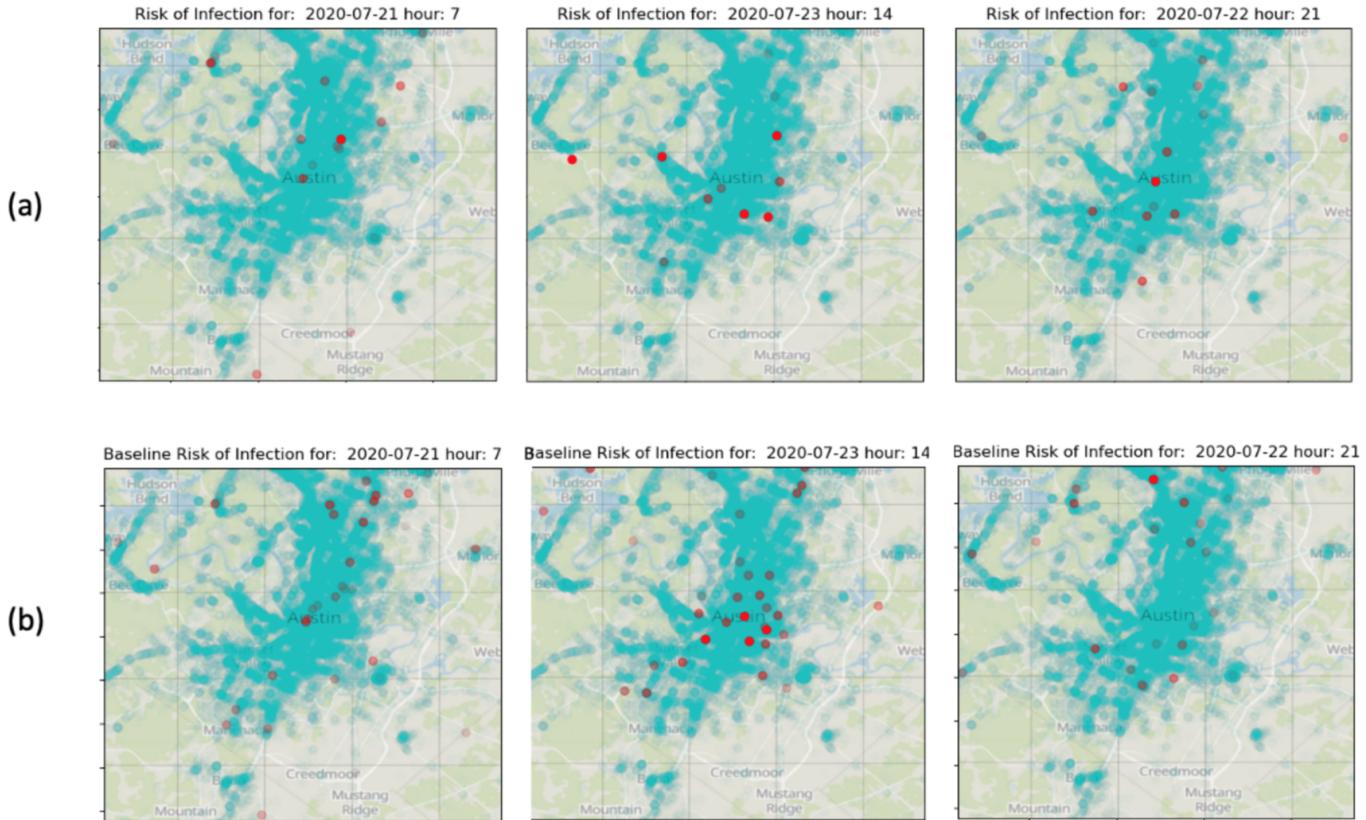


Fig. 9. (a) Risk of transmission at various POIs in Austin per day, per hour given by graph learning architecture A. (b) Baseline risk of transmission. Each POI is represented by a point in the map. A blue point represents a POI with 0 risk of transmission, and the opacity of a red dot corresponds to the value of risk (i.e., more red means a higher risk of transmission).

the same signal however the magnitude of risk prediction is consistent overestimation in A and underestimation in B.

Given that more people stay safe when adhering to an overestimation of risk per hour, we conclude that graph architecture A (that contains a Gated Recurrent Unit graph convolution layer) is the best suited for this node regression problem. Though this risk prediction results in overestimation, the social cost to a user is less severe than being told they were recently exposed and must isolate until test results are reliable. For example, a user can decide to delay their visit to an hour with less risk or choose to go to a similar location with lower risk all together.

We then perform a spatial-temporal visualization to investigate the difference between hourly risk of transmission prediction compared to the baseline in Figure 9. The blue nodes signify POIs with no risk of transmission, while the non-blue points in varying shades of red and purple represent the magnitude of transmission risk within the POI and hour.

#### E. Mitigation

After analyzing the graph learning architectures, we evaluate the efficacy of an informed population by simulating an intervention after the peak of an infection using mobility data from Austin TX in the month of July 2020. We emphasize the intervention after the peak in order to give a real-world example where there is a lag between mobility data collection, positive tests, and training the graph learning frameworks. Given these constraints, we train between July 1<sup>st</sup> – July 21<sup>st</sup> and then infer on the days of July 22<sup>nd</sup> – July 31<sup>st</sup> where, by July 21<sup>st</sup> over 50% of the Foursquare population has been either Infected, Incubating, or Recovered.

Once the Susceptible people get informed of the risk of transmission predictions on July 22nd, they can choose to go

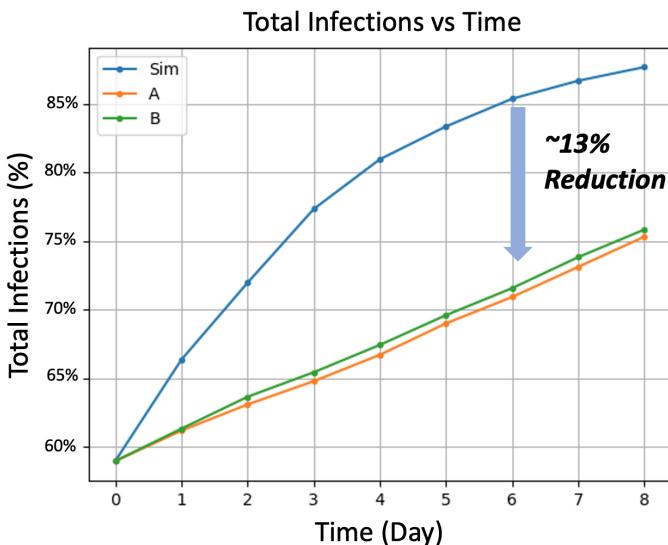


Fig. 10. Total infections (i.e., Incubating (I) + Infectious (I) + Recovered (R)) vs time comparison between the baseline (Sim), and the altered behavior from an informed population given risk of transmission estimations from graph learning architecture A (orange) and B (green).

to a destination (POI) during an hour where there is no risk of transmission or choose a similar destination. In Figure 10, we compare the baseline SEIR COVID-19 simulation to the inference produced by the graph learning architectures A and B. When given the chance to avoid POIs with non-zero risk of transmission, the simulated Foursquare population that has more than 50% is able to reduce the outbreak by roughly 13%.

Though architecture A tends to overestimate the magnitude of the risk transmission at locations (as seen earlier in Figure 8), it does not have a major advantage in reducing cases over architecture B. The advantage of using architecture B is that it is highly scalable and uses less runtime (from days to hours) to process large graphs. However, we hypothesize that when a real population has varying tolerance for risk of transmission that the overestimation in A will lead to more people avoiding POIs with high disease transmission and that B will underestimate leading them to ignore the risk.

## V. CONCLUSION

In this paper, we have formulated the highly granular disease transmission risk assessment as a graph learning node regression problem. We have utilized Foursquare mobility data to create a foot traffic network between POIs and run an SEIR infection model to gather features and calculate the risk of transmission. We have trained two different graph convolution strategies, namely Gated graph and SAGE and then compare their MSE. Finally, we have provided a proof-of-concept by allowing Susceptible people to avoid high risk POIs which results in a 13% reduction of new cases even after the peak of infection.

Though a 13% reduction seems small at the outset, we note that there is already a large number of people who are incubating and waiting to become infectious by the time an intervention is implemented. Rather than encouraging susceptible people to stay at home when there is an infectious outbreak surge (which is the current paradigm for *exposure* notification applications), we are instead informing them of POIs that can lead to real *transmission*.

In the real world, there would be a delay between those who test positive and their time of visit; however, by using an SEIR simulation, we can reduce uncertainty by knowing who got infected after each visit. While this work targets COVID-19 like diseases, this framework can serve as a starting point for other types of infectious diseases. We leave the back-tracing for future work; however, we reinforce the need to accurately capture the distinction between *exposure* and *transmission* at a highly granular level so that the information is actionable.

As the COVID-19 pandemic enters the endemic stages, we envision the exposure notification applications to extend to risk analysis and prediction. Given this information, we hope that human mobility can reorganize itself to be resilient against infectious diseases without resorting to costly lock downs.

## ACKNOWLEDGMENTS

This work is supported, in part, by NSF grants CCF 2107085 and 2200169.

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