Vaccination Strategies on a Robust Contact Network

Christopher Siu and Theresa Migler(✉)

California Polytechnic State University, San Luis Obispo, CA, USA
{cesiu,tmigler}@calpoly.edu

Abstract. Mathematical models of disease spreading are a key factor in ensuring that we are prepared to deal with the next epidemic. They allow us to predict how an infection will spread throughout a population, thereby allowing us to make intelligent choices when attempting to contain a disease. Whether due to a lack of empirical data, a lack of computational power, a lack of biological understanding, or some combination thereof, traditional models must make sweeping, unrealistic assumptions about the behavior of a population during an epidemic.

We present the results of granular epidemic simulations using a rich social network constructed from real-world interactions, demonstrating the effects of ten potential vaccination strategies. We confirm estimates by the WHO and the CDC regarding the virulence of measles-like diseases, and we show how representing a population as a temporal graph and applying existing graph metrics can lead to more effective interventions.

Keywords: Contact networks · Epidemics · Vaccination

1 Introduction

Epidemiology is the study of diseases that infect people, including the biological and social mechanisms involved in their outbreak, transmission, containment, and, hopefully, eventual eradication. Of that last goal, to date, only one disease that affects humans has been eradicated: a naturally occurring case of smallpox has not been reported since October of 1977, the conclusion of almost two hundred years of work immunizing the general population [5]. This required a dedicated program on the part of the World Health Organization, involving mass vaccinations, health surveillance, and targeted interventions on continental scales over more than a decade.

Should we ever be confronted with another smallpox-esque disease, computer models will be crucial to effective coordination and utilization of our limited resources, a logistical problem for which, in many respects, we are not currently prepared [7]. Developing models to simulate and predict the spread of diseases could allow us to contain outbreaks before they become epidemics, and, failing that, to determine the appropriate methods of intervention.

H. Cherifi et al. (Eds.): COMPLEX NETWORKS 2019, SCI 881, pp. 313–324, 2020.
https://doi.org/10.1007/978-3-030-36687-2_26

However, because of the complexity of the involved sociological and biological mechanisms, traditional mathematical models must make a handful of key unrealistic assumptions. In particular, they cannot account for the transmission of disease on an individual, per-person scale. Conventional *full mixing* models assume that every individual has an equal chance of coming into contact with any other member of the population: an assumption that is almost always incorrect.

We represent a real-world population as a temporal graph, capturing contact events with greater precision. We use this graph to investigate the possibility that existing graph metrics can inform more effective interventions.

2 Related Works

Kephart and White were, in 1991, among the first to propose modeling the spread of a virus using a graph [10]. Modeling networked computers as vertices in a directed graph, they apply a *Susceptible - Infectious - Susceptible* (SIS) model, assuming that every computer either is infected and capable of spreading the infection or is susceptible to being infected. Each edge represents a network connection, and they assign to each edge a probability of transmitting the virus.

The incorporation of individual movements, such as we might find in high resolution social networks, is not exclusive to models based on graphs. Granell and Mucha partition a population based on individuals' locations at discrete time steps, differentiating between residences and common spaces and between daytime and nighttime behavior, in order to account for patterns of movement [9]. Similarly, Gemmetto, Barrat, and Cattuto use temporal information to refine a conventional epidemic simulation, deriving their data from a real-world high resolution contact network obtained from sensors worn by children at a primary school in Lyon, France, which allows them to simulate the effects of varying degrees of school closure [8].

Frías-Martínez, Williamson, and Frías-Martínez construct and infect a dynamic social network of an entire city in Mexico [6]. Their location data is collected from cell towers, which they use to analyze the efficacy of the Mexican government's response to the 2009 H1N1 swine flu pandemic. Stopcyznski, Pentland, and Lehmann infected their Copenhagen network, using an SIR simulation to emphasize the structural differences between short- and long-range contact networks [13].

3 The Network

We develop our simulations using a network based on the Copenhagen Network Study. This study was conducted in two distinct iterations between 2012 and 2013, with the aim of creating a "high resolution" social network that was not owned by a private company or a government and could therefore be provided to researchers [14]. Not all of the data that was collected is relevant to disease spreading. We focus on face-to-face contact data, recorded based on phone-to-phone Bluetooth scans. This data encompasses the interactions of about seven

hundred individuals, over one month, reported every five minutes. The detail of this contact data gives us the opportunity to simulate transmission of disease with far more granularity, precision, and realism than would be possible in a full mixing model.

We highlight the number of interactions over time in the Copenhagen dataset (plotted in the Appendix, Fig. 5). We find that individuals' interactions also occur with a distinctive and immediately recognizable pattern: every day, the most interactions occur around midday, and there are significantly more on what we infer to be weekdays compared to weekends. These characteristics of the Copenhagen dataset reinforce the idea that full mixing simulations will not suffice: it is not a realistic assumption that every individual makes uniform, constant, random contact with every other.

4 Graph Representation

We model the Copenhagen dataset as undirected graphs, snapshots of a network over time. In each graph $G_i = (V_i, E_i)$, vertices represent individuals; there is an edge between vertex u and vertex v if individual u came into contact with individual v, or vice versa, at time t_i. We always assume that if u has come face-to-face with v, then v must have come face-to-face with u. We further observe that not every individual is present in every timestamp. For the purposes of our simulation, we add vertices to the network once their corresponding individuals appear, but we never remove them—since we are interested in simulating the spread of a disease, we need to keep track of individuals' states with respect to the infection at all times, regardless of whether or not they appear in the raw dataset at those times.

It is important to note that the vertices and their edges need not exclusively form little cliques within the network: if a comes into contact with b, and b comes into contact with c, that does not necessarily imply that a must have come into contact with c. This could mean that, within the five minute interval represented by each snapshot, b came into contact with a and c separately. It could also mean that the three individuals formed a line when they came into contact with each other, such that b came into contact with both a and c, but a and c were not close enough to be judged as having made face-to-face contact.

5 Simulation Model

As a basis for our simulated interventions, we infect the Copenhagen network with a measles-like disease using a *Susceptible-Exposed-Infected-Recovered* (SEIR) model: every individual begins in a Susceptible state, transitions first into an Exposed state once they have contracted the disease, then into an Infected state where they may transmit the disease, and eventually permanently move to a Recovered state.

Measles is highly contagious: nine out of ten susceptible individuals who come into contact with an infectious individual will contract the disease [4], which can

Table 1. Summary of ten simulated interventions

Strategy	Probability of intervention	Number of interventions	Requisite foreknowledge
Uniform vaccination	$p \in \{0.05, 0.10, \ldots, 0.95\}$	$\approx p \times 692$	*None*
Vaccination by degree	1	$\lambda \in \{10, 20, 30, \ldots, 690\}$	One month
	1	$\lambda \in \{10, 20, 30, \ldots, 650\}$	One week
	1	$\lambda \in \{10, 20, 30, \ldots, 610\}$	One Monday
Vaccination by cores	1	$\lambda \in \{10, 20, 30, \ldots, 690\}$	One month
	1	$\lambda \in \{10, 20, 30, \ldots, 650\}$	One week
	1	$\lambda \in \{10, 20, 30, \ldots, 610\}$	One Monday
Vaccination by rings	1	$\lambda \in \{10, 20, 30, \ldots, 690\}$	One month
	1	$\lambda \in \{10, 20, 30, \ldots, 650\}$	One week
	1	$\lambda \in \{10, 20, 30, \ldots, 610\}$	One Monday

continue to spread effectively even when less than 90% of the population is at risk [11].

We chose to test interventions using a measles-like disease for three reasons: firstly, because measles is so highly contagious, interventions should have a more pronounced effect in a shorter amount of time—if an individual escapes infection, that is more likely to be a result of the intervention than a result of random transmission chance. Secondly, while the measles virus is highly contagious, the measles vaccine is equally highly effective. Properly administered in two doses, the vaccine is 97% effective [3], so we may essentially ignore the possibility of ineffective vaccinations. Finally, at the time of this writing, measles outbreaks in the United States have recently risen drastically [2], so interventions that target measles are of greater immediate relevance.

One factor that makes measles so contagious is its ability to linger in airborne droplets for hours [11]. It is possible for a susceptible individual to contract the disease without ever coming into contact with an infected individual, simply by their occupying the same room within a few hours of each other. Because of the distinct lack of location data in the our dataset, we chose not to simulate this vector. Additionally, because the Copenhagen Study does not include interactions with the outside world, we do not simulate any chance of infection via such external contacts. We also note that contact events can only be recorded by active phones, and not every individual will realistically be holding a powered phone at all times. These factors all mean that our simulations will be conservative estimates of diseases' virulence.

6 Vaccination Strategies

Our baseline intervention is vaccination with uniform probability. Whenever an individual first appears in the Copenhagen dataset—whenever a new vertex is added to the network—that individual has a some probability p of gaining complete immunity to the disease. We simulated varying amounts of vaccination, from $p = 0.05$ to $p = 0.95$ in increments of 0.05.

We now imagine a scenario where there are a limited number of vaccines for our hypothetical, measles-like disease. Perhaps the vaccine is costly to manufacture, difficult to administer, or experimental in nature. In these situations, rather than randomly selecting individuals to vaccinate, we would like to vaccinate those that have the greatest effect on the spread of the infection.

Once an individual is vaccinated, they can neither contract nor spread the disease. Because the disease is spread along edges of the network, vaccinating an individual is analogous to removing all of their corresponding vertex's incident edges. If we are to contain an infection by removing a limited number of vertices, and the infection spreads along edges, then our ultimate goal is to remove vertices in order to disconnect the network into multiple connected components. If the network is so split, then any infection that begins in one component will not be able to spread to the others. Given this goal, if we have a limited number of vaccinations, one possible approach is to vaccinate those individuals who make the most contact with others.

Supposing that higher degree vertices would contribute to a faster or wider spread of the infection were they to be infected, and supposing that those vertices are responsible for connecting more components together, we simulated the vaccination of limited numbers of individuals, prioritizing those of highest degree. Because the network consists of multiple snapshots, one option is to *flatten* the entire month's worth of data into a single graph prior to computing the degree distribution. We can think of this as providing those in charge of administering vaccinations with advance knowledge of every individual's movements for the next month. While this would give us the most information about the degrees of vertices, it is somewhat unrealistic. Therefore, we tested two additional variations on this vaccination strategy: first, using the network flattened over the first week of the study, second, over just the first Monday.

With the same reasoning that motivated vaccination by degree, we next investigated vaccination informed by *k-cores*, induced subgraphs within which every vertex has degree at least k [12]. Vertices belonging to higher k-cores roughly correspond to vertices in denser regions of the network, thus, we consider the possibility that these individuals have a greater effect on the spread of an infection. As with the degree distribution, we first considered three methods of flattening the network: flattening the entire month's snapshots, flattening the first week, and flattening the first Monday. For each flattened graph, we computed every k-core. Given each set of k-cores, we then simulated limited numbers of vaccinations, and vaccinations were given to the individuals that appeared in the highest cores.

Similar to k-cores, the *density decomposition* partitions the vertices of a graph based on the density of their subgraphs, producing *rings* of vertices [1]. Specifically, an *egalitarian orientation* involves the addition of direction to edges such that vertices' indegrees are as balanced as possible. If k is the maximum indegree in such an orientation, then the ring R_k contains all vertices of indegree k along with their predecessors. Compared to the highest core, the highest ring better approximates the densest subgraph.

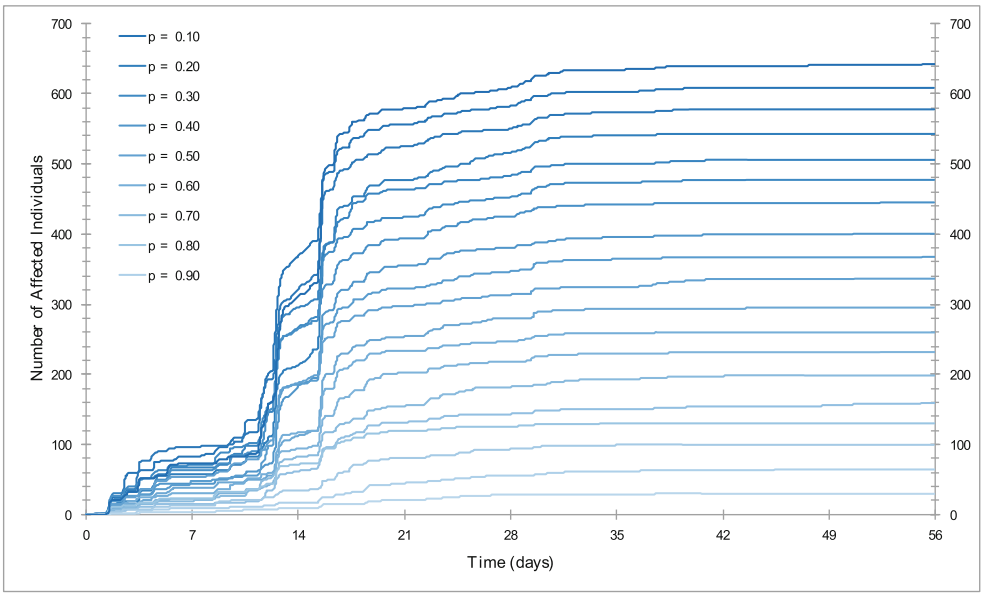

Fig. 1. Numbers of affected individuals by time in uniform vaccination scenarios. Each line is the median of ten averages of five simulations each (ten infection seeds, five simulations per seed).

As we did with k-cores, we suppose that the vertices in the highest rings represent individuals who are best positioned to propagate the infection. The density decomposition was computed for the network flattened over the first Monday, over the first week, and over the entire month. For each decomposition, we simulated vaccinating limited numbers of individuals from the highest rings.

In all cases of targeted vaccination, we simulated varying numbers of vaccinations, λ, in increments of 10. A summary of simulated interventions is given in Table 1.

7 Results

In all simulations, one individual was randomly chosen from the first snapshot to be the initially infected "seed" of the outbreak. As has been done in similar simulations, in order to allow ample time for infections to run their courses, the dataset was looped twice, creating eight weeks of individual contact events [8].

We refer to an *affected individual* as one that has contracted the disease at some point: one who is or has been in the Exposed or Infected states. For reference, the results of simulations with no interventions at all are given in the Appendix, Fig. 6. There, each curve plots the affected individuals over time in five simulations based on the same starting situation. Once randomly chosen, the seed of the infection was held constant, but the individual transmission events were not. This was repeated for thirty different random seeds.

The uniform vaccination strategy is summarized by Fig. 1, which plots the number of affected individuals for each simulated vaccination probability.

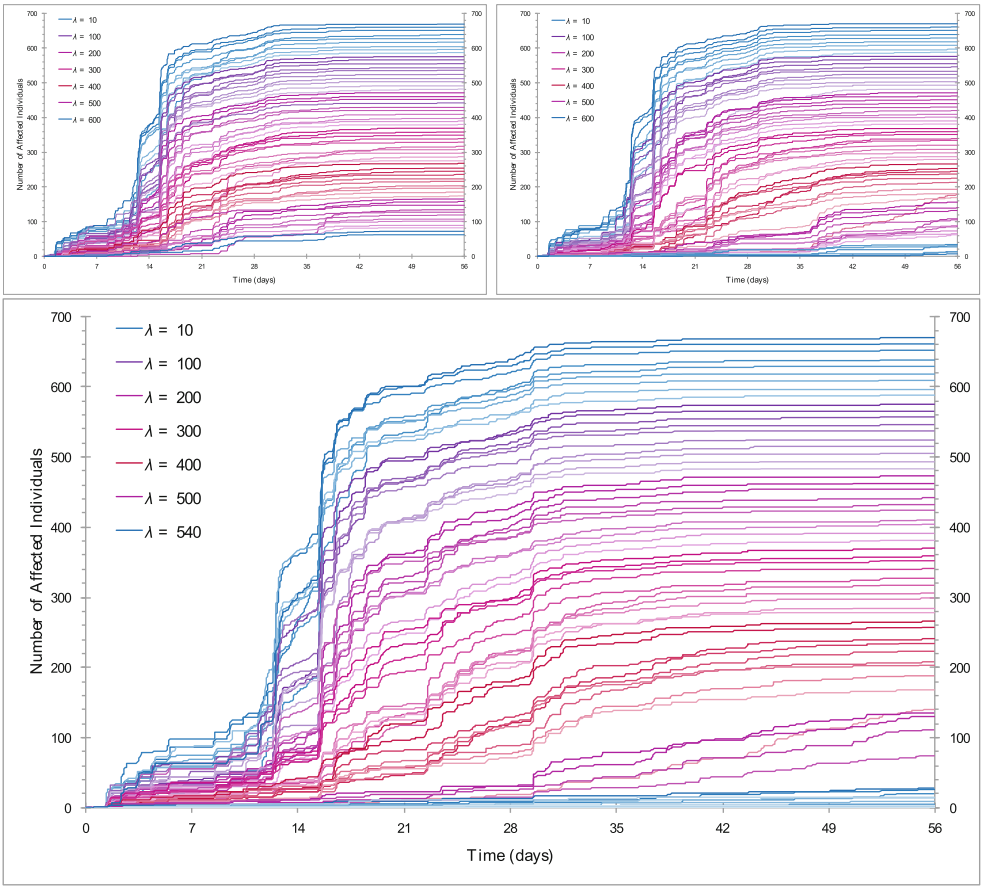

Fig. 2. Numbers of affected individuals for varying numbers of vaccinations by degree. Each curve is the median of five differently seeded simulations. Clockwise from top left: degrees computed from one Monday, from one week, and from one month.

Though dramatically subdued compared to the baseline curves in Fig. 6, these curves exhibit periods of faster-than-linear growth, and they flatten out as they approach the maximum number of susceptible individuals, indicating that almost every susceptible individual has been infected. We conclude that increasing the uniform probability of vaccination neither alters nor delays the general pattern of the outbreak; it merely places a cap on the number of individuals that can eventually be infected.

These results agree with existing estimates that measles outbreaks can continue to occur even when <10% of the population is susceptible [11]. We further infer that, due in part to the densely connected nature of the Copenhagen network, the *herd immunity threshold*, the percentage of individuals that must be immunized in order to prevent an outbreak, appears to be higher than 95% in our simulations. This confirms and strengthens existing estimates, including those by the WHO and the CDC, which place the threshold between 89% and 95% [4,11,15].

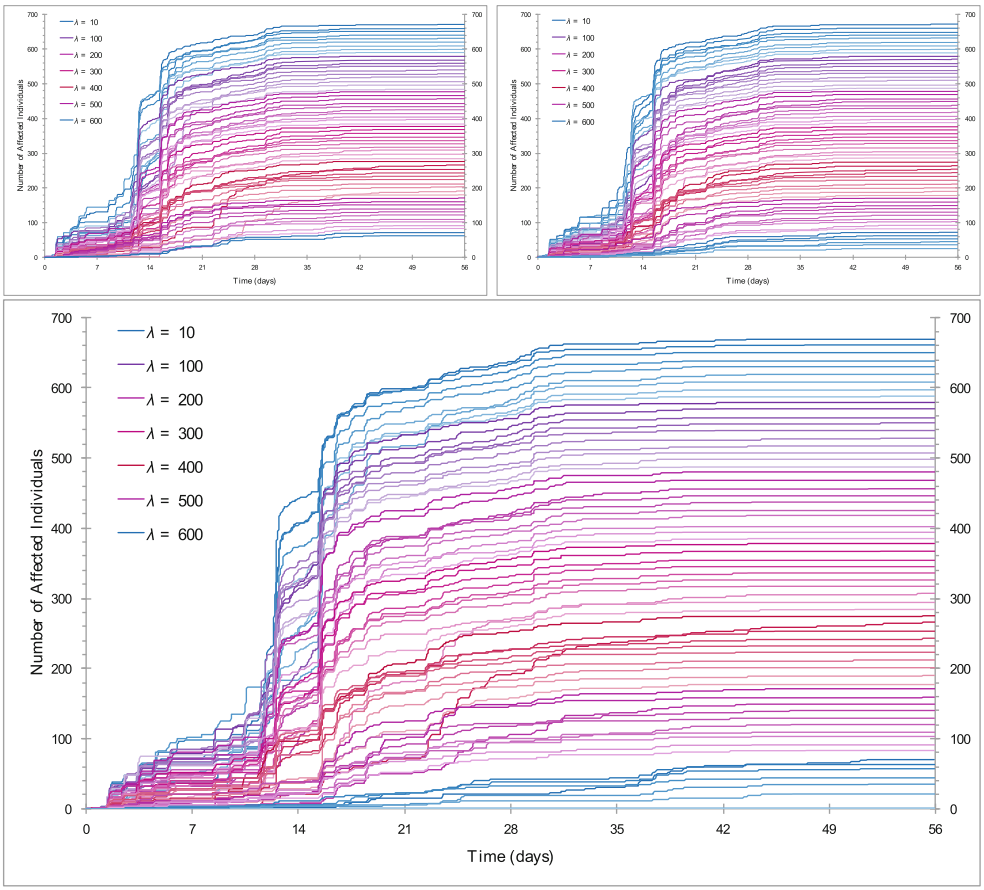

Fig. 3. Numbers of affected individuals for varying numbers of vaccinations by k-core. Each curve is the median of five differently seeded simulations. Clockwise from top left: k-cores computed from one Monday, from one week, and from one month.

Our first targeted intervention prioritizes individuals by the degrees of their vertices: in other words, those who made more unique contacts would receive the vaccine first. The results of this intervention are given by Fig. 2, where the simulations in the top-left plot compute the degree based on the first Monday; in the top-right, based on the first week; in the center, based on the entire month.

We observe that vaccination by degree using just the first Monday's data does not appear to make a difference compared to the uniform vaccination of Fig. 1. This makes intuitive sense: drawing from just the first Monday, there is simply not enough data about the contact patterns of vertices to make an intelligent decision regarding whom to vaccinate. Once we consider the data from the first week, we start to see some improvement at higher numbers of vaccinations. Starting at about $\lambda = 500$ vaccinations by highest degree, the outbreak has been delayed until the beginning of the fourth week. Should we be so fortunate as to have a month's worth of data, and we vaccinate according to highest degree, we find that, around $\lambda = 540$, the disease no longer infects the

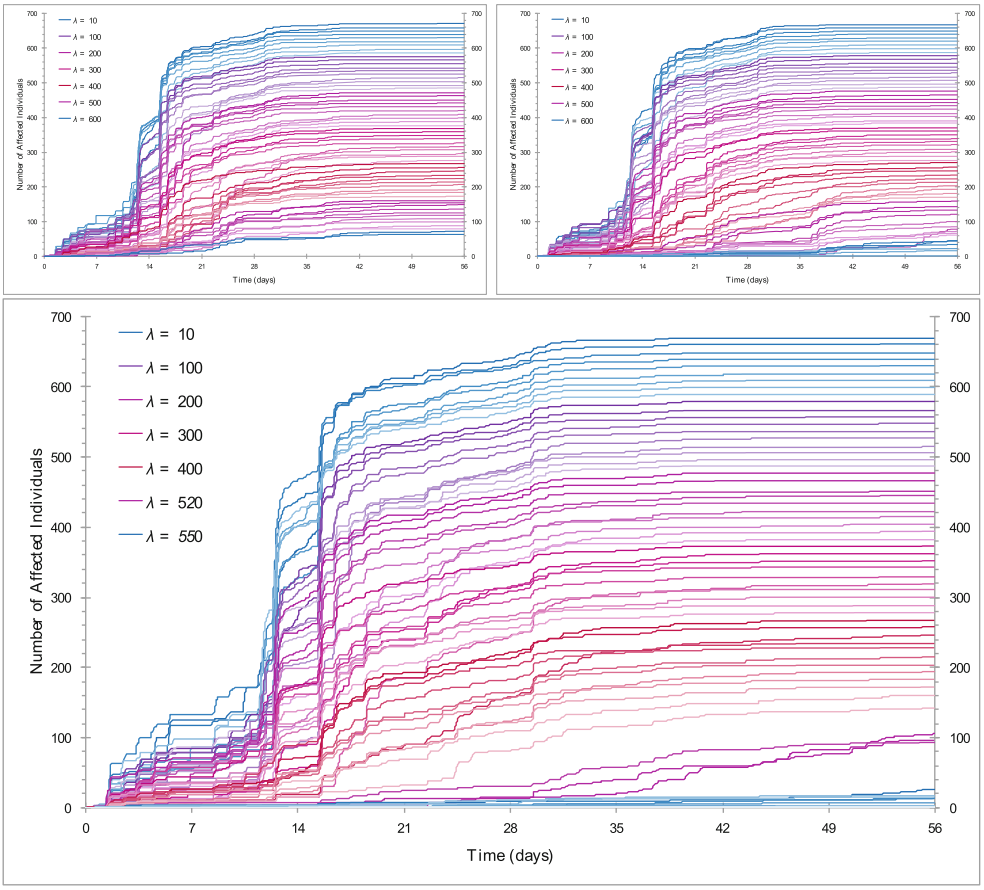

Fig. 4. Numbers of affected individuals for varying numbers of vaccinations by ring. Each curve is the median of five differently seeded simulations. Clockwise from top left: rings computed from one Monday, from one week, and from one month.

majority of susceptible individuals (540 vaccinated, thus, 152 susceptible, and a median of only 28 infected) over a two month period.

Our second targeted vaccination strategy involves k-cores. As with vaccination by degree, we simulated administering a limited number of vaccinations, prioritizing individuals whose vertices were in higher cores, and we computed those cores based on the first Monday, the first week, and the entire month. These results are shown in Fig. 3.

Disappointingly, we find that vaccination by k-core does not appear to perform any better than uniform random vaccination. In retrospect, however, this makes sense: higher k-cores identify subgraphs that are clique-like, whereas higher degrees identify the centers of subgraphs that are star-like. In a social network, we find it believable that there are more large stars than there are large cliques.

Finally, we simulate the vaccination of individuals whose vertices appear in higher rings of the density decomposition. These simulations are plotted in Fig. 4, and they show that vaccination by ring has better effects than vaccination by

k-core and similar effects to vaccination by degree. However, we note that whereas the degree distribution of a graph can be found in linear time, computing the density decomposition has runtime quadratic with the number of edges [1].

8 Conclusion

We have simulated disease spreading on a high resolution social network, using a real-world dataset that captures individual human interactions with extremely fine granularity. Using these simulations, we implemented ten strategies for preventing an epidemic. We first confirmed existing estimates with respect to measles-like diseases, with our results further suggesting that there exist non-trivial, not uncommon situations where those predictions are underestimates. We then showed that, by representing the network as a graph, we could apply existing graph metrics to inform more intelligent interventions. Notably, we showed that vaccination based on the degree distribution or the density decomposition of the network could delay or prevent a measles-like outbreak using fewer vaccinations than one based on a random distribution or the k-core decomposition.

Appendix

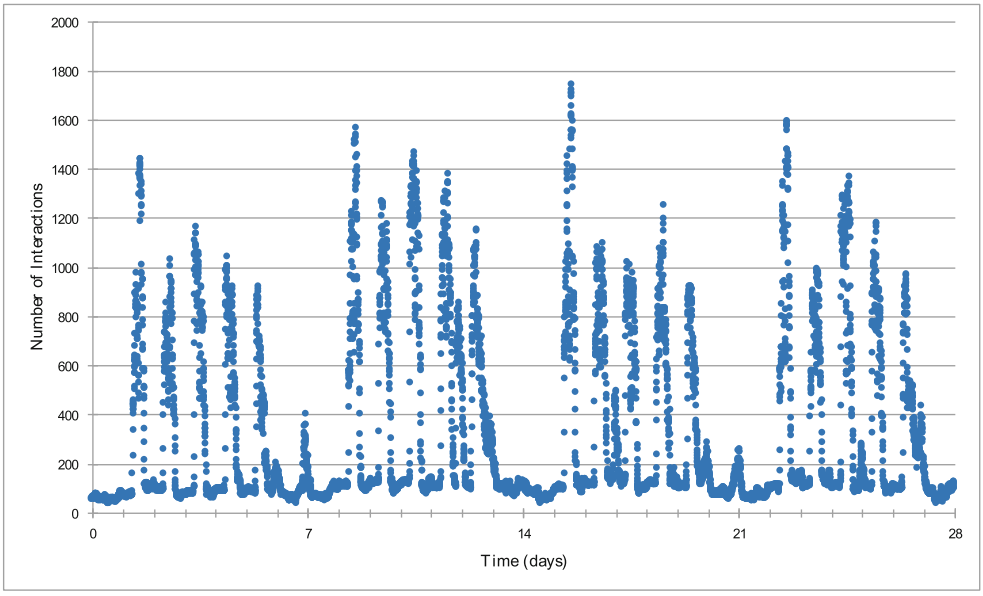

Fig. 5. Number of interactions by time in the Copenhagen dataset.

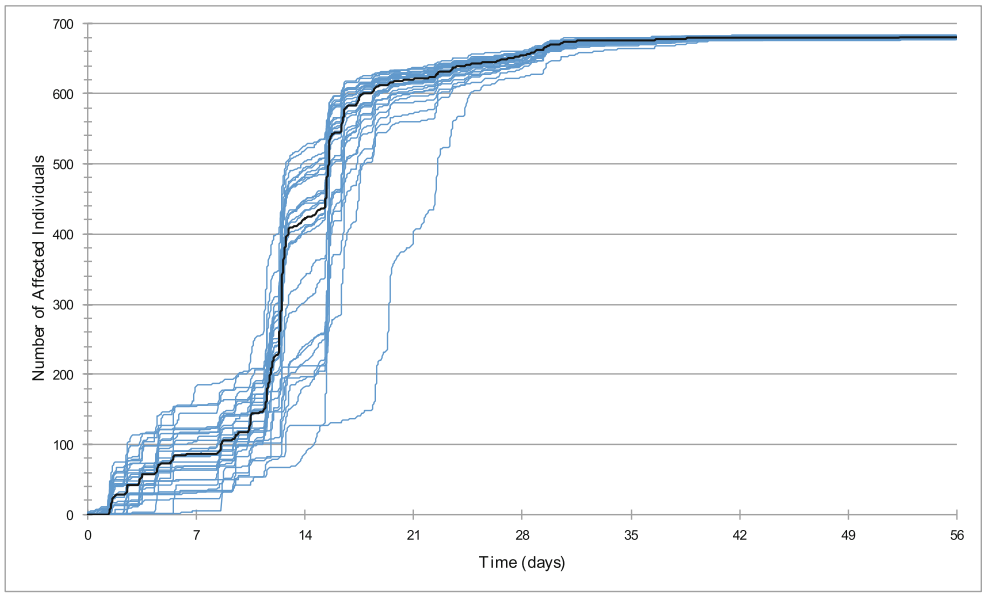

Fig. 6. Numbers of affected individuals by time in measles simulations without any interventions. Each curve is an average of five simulations with the same infection seed; the pointwise median of thirty curves is shown in black.

References

1. Borradaile, G., Migler, T., Wilfong, G.: Density decompositions of networks. In: Cornelius, S., Coronges, K., Gonçalves, B., Sinatra, R., Vespignani, A. (eds.) Complex Networks IX, pp. 15–26. Springer, Cham (2018)
2. CDC (Centers for Disease Control and Prevention). Measles—cases and outbreaks—CDC. Accessed 16 May 2019. https://web.archive.org/web/20190516082526/https://www.cdc.gov/measles/cases-outbreaks.html
3. CDC (Centers for Disease Control and Prevention). Measles—vaccination—CDC. Accessed 16 May 2019. https://web.archive.org/web/20190516074529/https://www.cdc.gov/measles/vaccination.html
4. CDC (Centers for Disease Control and Prevention). Pinkbook—measles—epidemiology of vaccine-preventable disease—cdc. Accessed 14 May 2019. https://web.archive.org/web/20190514200016/https://www.cdc.gov/vaccines/pubs/pinkbook/meas.html
5. Fenner, F., Henderson, D.A., Arita, I., Jezek, Z., Ladnyi, I.D.: Smallpox and its eradication. Number 6 in History of International Public Health. World Health Organization, Geneva (1988)
6. Frías-Martínez, E., Williamson, G., Frías-Martínez, V.: An agent-based model of epidemic spread using human mobility and social network information. In: 2011 IEEE Third International Conference on Privacy, Security, Risk and Trust and 2011 IEEE Third International Conference on Social Computing, pp. 57–64, October 2011
7. Gates, B.: The next epidemic—lessons from Ebola. N. Engl. J. Med. **372**(15), 1381–1384 (2015). PMID: 25853741
8. Gemmetto, V., Barrat, A., Cattuto, C.: Mitigation of infectious disease at school: targeted class closure vs school closure. BMC Infect. Dis. **14**(1), 695 (2014)

9. Granell, C., Mucha, P.J.: Epidemic spreading in localized environments with recurrent mobility patterns. Phys. Rev. E **97**(5), 5 (2018)
10. Kephart, J.O., White, S.R.: Directed-graph epidemiological models of computer viruses. In: Proceedings. 1991 IEEE Computer Society Symposium on Research in Security and Privacy, pp. 343–359, May 1991
11. Rota, P.A., Moss, W.J., Takeda, M., de Swart, R.L., Thompson, K.M., Goodson, J.L.: Measles. Nat. Rev. Dis. Primers **2**, 16049 (2016). EP – 07
12. Seidman, S.B.: Network structure and minimum degree. Soc. Netw. **5**(3), 269–287 (1983)
13. Stopczynski, A., Pentland, A.'Sandy'., Lehmann, S.: How physical proximity shapes complex social networks. Sci. Rep. **8**(1), 17722 (2018)
14. Stopczynski, A., Sekara, V., Sapiezynski, P., Cuttone, A., Madsen, M.M., Larsen, J.E., Lehmann, S.: Measuring large-scale social networks with high resolution. PLoS ONE **9**(4), 1–24 (2014)
15. WHO (World Health Organization). Measles vaccines: WHO position paper—April 2017. Wkly. Epidemiol. Rec. **92**(17), 205–228 2017