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or Early Detection of Contagious

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us outbreaks give contemporaneous information about the course of an epidemic at ter of a social network are likely to be infected sooner during the course of an hery. Unfortunately, mapping a whole network to identify central individuals who might icult. We propose an alternative strategy that does not require ascertainment of global the friends of randomly selected individuals. Such individuals are known to be more up could indeed provide early detection, we studied a flu outbreak at Harvard College vere either members of a group of randomly chosen individuals or a group of their ression of the epidemic in the friend group occurred 13.9 days (95% C.I. 9.9–16.6) in he population as a whole). The friend group also showed a significant lead time days before the peak in daily incidence in the population as a whole. This sensor ne to react to epidemics in small or large populations under surveillance. The amount bbreak and the network at hand. The method could in principle be generalized to other avioral contagions that spread in networks.

Social Network Sensors for Early Detection of Contagious Outbreaks. PLoS ONE al.pone.0012948

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in equity stake in a company, MedNetworks, that is licensed by Harvard and UCSD air work.

us outbreaks ideally give contemporaneous information about the course of an rs lag behind the epidemic.[1]–[3] However, the situation could be improved, possibly age of a potentially informative property of social networks: during a contagious 'k are likely to be infected sooner than random members of the population. Hence, the e of central individuals within human social networks could be used to detect he population-at-large.

ndividuals and then spreads from person to person in the network will tend, on ; more quickly than peripheral individuals because central individuals (as defined in number of steps (degrees of separation) away from the average individual in the h some contagions can spread via incidental contact, the duration of exposure ch higher than between strangers, suggesting that the social network itself will be an ak.[5], [7] As a result, we would expect the S-shaped epidemic curve [8], [9] to be / located individuals compared to the population as a whole (see Figure 2). This shift, lection of an outbreak.

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variation in structural attributes and topological position. Each circle represents a hip tie. Nodes A and B have different “degree,” a measure that indicates the number I to exhibit higher “centrality” (node A with six friends is more central than B and C ons infect people at random at the beginning of an epidemic, central individuals are e a shorter number of steps (on average) from all other individuals in the network. same degree, they differ in “transitivity” (the probability that any two of one’s friends its high transitivity with many friends that know one another. In contrast, node C’s .nd therefore they offer more independent possibilities for becoming infected earlier

[48.g001](#)

in contagion between central individuals and the population as a whole.

phases, one in which the number of infected individuals exponentially increases as incidence exponentially decreases as susceptible individuals become increasingly y a logistic function. Central individuals lie on more paths in a network compared to 3 therefore more likely to be infected early by a contagion that randomly infects erson to person within the network. This shifts the S-shaped logistic cumulative al individuals compared to the population as a whole (left panel). It also shifts the

[48.g002](#)

ating central individuals in networks could enhance the population-level efficacy of a work suggests that optimal placement of sensors in physical networks (such as water ner.[14] However, mapping a whole network to identify particular individuals from isuming, and often impossible, especially for large networks.

tegy that does *not* require ascertainment of global network structure, namely, *idividuals*. This strategy exploits an interesting property of human social networks: on pple possess more links (have higher degree) and are also more central (e.g., as etwork than the initial, randomly selected people who named them.[15]–[19] ds to get infected earlier than a set of randomly chosen individuals (who represent the ndom sample of individuals from a social network will have a mean degree of μ (the ds of these random individuals will have a mean degree of μ plus a quantity defined ded by μ . Hence, when there is variance in degree in a population, and especially r of contacts for the friends will be greater (and potentially much greater) than the ies known as the “friendship paradox” (“your friends have more friends than you do”)

andomly chosen people has previously been explored in a stimulating theoretical ises nominated friends as *sensors* for early detection of an outbreak has not ited on any sort of real outbreak. To evaluate the effectiveness of nominated friends as 3d the spread of flu at Harvard College from September 1 to December 31, 2009. In ally kills 41,000 Americans each year [20]) and the H1N1 strain were prevalent in the 9 have been attributed to the latter.[1] It is estimated that this H1N1 epidemic, which million Americans. Unlike seasonal flu, which typically affects individuals older than nally, according to the CDC, the epidemic peaked in late October 2009, and 3ecember 2009. Whether another outbreak of H1N1 will occur (for example, in areas 3ared) is a matter of some debate,[1] but many scholars have been studying the pectives.[21], [22]

3ents from Harvard College, discerned their friendship ties, and tracked whether they from the start of the new academic year) to December 31, 2009. This sample was 3ents of essential analytic interest: (1) a sample chosen randomly from the 6,650 friends” sample (N=425) composed of individuals who were named as a friend at le (see Supporting Information [Text S1](#) for more details).

3 foregoing group of 744 students, we wound up having information about a total of dents (who either participated in the study or who were nominated as friends or as 3 draw the social network of part of the Harvard College student body (see Supporting

3estionnaire soliciting demographic information, flu and vaccination status since measures of popularity. We also obtained basic administrative data from the Harvard 3ent, and inter-collegiate sports participation.

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enza among the students in our sample as recorded by University Health Services on December 31, 2009. Presenting to the health service indicates a more severe level of illness. We do not expect the same overall prevalence using this diagnostic standard as with self-reported data offer the advantage of allowing us to obtain information about flu symptoms as

collected self-reported flu symptom information from participants via email twice weekly on December 31, 2009. The students were queried about whether they had had a fever and there was very little missing data (47% of the subjects completed *all* of the surveys).

al testing is the current standard for flu diagnosis. Similar to previous studies,[23] whether seasonal or the H1N1 variety) if they reported having a fever of greater than 100.4°F (38°C) or symptoms: sore throat; cough; stuffy or runny nose; body aches; headache; chills; findings by using definitions of flu that required more symptoms, and our results did not differ. As part of the foregoing biweekly self-reports, in order to complement the UHS data, we asked whether the students reported having been vaccinated (with seasonal flu vaccine or H1N1 vaccine) at the UHS.

son's precise position in the observed network, nor indeed whether he was nominated as a friend by the *actual path* by which he acquired (or did not acquire) the flu. The topological fact that a person was deemed to be a member of the friend group, serve as *proxies* for an essentially unobservable social network (including real friends, relatives, casual acquaintances, and contacts by inter-personal means. Being a "friend" is a marker for a person's social network, but whether this person actually is. Of course, it is likely that measured friendship networks are noisy: for instance, people with more friends should come into greater contact with more friends.

Prevalence of flu in our sample was 8% based on diagnoses by medical staff, and it was 32% based on self-reported flu symptoms. In studies of school-based outbreaks and also contemporaneous national estimates for influenza, the prevalence was higher by the self-report standard. We studied the effect of various variables with cumulative flu incidence at day 122 (the last day of follow-up) to see if any were associated with risk. None of these variables was significantly associated with flu diagnoses by medical staff ($p > 0.05$), so we focused on the effect of these variables on *shifts in the timing* of the

curves for the friend group and the random group diverge and then converge (Figure 3). The time to flu diagnosed by medical staff is shifted 13.9 days forward in time (95% C.I. 9.9–17.9 days), which represents approximately 60% of one standard deviation in the time-to-event in the whole population, but a smaller shift in self-reported flu symptoms (3.2 days, 95% C.I. 2.2–4.3). In the absence of a gold standard diagnostic standards, the estimates are robust to a number of control variables including sex, college class, and inter-collegiate sports participation (see Supporting Information

between "friend" group and randomly chosen individuals.

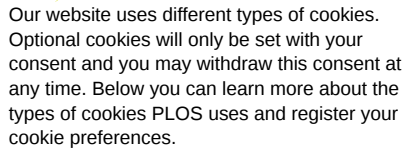
of individuals randomly selected from our population, and one composed of individuals nominated by members of the random group. The friend group was observed to have higher betweenness centrality than the random group (see Supporting Information Text S1). The maximum likelihood estimate (NPMLE) of cumulative flu incidence (based on data from individuals in the friend group) tended to get the flu earlier than individuals in the random group. The incidence from a nonlinear least squares fit of the data to a logistic distribution of flu is shifted forward in time for the friends group by 13.9 days (right panel). A comparison of the friend group was first detected with data available up to Day 16. Raw data for daily flu incidence in the friend group (red) is shown in the inset box (right panel).

[Fig 48.g003](#)

on *ex post*, but we wondered when it would also be possible to detect a difference in time, given less complete data. We therefore estimated the models each day using data on flu diagnoses by medical staff, the friend group showed a significant lead time ($p < 0.05$) in the peak in daily incidence in visits to the health service. For self-reported flu symptoms, the peak occurred by day 39, which is 83 days prior to the estimated peak in daily incidence in self-reported flu symptoms. The difference in the timing of the peak in the friends group and the randomly chosen group could be an effective measure of an epidemic.

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ation procedure would be to rely on self-reported popularity or self-reported counts of risk group. We measured our subjects' self-perceptions of popularity using an eight-point scale. The time to flu diagnosed by medical staff is shifted 13.9 days forward in time for flu diagnoses (see Supporting Information Text S1). Moreover, the difference in the timing of the lead time provided by the friend group for either flu



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symptoms. These results suggest that being nominated as a friend captures more (to be central in the network) than self-reported network attributes. Such information might also be more accurate [12].

t require information about the full network, our survey took place on a college campus nominated, and the same person was frequently nominated several times. Hence, our information about 1,789 unique, inter-connected students who were either surveyed or part in the study. A connected component of 714 people was in turn apparent within a part of flu in this component in Figure 4, which shows the tendency of the flu to “bloom” over a 122-frame movie of daily flu prevalence available online (see Supporting

friendship network over time. The network (714 people) for a specific date, with each line representing a friendship between two people. Infected individuals are colored red, and the size of the red area is proportional to the number of friends infected. All available information for all 122 days of the study are available in a movie of the epidemic posted in the [48.g004](#)

n also allowed us to actually measure egocentric network properties like in-degree (a friend), betweenness centrality (the number of shortest paths in the network that number of friends an individual has when all individuals with fewer friends are iteratively removed) or probability that two of one's friends are friends with one another). This would not be unique in larger populations (wherein surveyed individuals would be much less likely to overlap). Results showed that, as expected, the friend group differed significantly from the random network (Mann Whitney U test $p < 0.001$), higher centrality ($p < 0.001$), higher k -value ($p = 0.039$).

s could help to identify groups that could be used as social network sensors when full (Figure 5). For example, we expect in-degree to be associated with early contagion in the network who might be infected. NLS estimates suggest that each on average 5.7 days (95% C.I. 3.6–8.1) for flu diagnoses by medical staff and 8.0 days (95% C.I. 5.7–10.3) for flu diagnoses by family and friends. On the other hand, the same is not true for out-degree (the number of friends a person has). In-degree would be straightforwardly ascertainable by asking respondents about themselves. This is the case in the present setting since most people named three friends (the maximum allowed).

ness are computed based on the mapping of the network. The high in-degree indicates a higher-than-average number of other people in the network who name them as friends. The low probability indicates that individuals with below-average probability that any two of their friends are both named by the same person form a group which is composed of individuals with a higher-than-average betweenness, which is the number of shortest paths through all individuals in a network that pass through a given person. The high coreness indicates a higher-than-average coreness, which is the number of friends a person has once all other individuals have been eliminated from the network. Analyses were conducted separately for data based on self-reported flu symptoms (green bars) and data based on self-reported flu symptoms (green bars). Estimates and 95% confidence intervals are shown for each measure. Linear least squares fit of the flu data to a logistic distribution function (see Supporting Information S1) shows that flu outbreaks occur up to two weeks earlier in each of these groups.

[48.g005](#)

associated with early contagion. NLS estimates suggest that individuals with τ_e left by 16.5 days (95% C.I. 1.9–28.3) for flu diagnoses by medical staff and 22.9 days, relative to those with minimum centrality. A related measure, k -coreness, network get the flu earlier. NLS estimates suggest that increasing the measure k by 1 leaves τ_e left by 4.3 days (95% C.I. 1.8–6.5) for flu diagnoses by medical staff and 7.5 days by friends. Moreover, both betweenness centrality and k -coreness remain significant even after controlling for other variables. These results suggest that individuals who agree, suggesting that it is not just the number of friends that is important with respect to contagion, but also the quality of the relationships, such as friends with respect to friends, friends of friends of friends, and so on [6].

associated with early contagion. People with high transitivity may be poorly connected and tend to know one another and exist in a tightly knit group. In contrast, those with low centrality are more likely to be in independent groups, and each additional group increases the possibility that the disease spreads to the subject. NLS estimates suggest that individuals with minimum observed

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(95% C.I. 23.5–43.5) for flu diagnoses by medical staff and 15.0 days (95% C.I. 12.7–) those with maximum transitivity. Moreover, transitivity remains significant even when

lge of when – or whether – an epidemic is unfolding is crucial to policy makers and populations, whether small or large. In fact, with respect to flu, models assessing the olis such as New York City suggest that vaccinating even one third of the population e epidemic, but only if implemented a month earlier than usual.[25], [26] A method like it such early detection.

targeted populations of any size, in real time. For example, a health service at a a sample of subjects who are nominated as friends and who agree to be passively e form of visits to health care facilities); a spike in cases in this group could be read as ealth officials responsible for a city could also empanel a sample of randomly chosen s (perhaps a thousand people in all) who have agreed to report their symptoms using ey system (like the one employed here). Regional or national populations could also nominated friends being periodically surveyed instead of, or in addition to, a random ice public health officials often monitor populations in any case, the change in practice entral individuals might not be too burdensome.

single, relatively small institution might possibly actively seek out central individuals to g the utility of such individuals as sensors), such a focused vaccination effort would be al sample, given the likely irrelevance of vaccinating the actual sensor sample le epidemic. Regardless, since the people being followed as sensors would, in most al people in a population (let alone of all the people in the population as a whole), idemic were noted to have affected them), it seems unlikely that this would materially ise the utility of the central individuals as sensors. Nevertheless, mathematical o better understand what role sensors might play in helping to reverse the course of

re epidemic in the friend and random groups could be exploited in at least two o were being monitored, an analyst tracking an outbreak might look for the first among the friends group rose above a predetermined rate (e.g., a noticeable increase ld indicate an impending epidemic. Second, in a strategy that would yield more mple of friends and a sample of random subjects, and the harbinger of an epidemic re seen to first diverge from each other. Especially in the case of the spread of re difference between these two curves provides additional information: the adoption idence of secular trends in the population, whereas the *difference* between the two personal) effect, over and above the baseline force of the epidemic.

method of surveying friends could provide early detection of contagious outbreaks in ase of the flu, the method we evaluated appears to provide longer lead times than ics. Current surveillance methods for the flu, such as those implemented by the CDC eeking outpatient care or having lab tests, are typically lagging indicators about the r one to two weeks behind the actual course of the epidemic).[1] A proposal to use information about the flu suggests that this approach could offer a better indicator, week before published CDC reports.[2], [3] Another innovative proposal involved the ed the warning [27]. However, while potentially instantaneous, the Google Trends and t, give *contemporaneous* information about rates of infection. In contrast, we show that an outbreak of flu two weeks *in advance*. That is, the sensor network method *warning*.

n conjunction with online search. By following the online behavior of a friend group, or example, based on e-mail records which could be used to reconstruct social network ght be able to get high-quality, real-time information about the epidemic with even s even more time to plan a response.

ved for other pathogens or in populations of different size or composition remains to detect outbreaks early, and how early it might do so, will depend on intrinsic the biology of the pathogen); how this thing is measured; the nature of the population, e or affected individuals; the number of people empanelled into the sensor group; the ree distribution and its variance, or other structural attributes) [6], [28]; and other is the structure of the network as it spreads (for example, by killing people in the ion, perhaps by affecting the tendency of any two individuals to remain connected unt of time, in terms of early detection, provided could thus vary considerably, g.

been illustrated with a particular outbreak (flu) in a particular population (college o other phenomena that spread in networks, whether biological (antibiotic-resistant rative (altruism) [30], informational (rumors), or behavioral (smoking) [31]. Outbreaks onditions could be detected before they have reached a critical threshold in

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11 participants and the study was approved by and carried out under the guidelines of the Institutional Review Board in Research at Harvard University.

Participants completed a set of 8 questions previously used to assess the popularity of co-workers.[32]

Participants were asked to provide us with the names and contact information of 2-3 [of your] friends... 3 Harvard College students who you know and who you think would like to participate

the *in-degree* (the number of times an individual is named as a friend by other individuals each person names as a friend) of each subject. The in-degree is virtually 1, the total number of other people in the network) but the out-degree is restricted to a maximum of 3 (the number of friendship information).

we identified the extent to which an individual lies on potential paths for contagions through the network; this quantity summarizes how central an individual is in the network and is called *k-core-ness*, which identifies the number of friends a person has after all individuals with a lower *k* are removed from the network. Recent work suggests this measure may be more appropriate than degree centrality in correlated networks [6]. We measured *transitivity* as the empirical probability that two friends of a person are themselves friends, forming a triangle (see Figure 1). This measure is just the total number of triangles in the network divided by the total possible number of triangles.

we used pictures of the network, and we implemented the Kamada-Kawai algorithm, which assigns positions to nodes in the network and repositions nodes in an attempt to minimize the difference between the plotted distances and the network distances.[35] A movie of the network evolution over the days of the study is available online (see Supporting Information [Text S1](#)).

For both the friend group and the random group using a nonparametric maximum likelihood method we calculated the predicted daily incidence using an estimation procedure designed to account for the unknown outbreak associated with a given independent variable (see Supporting Information [Text S1](#)). The observed probability of flu to a cumulative logistic function via nonlinear least squares and 95% confidence intervals, we used a bootstrapping procedure in which we sampled with replacement and re-estimated the fit [38]. This procedure produced estimates based on asymptotic approximations, so we report only the more conservative estimates of how many days of early detection was possible for groups with various network topologies. We calculated the confidence intervals in the foregoing models by the mean difference between the above-mentioned models (see Supporting Information [Text S1](#)).

network over time.
[.s001](#)

[.s002](#)

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