The Spread of Behavior in an Online Social Network Experiment

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Abstract

How do social networks affect the spread of behavior? A popular hypothesis states that networks with many clustered ties and a large diameter will be less effective for behavioral diffusion than "randomized" networks, in which locally redundant ties are rewired to provide shortcuts across the social space. A competing hypothesis argues that when behaviors require social reinforcement, random networks lack the local structure to support behavioral adoption, suggesting that networks with more clustering and a larger diameter may be more advantageous for some diffusion processes. We investigated the effects of network structure on diffusion experimentally by studying the spread of health behavior through artificially structured online communities. The results show that individual adoption was much more likely when participants received social reinforcement from multiple neighbors in the social network. This produced the striking finding that the behavior spread farther and faster across clustered lattice networks than across corresponding random networks.

The Spread of Behavior in an Online Social Network Experiment

Many behaviors spread through social contact (*1-3*). As a result, the network structure of who is related to whom can critically impact the extent to which a social behavior is adopted in a population (*2-8*). There are two competing hypotheses about how network structure affects diffusion. The 'strength of weak ties' hypothesis predicts that networks with many "long ties" (e.g., small world topologies) will spread a social behavior farther and more quickly than a network in which ties are highly clustered (*4-6*). This hypothesis treats the spread of behavior as a *simple contagion*, such as disease or information: a single contact with an "infected" individual is usually sufficient to transmit the behavior (*2*). The power of long ties is that they reduce the redundancy of the diffusion process by connecting people whose friends do not know each other, thereby allowing a behavior to rapidly spread to new areas of the network (*3-5*). The "ideal" case for this lack of redundancy is a "random" network – where (in expectation in a large population) all of an individual's ties each reach out to different neighborhoods (*4,9*). The other hypothesis states that, unlike disease, social behavior is a *complex contagion*: people usually require contact with multiple sources of "infection" before being convinced to adopt a behavior (*2*). This hypothesis predicts that because clustered networks have more redundant ties, which provide social reinforcement for adoption, they will better promote the diffusion of behaviors across large populations (*2,7*). Despite the scientific (*6,7,10*) and practical (*1,2,11*) importance of understanding the spread of behavior through social networks, an empirical test of these predictions has not

been possible because it requires the ability to independently vary the topological structure of a social network.

We adopted an experimental approach to testing the effects of network structure on diffusion (*12*). We studied the spread of a health behavior through a network-embedded population by creating an Internet-based health community, comprising 1,528 participants recruited from health-interest World Wide Web sites (*13*). Each participant created an on-line profile, including an avatar, a username, and a set of health interests. They were then matched with other participants in the study – referred to as "health buddies" – as members of an on-line health community. Participants made decisions about whether or not to adopt a health behavior based on the adoption patterns of their health buddies. Arriving participants were randomly assigned to one of two experimental conditions – a clustered lattice network and a random network – which were distinguished only by the topological structure of the social networks. In the clustered lattice network condition, there was a high level of clustering (*5,6,13*) created by redundant ties that linked each node's neighbors to one another. The random network condition was created by rewiring the clustered lattice network using a permutation algorithm based on the small world network model (*14,15,6,12*). This ensured that each node maintained the exact same number of neighbors as in the clustered network (i.e., constant degree), while at the same time dramatically reducing the clustering in the network, and eliminating redundant ties within and between neighborhoods (*14,6,4*).

The network topologies were created before the participants arrived, and the subjects could not alter the topology in which they were embedded (e.g., by making new ties). In both conditions, each participant was randomly assigned to occupy a single node

in one network. The occupants of the immediately adjacent nodes in the network – i.e., the network neighbors – constituted a participant's health buddies (*12*). Each node in a social network had an identical number of neighbors as the other nodes in the network, and participants could only see the immediate neighbors to whom they were connected. Consequently, the size of each participant's social neighborhood was identical for all subjects within a network and across conditions. More generally, every aspect of a participant's experience prior to the initiation of the diffusion dynamics was equivalent across conditions (*12*), and the only difference between the conditions was the pattern of connectedness of the social networks in which the participants were embedded. Thus, any differences in the dynamics of diffusion between the two conditions can be attributed to the effects of network topology.

This experimental design has four advantages over observational data. (i) The present study isolates the effects of network topology independent of frequently co-occurring factors such as homophily(*16,3*), geographic proximity (*17*), and interpersonal affect (*4,18*), which are easily conflated with the effects of topological structure in observational studies (*2,3,19*). (ii) We study the spread of a health-related behavior that is unknown to the subjects before the study (*13*), thereby eliminating the effects of non-network factors from the diffusion dynamics, such as advertising, availability, and pricing, which can confound the effects of topology on diffusion when, e.g., the local structure of a social network correlates with greater resources for learning about or adopting an innovation (*11,19,20*). (iii) This study eliminates the possibility for social ties to change, and thereby identifies the effects of network structure on the dynamics of diffusion without the confounding effects of homophilous tie formation (*1,21*). (iv)

Finally, this design allows the same diffusion process to be observed multiple times, under identical structural conditions, thereby allowing the often stochastic process of individual adoption (*22*) to be studied in a way that provides robust evidence for the effects of network topology on the dynamics of diffusion.

We report the results from six independent trials of this experimental design, each trial consisting of a matched pair of network conditions. In each pair, subjects were randomized to either a clustered lattice network or a corresponding random network (*13*). This yielded twelve independent diffusion processes. Diffusion was initiated by selecting a random "seed node," which sent signals to its network neighbors encouraging them to adopt a health-related behavior – *viz*., registering for a health forum website that offered access and rating tools for online health resources (*13*). Every time a participant adopted the behavior (i.e., registered for the health forum), messages were sent to her health buddies inviting them to adopt. If a participant had multiple health buddies who adopted the behavior, then she would receive multiple signals, one from each neighbor. The more neighbors who adopted, the more reinforcing signals a participant received. The sequence of adoption decisions made by the members of each social network provides a precise time series of the spread of the behavior through the population. It also provides an exact record of the number of signals required in order for individuals to adopt. The starting time (i.e., time = 0) for each diffusion process corresponds to the instant when the seed node was activated, and the initial signals were sent. For each trial, the diffusion process was allowed to run for three weeks (approximately 1.8 million seconds). To test for the possible effects of population size (N) and neighborhood size (Z) on the diffusion

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dynamics, three different versions of the experiment were used i) $N=98$, $Z=6$; ii) $N=128$, $Z=6$; iii) $N=144$, $Z=8$ (*13*).

The results show that network structure has a significant effect on the dynamics of behavioral diffusion. Surprisingly, the topologies with greater clustering and a larger diameter were much more effective for spreading behavior. Figure 1 shows the time series generated by the six independent trials of the experiment. Adoption typically spread to a greater fraction of the population in the clustered networks (filled circles) than in the random networks (open triangles). On average, the behavior reached 53.77% of the clustered networks, while only 38.26% of the population adopted in the random networks (*13*). The results in figure 1 also show that the behavior diffused more quickly in the clustered networks than in the random networks. The average rate of diffusion in the clustered networks was more than four times faster than that of the random condition. (Differences in both the success and the rate of diffusion between network conditions are statistically significant, $P<0.01$)(*13*).

These findings were qualitatively the same across different network sizes and different neighborhood sizes. However, networks with more redundancy ($Z=8$) and greater local clustering, performed better than those with less redundancy ($Z=6$) and less clustering (*13*). These results are consistent with the hypothesis that more redundant ties between clustered neighborhoods can improve the global spread of behavior.

At the individual level, the results (Fig.2) show that redundant signals significantly increased the likelihood of adoption – social reinforcement from multiple health buddies made participants much more willing to adopt the behavior. Figure 2 compares the baseline likelihood of adoption after receiving one social signal, to the

increased likelihood of adoption for nodes receiving second, third, and fourth reinforcing signals. Participants were significantly more likely to adopt after receiving a second signal than after receiving only one signal ($P<0.001$). Receiving a third signal also significantly increased the likelihood of adoption, but with a smaller effect size ($P<0.05$) (*13*). Additional signals had no significant effect. This can be attributed to the attenuation of the sample size as the number of signals increased.

As with all experiments, design choices that aided our control of the study also put constraints on the behaviors that we could test. A key limitation of our design is that unlike the behavior we studied, in the real world adopting a new health behavior is often extremely difficult. In order to adopt behaviors such as getting a vaccination, going on a diet, starting an exercise routine, or getting a screening, people may be required to pay the costs of time, deprivation, or even physical pain. Because of this, we expect that the need for social reinforcement would be greater for adopting these health behaviors than it was for the behavior in our study. Consequently, the diffusion of real world health behaviors may depend even more upon clustered network structures than did the diffusion dynamics reported in our results.

An additional constraint of our study was that participants did not have any direct communication with their health buddies, or information about their identities. Previous studies have shown how factors such as homophily and strong interpersonal affect in social ties can improve the diffusion of behaviors through social networks (*3,18*). Our study explicitly eliminated these factors from the social interaction in order to isolate the effects of network structure. However, in the real world, these features of social relationships tend to be highly correlated with the formation of clustered social ties

(*3,23,24*). Consequently, we expect that these reinforcing factors would amplify the observed effects of clustered social networks in promoting the diffusion of health behaviors across a large population.

Evidence in support of the 'strength of weak ties' hypothesis has suggested that that networks with high levels of local clustering and tightly-knit neighborhoods are inefficient for large scale diffusion processes (*4,9,5*). Our findings show that not only is individual adoption improved by reinforcing signals that come from clustered social ties (Fig. 2), but this individual-level effect translates into a system-level phenomenon whereby large scale diffusion can reach more people, and spread more quickly, in clustered networks than in random networks (Fig. 1). While locally clustered ties may be redundant for simple contagions, like information or disease (*25,4,6*), they can be highly efficient for promoting behavioral diffusion. Based on these findings, we conjecture that public health interventions aimed at the spread of new health behaviors (e.g., improved diet, regular exercise, condom use, or needle-exchange) may do better to target clustered residential networks than the casual contact networks across which disease may spread very quickly (*26*) – particularly if the behaviors to be diffused are highly complex, e.g., because they are costly, difficult to do, or contravene existing norms.

Like previous web-based experiments (*22,27*), this experiment has important methodological advantages over studies conducted in physical laboratories. Web-based experiments provide a natural tool for studying the dynamics of social aggregation, which has traditionally been restricted to mathematical models due to the inherent limitations of data collection. Particularly for the study of socially interdependent behaviors embedded in social networks, a web-based design allows us to create large topological structures

necessary to test aggregation on a scale that is relevant to the dynamics observed in the

real world. Additionally, we were able to create a sufficient number of realizations to

characterize the interaction between the individual (micro) level behaviors and collective

(macro) phenomena. Because interdependent social processes are frequently stochastic

(*22*), the reproducibility of an aggregation process is essential for identifying how a

specific structural variable – such as network topology – affects the collective dynamics.

Web-based experiments make this possible on a new scale, offering a powerful

methodology for understanding the dynamics of behavior on social networks.

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Supporting Online Material
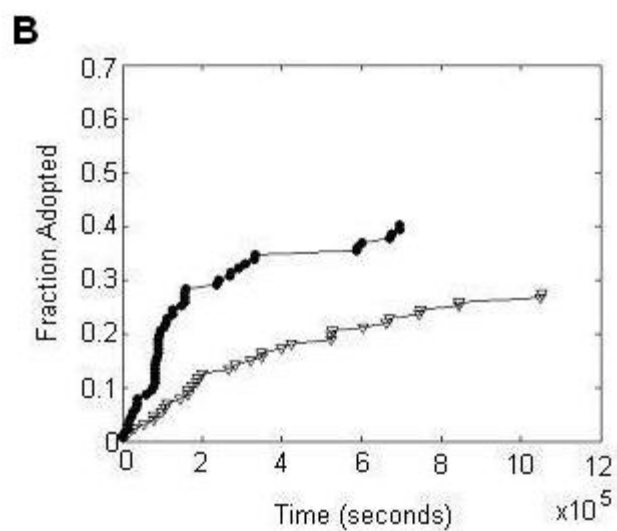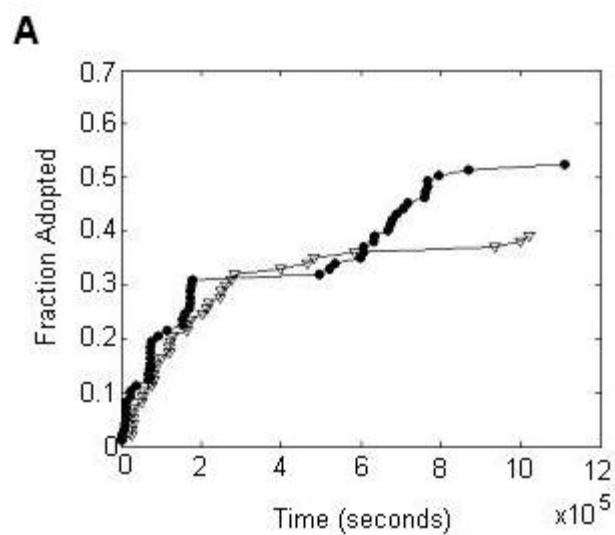www.sciencemag.org
Materials and Methods
SOM Text
Figs. S1 to S7
Tables S1, S2
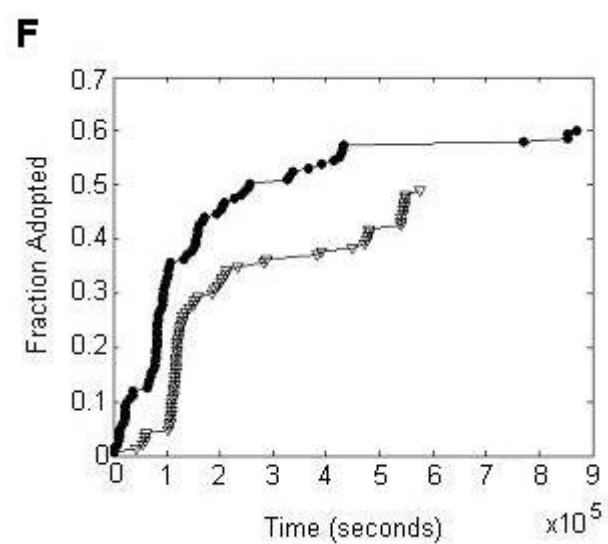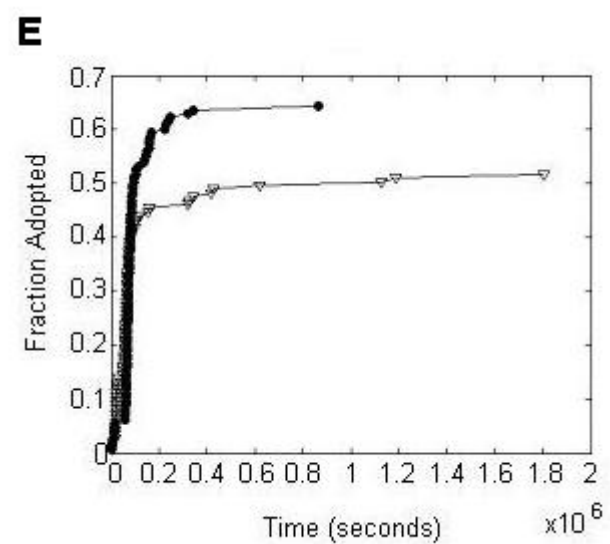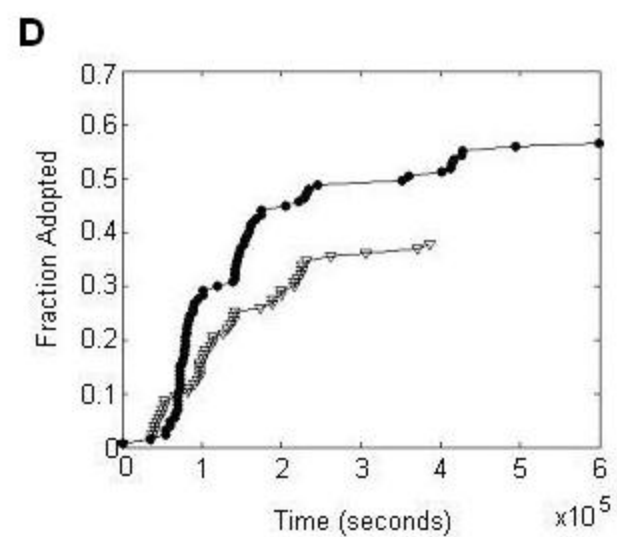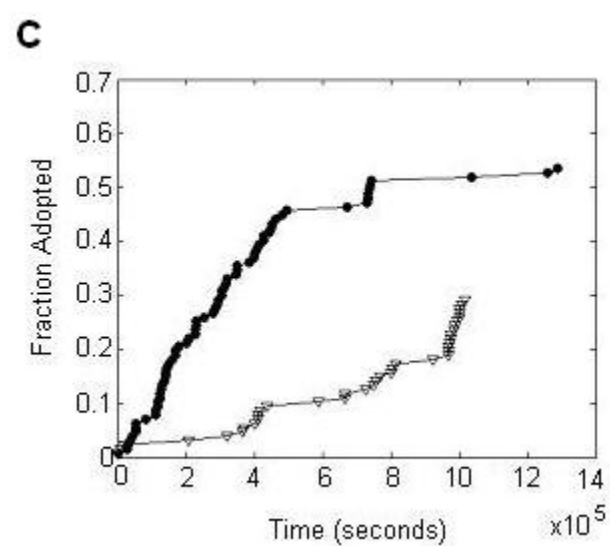
Fig. 1. Time series showing the adoption of a health behavior spreading through clustered lattice (solid circles) and random (open triangles) social networks. Six independent trials of the study are shown, including (**A**) N=98, Z=6, (**B-D**) N=128, Z=6, and (**E,F**) N=144, Z=8. The success of diffusion was measured by the fraction of the total network that adopted the behavior. The speed of the diffusion process was evaluated by comparing the time required for the behavior to spread to the greatest fraction reached by both conditions in each trial. Differences in both the success and the rate of diffusion between network conditions are significant (P < 0.01)(*12*).
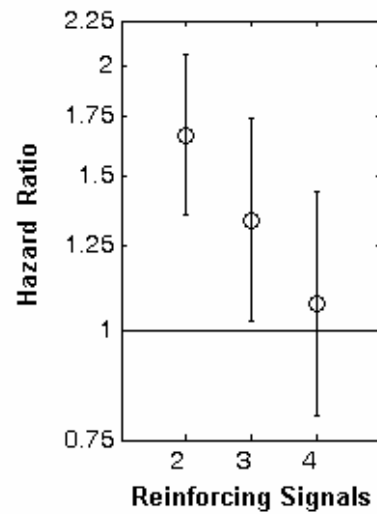
Fig. 2. Hazard ratios for adoption for individuals receiving 2, 3, and 4 social signals. The hazard ratio g indicates that the probability of adoption increases by a factor of g for additional signals compared to the baseline hazard of adoption from receiving a single signal ($g=1$). Shown are the 95% confidence intervals from the Cox proportional hazards model. The effect of an additional signal on the likelihood of adoption is significant if the 95% confidence interval does not contain $g=1$ (*12*).

Supporting Online Materials

<u>Experimental Design</u>

As described in the text, each trial of the study consisted of a pair of networks, one of each condition – a *clustered lattice network* condition and a *random network* condition –between which subjects were randomly assigned. The schema for this design is shown in Figure S1. Once subjects were assigned to a network condition, they were randomly assigned to one node in the network. In each condition, a single, randomly selected node was not filled with a subject – this node was used as the "seed node" for initiating the diffusion dynamics once the network was populated. In each trial, both networks had the same degree (each node had the same number of neighbors as every other node), and the same overall size (each network had the same total number of nodes). Within each trial, the only difference between conditions was the topological structure of the ties that connected the participants. Consequently, any difference in the dynamics of diffusion between conditions was due to the effects of network topology on the spread of behavior. Six independent trials of the study were run. Across all six trials, 50% of subjects were enrolled in the clustered lattice network condition and 50% were enrolled in the random network condition.

Diffusion dynamics were initiated by sending an email signal from the randomly chosen seed node to its neighbors in the social network, inviting them to register for a health forum website that offered access and rating tools for online health resources. If any of these subjects registered for the site, their network neighbors (i.e., "health buddies"), in turn, received an email message inviting them to adopt the behavior. If a

subject had multiple network neighbors who adopted the behavior, then she would receive multiple email signals, one from each neighbor. The sequence, timing, and number of signals that a subject received was entirely determined by the adoption pattern of the members of the social network. All email signals were sent from the "Healthy Lifestyle Network," and subjects had no access to identifying information about who their health buddies were, or how to contact them directly.
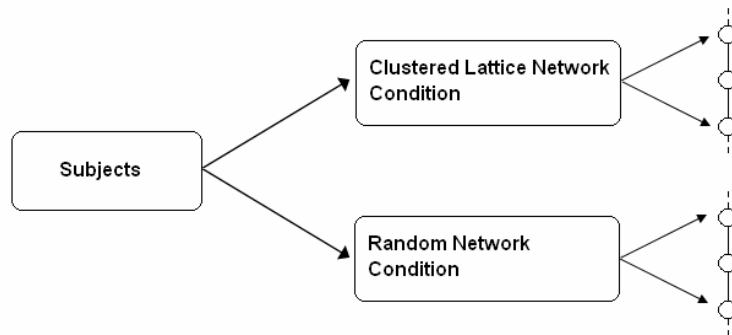

Figure S1. Schema of the experiment. Each subject is randomly assigned to a network condition, and then randomly assigned to a single node in that condition.

Subject Experience During the Experiment

The design of the experiment was unknown to the subjects. Upon arriving to the study, subjects were told that they would be matched with "health buddies" with whom they could share recommendations about on-line health resources. Subjects then provided their email addresses, agreed to a consent form, and chose usernames and avatars to represent themselves in the on-line community. Finally, each subject was shown a health buddy page, which displayed her own user avatar and health interests, as well as the avatars and health interests of her health buddies. Figure S2 shows a health

buddy page. Because of the similarity of the networks across conditions within a given

trial of the study, subjects' health buddy pages showed the same number of health

buddies regardless of which condition they were randomly assigned to.
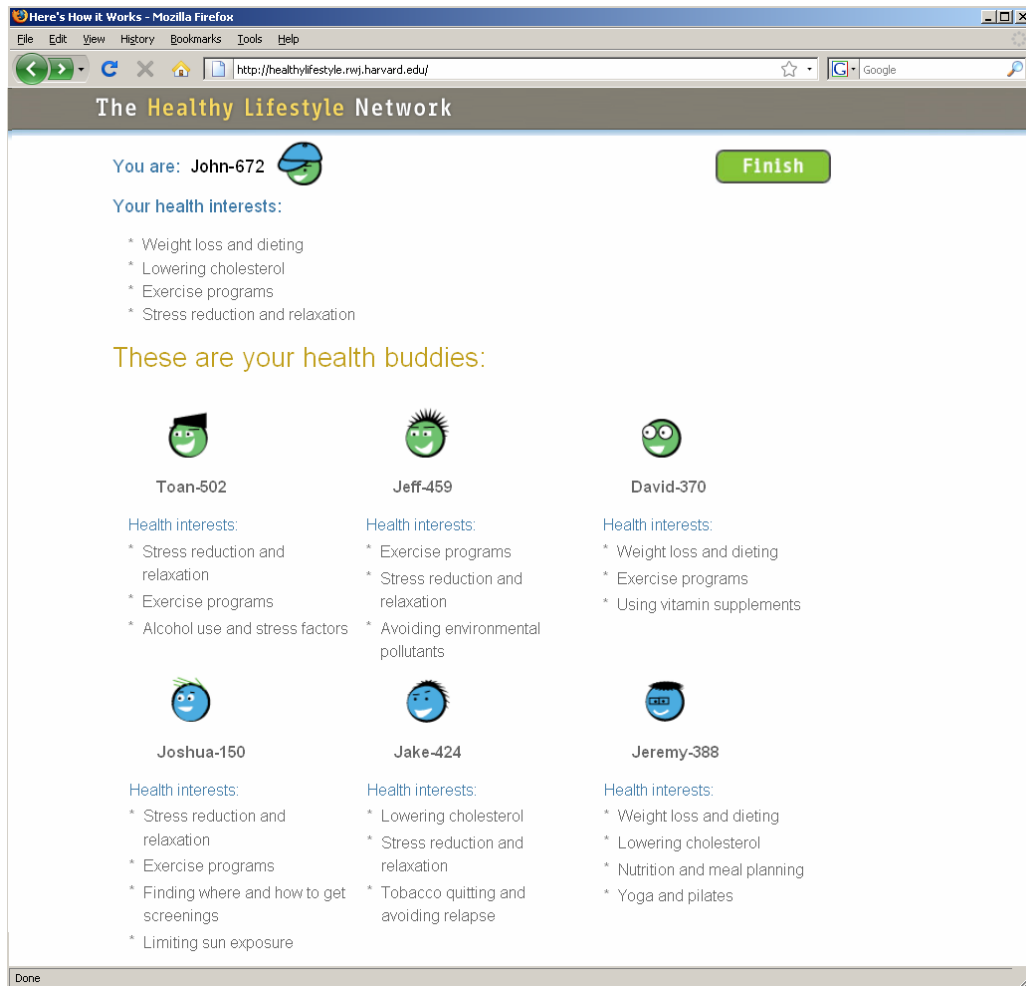
Figure S2. Screenshot of a health buddy page.

Once a subject completed the sign-up process, she received a confirmation email

asking her to verify that her email address was working. This allowed us to make sure

that all subjects in the study could be reached by email. For the duration of the study,

subjects only received email signals if their neighbors in the network adopted the

behavior. Each subject could receive at most one email from each health buddy. Each email let the subject know which of their health buddies had registered for the health forum website, and provided a web-link to the health forum registration page. An email signal is shown in figure S3.
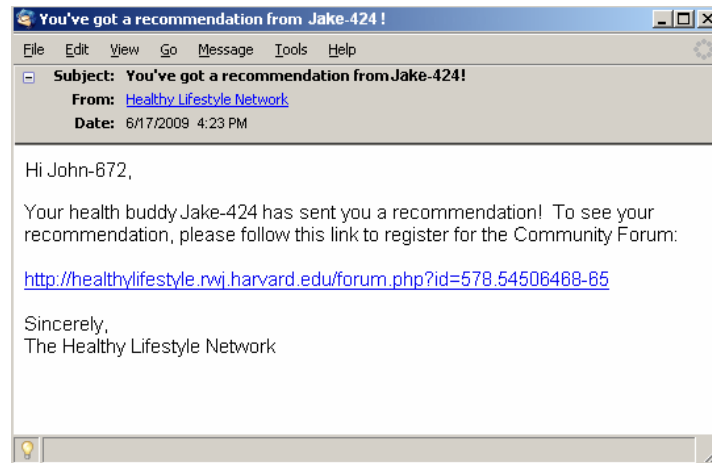

Figure S3. Email signal inviting a subject to join the health forum.

Once subjects registered for the forum, they could visit any of the websites listed under the different category headings (including "Healthy Lifestyle," "Fitness," "Nutrition", "Smoking Cessation", and "Weight Loss"), and rate the quality of the websites. Figures S4 and S5 show the registration page, and the home page, respectively, of the health forum. Every subject who registered for the forum saw the most current list of sites and ratings, available to all members. The only difference in the content of the health forum across subjects was the list of health buddies shown in the lower left panel – this was determined by which of the subject's health buddies had already registered for

the forum. The ratings for the websites, and the listed order of the websites, changed in

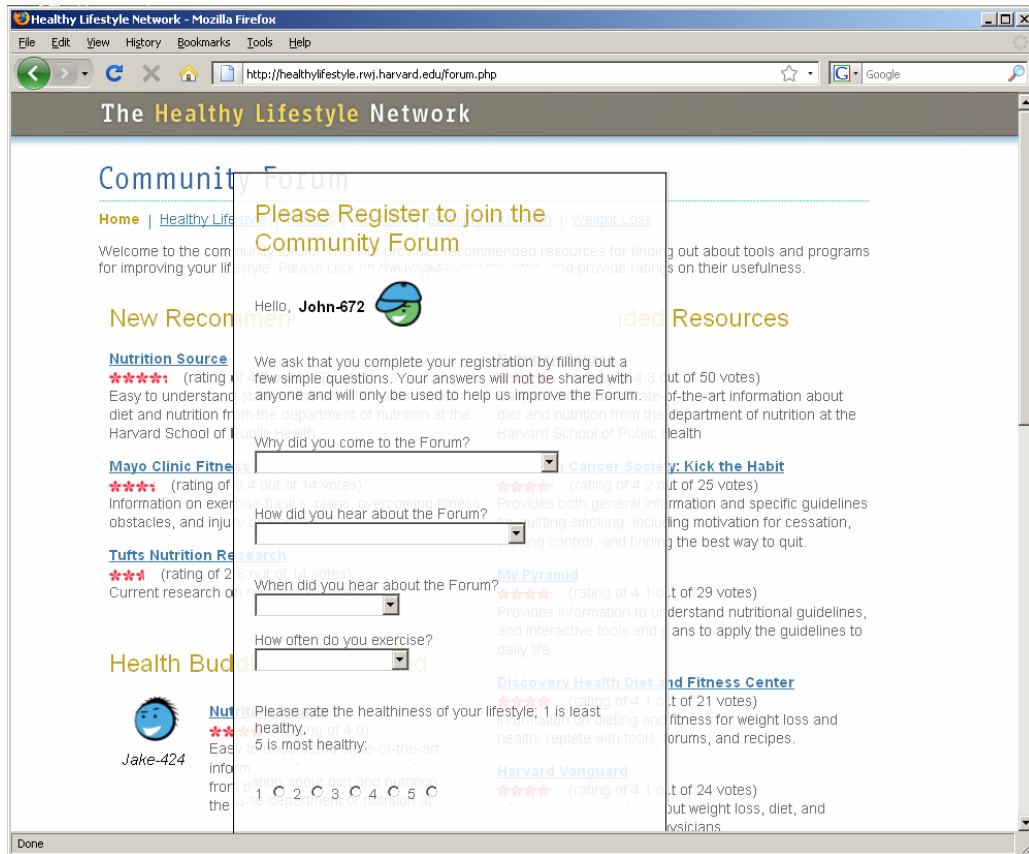real-time as subjects interacted with the health forum.

Figure S4. Registration page for the health forum website. Subjects were required to

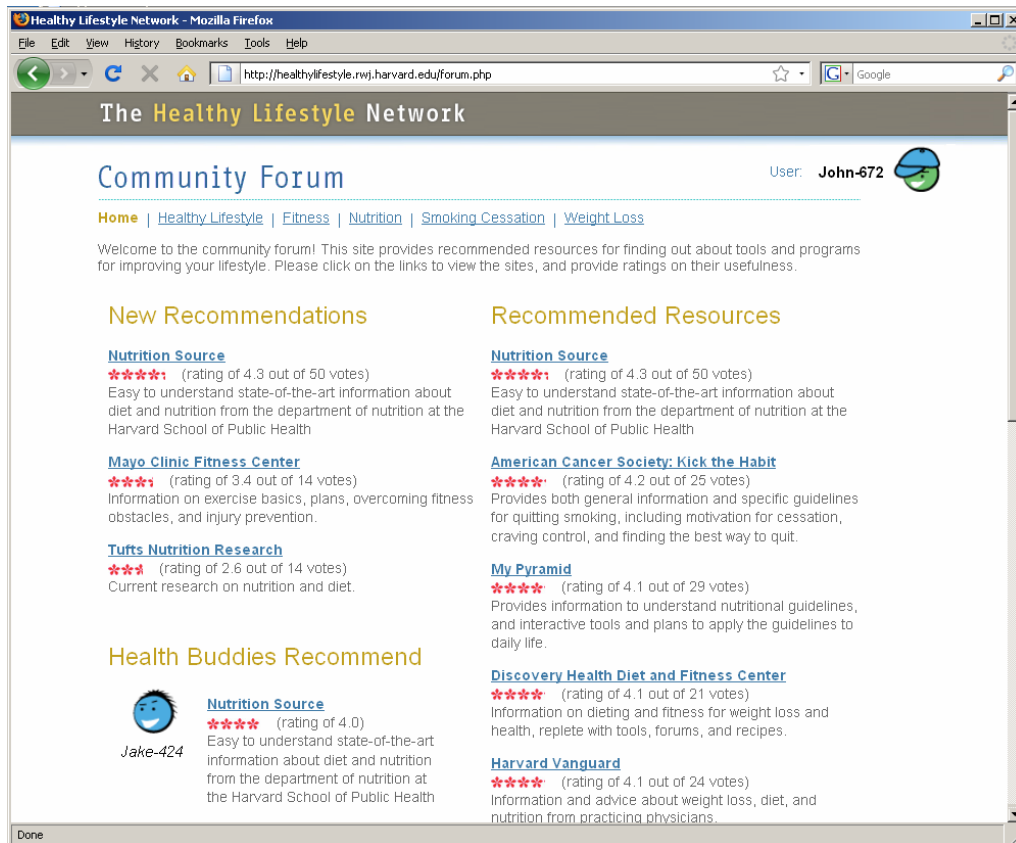register in order to access the forum.

Figure S5. Home page for the health forum website.

Subjects' activity in the health forum did not affect the experiment. Once subjects registered for the forum their actions did not result in additional email signals being sent, nor could they receive additional email signals. Entry to the health forum was treated as a binary and irreversible adoption decision, which was recorded as a one time event, resulting in a single message being sent to each of the subject's health buddies who had not already adopted the behavior.

If subjects returned to the initial sign-up website for the experiment, or to the health forum website, their most recent information was displayed, and they were not given the option to re-register either for the study or for the forum. However, subjects could return to the health forum as often as they liked (which logged them in

automatically once they were registered), and were able to visit new sites, add new ratings, and see the most recent ratings of their health buddies.

Subject Recruitment

The study was run for a 124-day period from May 4, 2009 through September 5, 2009, over which time a series of recruitment campaigns were used to attract subjects to the experiment. In total, 1,528 subjects participated in the study, 764 in the clustered lattice network condition, and 764 in the random network condition. Most subjects were recruited through email advertisements sent to members of health websites such as Prevention (http://www.prevention.com), Self (http://www.self.com), Men's Health (http://www.menshealth.com), Women's Health (http://www.womenshealthmag.com), and Shape (http://www.shape.com). Figure S6 shows examples of recruitment advertisements. Additionally, a small fraction of subjects were recruited from Your Disease Risk, a cancer risk evaluation site run by Washington University in St. Louis (http://www.yourdiseaserisk.wustl.edu).
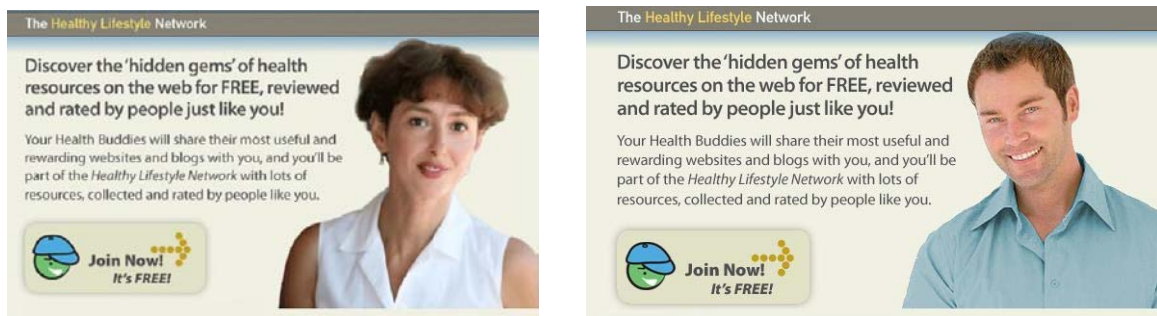

Figure S6. Advertisements used to recruit subjects to the study.

Network Structures

Each trial was comprised of a clustered lattice condition and a random network condition. Clustering in the network was measured using the clustering coefficient (CC), which reports the fraction of a node's neighbors that are neighbors with one another (averaged over the entire population). Trials 1, 2, 3, and 4 used a hexagonal lattice network ($Z=6$, $CC=0.4$) for the lattice condition (fig. S7A shows the hexagonal neighborhood structure) and a randomized version of the lattice network for the random condition. Randomization used the Maslov-Sneppen small world rewiring technique (*13,14*), which entails rewiring each tie to a random location in the network while preserving each node's degree, resulting in a network with the same degree distribution ($Z=6$), but with a completely random topology ($CC< 0.05$). Trials 5 and 6 used a Moore lattice network ($Z=8$, $CC=0.43$) for the lattice condition (fig. S7B shows the Moore neighborhood structure), and used the same randomization procedure described above to create the corresponding random networks ($Z=8$, $CC<0.05$). Both the hexagonal and Moore lattice networks were located on tori (i.e., toroidal surfaces), so there were no boundary effects in the networks.
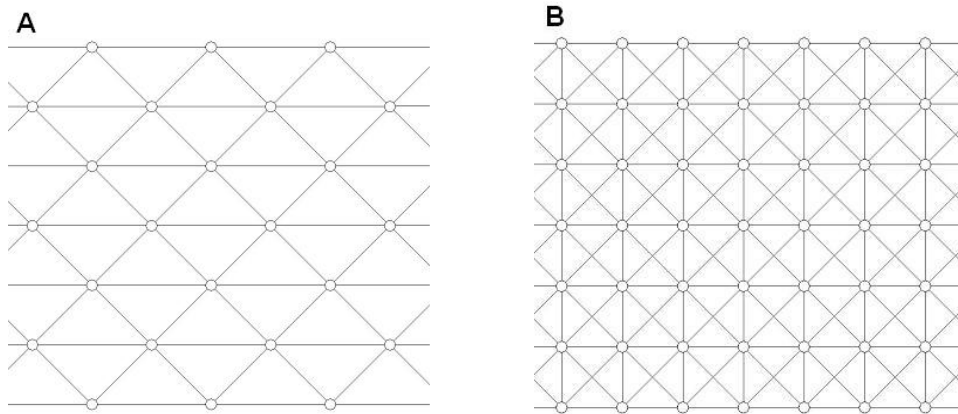

Figure S7. Neighborhood structure for the **A)** Hexagonal and **B)** Moore lattice networks.

<u>Data Analysis</u>

We measured the success of diffusion in terms of the fraction of the population that ultimately adopted the behavior. The fraction of adopters, S_j, in network j, is defined as:

$$S_j = \frac{\sum_{i=1}^{(N_j-1)} a_i}{(N_j-1)}, \quad (1)$$

where N_j is the number of nodes in network j (1 is subtracted to account for the seed node), and $a_i = 1$ iff node i adopted, otherwise $a_i = 0$. Within each trial, both networks in both conditions had the same size and degree distribution. However, across trials some networks had different sizes and degree distributions. This was done to ensure that the results from this study were not an artifact of a specific choice of neighborhood size or network size. To make comparisons across trials possible, success is measured in terms of the *fraction* of the population that adopted, not the absolute number. The success of diffusion for each condition of each trial, and mean and standard deviation of these values across all trials, are shown in Table S1.

We used the Wilcoxon Rank Sum Test (also known as the Mann-Whitney U test) to evaluate the statistical significance of differences in success across the six trials. The Wilcoxon is a non-parametric test of the likelihood that observations drawn from one population will be greater than those drawn from another population. In essence, it tests whether there is a statistical significance in the difference of the medians of two populations. Thus, it is very similar to the two-sample *t*-test, however it provides a more conservative estimate of significance since it does not rely on the assumption of normality in the distribution. The Wilcoxon test shows that the null hypothesis that there

is no difference in the success of diffusion between the two conditions can be accepted

with a probability of $p<0.01$.

	Random Network Condition (Total Fraction Adopted)	Clustered Lattice Network Condition (Total Fraction Adopted)
Trial 1 (N=98, Z=6)	0.3814	0.5154
Trial 2 (N=128, Z=6)	0.2677	0.3937
Trial 3 (N=128, Z=6)	0.2834	0.5275
Trial 4 (N=128, Z=6)	0.3700	0.5590
Trial 5 (N=144, Z=8)	0.5104	0.6363
Trial 6 (N=144, Z=8)	0.4825	0.5944
Mean	0.3826	0.5377
Standard Deviation	0.0995	0.0833

Table S1. Success of Diffusion in Clustered Lattice and Random Networks

To measure the rate of diffusion, we compared the time it took for the diffusion

process to reach the farthest node that was reached by both conditions in a given trial.

For example, in trial 1 diffusion in the random network condition reached 38.14% of the

network (37 nodes), while diffusion in the clustered lattice network condition reached

51.54% of the network (50 nodes). Thus, the rates of diffusion for trial 1 are compared

by evaluating the time it took each network to reach 37 nodes. More generally, the rate

of diffusion in network j in trial T, R_{Tj}, is defined as:

$$R_{T_j} = \frac{\min(S_{T_0}, S_{T_1})}{time_{T_j}[\min(S_{T_0}, S_{T_1})]}, \quad (2)$$

where S_{T_0} and S_{T_1} are the fraction of adopters in conditions 0 (random network) and 1

(clustered lattice network) of trial T, respectively. $time_{T_j}[\min(S_{T_0}, S_{T_1})]$ reports the time it

took in network j of trial T for the behavior to reach the largest fraction of nodes reached

by both networks in trial T. Table S2 shows the distances, times, and rates corresponding

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to each condition in each trial, and the mean and standard deviation of the rates of diffusion across all trials.

An alternative approach to measuring diffusion rates is to pick a specific prevalence (say 50% adoption), and compare all networks at this same prevalence point. However, since many of the random networks did not reach 50%, this comparison would omit some of the data. In order to include all of the data in such a comparison, the prevalence point would have to be below 27% adoption. Yet, since many of the networks (both clustered lattice networks and random networks) spread well past 27%, this measure does not provide a good representation of the overall diffusion processes recorded in these trials.

The approach that we adopted of comparing the network conditions on a trial-by-trial basis ensures that all networks are included in the comparison. Further, this approach also ensures that the greatest possible number of data points are included to give the most accurate picture of the rate at which the behavior spread through each of the networks. Finally, because the network conditions are already paired into trials, comparing the time it takes to reach an equivalent distance within each trial is a natural way to evaluate the rate of diffusion across conditions. Because these rate measurements have commensurate units across trials (i.e., nodes/sec), they can be aggregated to provide a summary statistic, as shown in the last two rows of table S2.

To evaluate the significance of the differences in rates across the six trials we used the same Wilcoxon Rank Sum Test described above. The logic for using this test to compare rates is the same as it was for the evaluating the differences in success: we are trying to determine the likelihood that one condition will consistently produce

observations that are greater than those for the other condition. The Wilcoxon test shows that the null hypothesis that there is no difference in the rates of diffusion between the two conditions can be accepted with a probability of $p<0.01$.

	Max. Nodes Adopted in Both Conditions	Random Network Condition		Clustered Lattice Network Condition	
		Time (seconds)	Rate (x 10^{-3} nodes/sec)	Time (seconds)	Rate (x 10^{-3} nodes/sec)
Trial 1 (N=98, Z=6)	37	1021564	0.0362	634444	0.0583
Trial 2 (N=128, Z=6)	34	1051161	0.0323	157112	0.2164
Trial 3 (N=128, Z=6)	36	1016415	0.0354	294609	0.1221
Trial 4 (N=128, Z=6)	47	386516	0.1215	152509	0.3081
Trial 5 (N=144, Z=8)	73	1803602	0.0404	101640	0.7182
Trial 6 (N=144, Z=8)	69	575523	0.1198	256616	0.2688
Mean	-	-	0.0643	-	0.2820
Standard Deviation	-	-	0.0437	-	0.2328

Table S2. Rates of Diffusion in Clustered Lattice and Random Networks

The effect of social reinforcement on the individual likelihood of adoption was calculated using the Cox proportional hazards model. The Cox model is a semi-parametric test of hazard rates, which does not assume an underlying functional form for the hazard of adoption. The baseline hazard for adoption is based on the individuals who adopted after one signal. This hazard function was then used to evaluate the conditional hazard of adoption for individuals receiving additional signals. This test thus measures the increase in likelihood that an individual will adopt the behavior from receiving multiple social signals, conditioned on the likelihood of adoption from receiving a single social signal.

The results of the Cox Model showed that receiving a second social signal increased the probability of adoption by 1.67 times, with 95% confidence intervals

ranging from 1.35 to 2.05. The null hypothesis – that there was no effect of receiving a second signal on the likelihood of adoption – can be accepted with a probability of $p<0.001$. Receiving a third signal increased the likelihood of adoption by 1.32 times, with 95% confidence intervals ranging from 1.01 to 1.73. The null hypothesis can be accepted with a probability of $p < 0.05$. There was no significant effect of additional social signals on the likelihood of adoption.

Ensuring Data Quality

In all experiments researchers must take steps to ensure that the subjects do not violate the design of the experiment, either through accidental behaviors, or through malicious intent. This can be more difficult in on-line experiments, where researchers have less control over the behavior of the subjects than in traditional laboratory settings. We took several steps to ensure that the data collected were sound.

For example, we designed the health forum website so that it would be an unknown behavior to subjects before they enrolled in the experiment. However, it is possible that subjects could tell people about the health forum outside the context of the experiment. We ensured that individuals could not access the health forum without being enrolled in the experiment by giving each individual a unique log-in identifier, without which an individual could not log-in to the health forum. It is also possible that subjects could encourage peers to sign up for the study in order to get access to the health forum. To control for this possibility, subjects were asked upon registering for the health forum to tell us how they found out about it (from a list of options including: "From a health buddy", "From my doctor", "From a friend", etc.). This allowed us to track subjects who

might have come to the study with preexisting knowledge of the health forum. Given that such knowledge would make subjects more likely to adopt after a single signal, we suspect that the presence of these individuals in the study would only have weakened the effects shown in our findings.

We also intended for social influence among participants in the study to be based entirely on the on-line networks that we created, and not confounded by peer relationships outside the study. In order to prevent people from trying to identify friends who may have also signed up for the study, or from trying to contact health buddies outside the context of the experiment, we blinded the identifiers that people used. Thus, subjects could not see the true usernames used by their health buddies. Because a message from a friend from outside of the study would be more likely to promote adoption with fewer signals, we expect that a more effective means of eliminating these relationships from our study would only increase the effects that are shown in our findings.

An additional concern with an on-line study is that subjects might return to the health forum, or to the initial study sign-up website, and their data might be re-entered into the experiment. To prevent this from happening, once a subject registered for the health forum, her unique identifier in the study was flagged, and her subsequent behavior no longer affected any aspect of the experiment. However, while subjects could no longer affect the experiment, once they joined the health forum, they were permitted to return as many times as they liked, where they were automatically logged in, and any additional recommendations and ratings they made were included in the forum to be shared with the other members.

Subjects could also return to the initial enrollment website, where they had joined

the study. To ensure that no subjects were re-enrolled in the study, we placed cookies

into the web-browsers of the subjects, which automatically populated the sign-up pages

with their user information, and prevented us from collecting this information a second

time (even if the users altered it). Users without cookie-compatible browsers (or who had

cookies disabled) were not able to sign up for the study. A subject with malicious intent

could figure out how to destroy the cookies in her web-browser and then re-enroll in the

study. However, we also double-checked each new user's profile against existing users

(from the entire history of the study), and would not allow a new user to register if her

profile information or email address matched an existing user. Our attempts to detect

patterns in the data that revealed the presence of this kind of malicious behavior did not

find any instances of it.

Robustness to Design Choices

The six trials of this experiment represent a small portion of the parameter space

of possible experiments using this design. For example, parameters like the size of the

networks (N), the neighborhood size (Z), and the kind of behavior being diffused may all

influence the dynamics of social diffusion. The results from these studies suggest some

predictions.

We anticipate that increases in the size of the network (N) will make the observed

differences in diffusion between the random and clustered lattice networks more

pronounced. As the networks become larger (and neighborhood size, Z, is kept constant)

the probability of nodes in a random network receiving redundant signals becomes

smaller, which we expect will make the effect of local structure more important for the diffusion of behaviors. Similarly, these anticipated effects are also relevant for changes to neighborhood size since we suspect that reductions in neighborhood size, Z (for a fixed population N), will equally reduce the probability that nodes in random networks will receive redundant signals. Conversely, we anticipate that decreasing network size (while keeping Z constant) will ultimately eliminate the effects of topology by making the density of the networks so great that differences in topology are insignificant. Equivalently, we expect that increasing the neighborhood size while keeping N fixed will have the same effect of increasing density to the point where topological differences are no longer significant.

More generally, for the scope condition that $N>>Z$ we expect that the results of this experiment represent the lower bound of the effects of topological structure on behavioral diffusion. As neighborhood size becomes a much smaller fraction of the total population (which naturally happens as population size increases to the order of magnitude of large societies), the confounding effects of density are eliminated. As this happens, we expect that the observed differences in the diffusion dynamics between topologically diverse network conditions will become even greater.

We suspect that the results of this experiment will also generalize to other kinds of behavior. Our focus on health behavior necessitated recruitment from a population of individuals who were interested in health. However, this design could easily be replicated for other behaviors (such as adopting a product or financial service) in which the subject pool would be drawn from a population of individuals interested in those behaviors. Further, the behavior studied in this experiment is relatively easy to do

compared with health behaviors such as getting screenings, changing diet, quitting smoking, or improving insurance coverage, and is available free of charge. We expect that the more difficult, or costly, the behavior is, the more dependent the success of diffusion will be on social reinforcement from locally clustered network neighborhoods. Further empirical work in this area is needed.

An important feature of the design of this experiment is that personal information about the subjects was not revealed to their health buddies. This allowed us to isolate the effects of the network topology on the dynamics of diffusion without the presence of confounding variables. But, it also raises the question of what the strength of the effects of network topology would be when allowed to interact with the effects of interpersonal relationships. New experimental designs are required to test the interaction effects of these variables (and other variables, such as gender, affect, and frequency of interaction) on the spread of social behaviors. Such experimental designs will require the ability to carefully integrate each additional variable into the study, while still isolating the effects of each mechanism on the diffusion process. We anticipate many new studies in this growing area of research.