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**Social Networks and Health:
New Developments in
Diffusion, Online and Offline**

Jingwen Zhang¹ and Damon Centola²

¹Department of Communication, University of California, Davis, California 95616, USA

²Annenberg School for Communication, University of Pennsylvania, Philadelphia, Pennsylvania 19104, USA; email: dcentola@asc.upenn.edu

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Abstract

The relationship between social networks and health encompasses everything from the flow of pathogens and information to the diffusion of beliefs and behaviors. This review addresses the vast and multidisciplinary literature that studies social networks as a structural determinant of health. In particular, we report on the current state of knowledge on how social contagion dynamics influence individual and collective health outcomes. We pay specific attention to research that leverages large-scale online data and social network experiments to empirically identify three broad classes of contagion processes: pathogenic diffusion, informational and belief diffusion, and behavioral diffusion. We conclude by identifying the need for more research on (a) how multiple contagions interact within the same social network, (b) how online social networks impact offline health, and (c) the effectiveness of social network interventions for improving population health.

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INTRODUCTION

The variety of ways that social networks can influence health is staggering (Berkman et al. 2000, Cohen 2004, Moren-Cross & Lin 2006, Smith & Christakis 2008, Valente 2010). Because we live in multiple social networks and occupy different social positions in different settings, the relationship between social networks and health encompasses everything from the flow of viruses and information, to the diffusion of emotions, opinions, behaviors, and resources, all of which may spread in different ways and through different parts of our social networks. In short, networks offer an abundance of causal pathways for influencing individual well-being (Berkman et al. 2000, Berkman & Glass 2000).

While this observation has become commonplace, it also means that the underlying dynamics of network formation, such as choice homophily (McPherson et al. 2001), social stratification (House et al. 1992, Parsons 1940), and social exclusion (MacDonald & Leary 2005, Maner et al. 2007), can also have both direct and indirect consequences for individual and collective health (Centola & van de Rijt 2015, de la Haye et al. 2011, Flatt et al. 2012, House et al. 2005, Phelan et al. 2010). As these layers of social influence are considered—that is, the factors that affect both network formation and the ways that networks in turn affect morbidity and mortality—the opportunities for interventions at different levels of social structure become increasingly interesting for researchers working to identify and shape the impact of social networks on population welfare (Centola 2018, Valente 2012).

This review is focused on addressing the vast and multidisciplinary literature that studies social networks as a structural determinant of health, in particular their role in mediating the spread of social contagions that impact health outcomes. The literature on social contagions and health stretches across the fields of sociology, epidemiology, social epidemiology, social psychology, communication, public health, and dozens of other disciplines and subdisciplines, including even computer science and physics. Over the past three decades, summary articles and books on social networks and health have worked to clarify terms, propose unifying models, and synthesize evidence across many disciplines and domains (Berkman et al. 2000, Moren-Cross & Lin 2006, Smith & Christakis 2008, Southwell 2013, Valente 2010). Instead of summarizing the large array of work discussed in previous reviews, we focus on new developments in understanding health diffusion. We structure our review in terms of the primary mechanisms through which social contagions affect health outcomes: namely, pathogenic diffusion, informational and belief diffusion, and behavioral diffusion.

In recent years, the rapidly expanding fields of data science and computational social science have offered many new insights into these topics. Here, we pay particular attention to research that leverages large-scale online data and social network experiments to empirically identify the causal effects of social networks on health. We conclude this review by suggesting promising new directions for future research and by discussing the implications of this work for the growing field of network-based interventions for health.

SOCIAL NETWORKS: A STRUCTURAL LOGIC

Any introduction to social networks and health must begin, if only briefly, with Durkheim's study of suicide. Coarsely summarized, Durkheim argues that individual health behavior (in particular, suicide) can be directly caused by the structure of social integration in a society (Durkheim 1897). Durkheim's notion of social integration encompasses multiple dimensions of relationships, ranging from immediate families, to friends and neighbors, to organizations and communities (Bille-Brahe 1996, Pope 1975). Although Durkheim never conceptualized social integration from a networks perspective—and although he vehemently argued against the explanatory importance

of social contagion in his treatise on suicide—his conception of integration in terms of attachment and regulation inspired later scholars to recast and unify his ideas in the framework of network theory.

Modern network theory started with a major methodological innovation by Moreno (1937a), who developed sociograms to graphically represent individuals as nodes and the relationships between them as ties (Moreno 1937b)—a convention that is still predominantly used today. Building on this formal representation of networks, in the 1950s, the field of social network analysis expanded to include new mathematical methods developed by sociologists and anthropologists who were interested in understanding how the density and connectivity of large social networks might impact social stratification, the provision of welfare, and health outcomes (Barnes 1954, Bott 1957, Menzel & Katz 1955, Stewart 1958, Suttles 1960).

These network theories suggested new structural explanations for disparities in health. For instance, since the 1980s, a prominent line of medical sociology research has started to retheorize Durkheim's integration-suicide link in terms of network connections. Pescosolido & Georgianna (1989) argue that religious affiliations can have either protective or aggravating effects on suicide, depending on the density of religious networks. Using the Add Health data set, Bearman & Moody (2004) found evidence that being part of a school with a higher relative density of friendship ties strongly reduced adolescents' attempts at suicide, suggesting a direct relationship between the network structure of social integration and individuals' subjective wellbeing.

As these structural approaches to health have matured, they have increasingly brought new network theoretic properties of relationships to researchers' attention, illuminating how quantifiable features of social structure may shape individuals' ideas, beliefs, and behaviors. In the past two decades, many excellent reviews of this work have explored the social and psychological mechanisms underlying peer effects in interpersonal networks. To avoid redundancy with the foundational work already done here, the following discussion of social and psychological mechanisms briefly reviews three primary ways that peer effects operate in social networks—social support, social capital, and social influence—and the recent studies that have sought to address these topics. Detailed discussions of related theories and empirical findings can be found in several well-known review articles (Berkman et al. 2000, Kawachi & Berkman 2000, Luke & Harris 2007, Luke & Stamatakis 2012, Pampel et al. 2010, Smith & Christakis 2008). After briefly discussing this literature in the paragraphs below, the rest of this review focuses on addressing recent work that has sought out new directions in health research using computational studies of large-scale networks to identify the spreading dynamics of health-related contagions.

Over the past several decades, research in psychology, social psychology, and social epidemiology has produced an impressive number of theoretical and empirical studies addressing peer effects through a variety of social and psychological mechanisms. To understand why and how individuals' health is directly or indirectly influenced by their social contacts, the emphasis in this literature has been on identifying the specific kind of content (e.g., social support, material resources, social pressure) that flows across social ties, and the implications it has for how social networks mediate broader structural influences. Berkman et al. (2000) proposed a conceptual model of how social networks impact health through providing support and influence. Smith & Christakis (2008) reviewed the debate over whether patterns of social clustering on health outcomes were better explained by homophilous social selection or direct interpersonal influence. In addition, several other review articles have systematically surveyed these social psychological factors (Kawachi & Berkman 2000, Luke & Harris 2007, Luke & Stamatakis 2012, Pampel et al. 2010). In brief, three mechanisms have attracted the bulk of research attention: social support, social resources (referred to here as social capital), and social influence. While each of these has been discussed distinctly in various contexts, the boundaries between them are far from clear-cut.

Here, we refer to social support as the actual and perceived positive emotional engagement with friends, family, and acquaintances (Faber & Wasserman 2002). Much of the work on social networks and social support concludes that greater support networks are generally associated with greater health and reduced mortality (Berkman & Glass 2000, Thoits 2011). More recent research also examined network activation, looking into how people actively selected different supporters in their networks to cope with mental illnesses (Perry & Pescosolido 2015).

Social capital has many meanings. In this context, we restrict our attention to research that identifies how individuals' membership in social networks facilitates access to vital resources (Lin 1999, Kawachi et al. 2008). Access to social capital (such as childcare) can be measured at the group, neighborhood, and community levels and has been shown to be strongly associated with better subjective wellbeing and lower rates of mortality. Recent studies focused on studying social capital in more specific and underrepresented networks. For instance, Kelly et al. (2014) found greater connectivity with other gay men was positively associated with perceived community cohesion among urban gay men, whereas living in a gay neighborhood was not. Hurlbert et al. (2017) found network social capital mediated the effect of neighborhood disadvantage on depressive symptoms, even after adjusting for perceived neighborhood disorder.

Finally, the effects of interpersonal influence have been measured by showing a correlation between the health outcomes of a person and the health outcomes of his or her network contacts. There are many potential ways for social influences to affect health, including social learning, adopting social norms, peer imitation, and social pressure, among others. In studies of social influence on suicide, using the longitudinal Add Health network data set, both Bearman & Moody (2004) and Abrutyn & Mueller (2014) found that individuals with friends who attempted suicide had increased likelihoods of suicidal ideation and suicide attempts. Studying the effects of peer influence on smoking, Haas and Schaefer (2014) found that peer influence was stronger for the initiation of smoking than for smoking cessation. Consequently, peer influence is considered an important factor for understanding the spread of both positive and negative health behaviors.

As the literature on social networks has expanded to address the population-level implications of social influences on health, one perennial challenge has been the difficulty of identifying causal mechanisms that operate between the micro and macro scales. Only a decade ago, the limited number of large-scale network data sets and the complete absence of large-scale network experiments made it difficult to identify the precise pathways through which social contagions might generate observed correlations among health outcomes in social networks. Many scholars, including Luke & Harris (2007), Luke & Stamatakis (2012), and Pampel et al. (2010), brought attention to these shortcomings and called for intensified scientific efforts to develop methods that could identify the processes by which social networks control the spread of social contagions affecting health outcomes.

The rest of this review reports on the broad array of new work on social networks and health that has answered this call. This review addresses the vanguard of theoretical, experimental, and observational studies that have worked to identify the social contagion processes underlying individual and collective health. In particular, our emphasis is on the diffusion mechanisms through which social networks influence population health outcomes: namely, pathogenic diffusion, informational and belief diffusion, and behavioral diffusion.

Contagion of Pathogens

One of the most direct ways for social networks to influence health is by restricting or promoting exposures to infectious diseases. For epidemiologists working on understanding the diffusion of pathogens, the underlying physical contact network is crucial for tracing how infections reach across diverse parts of a population (Bansal et al. 2010, Klodahl et al. 1994, Mossong et al. 2008).

Early work applying mathematical modeling of networks in epidemiology of sexually transmitted infections (STIs) made significant contributions in this domain. In particular, the presence of a small number of individuals who have a large number of partners and racial segregation of sexual contact linkages have been shown to accelerate the transmission of HIV, syphilis, and gonorrhea (Adimora & Schoenbach 2005). Laumann & Youm's (1999) simulation work revealed two network explanations for the disproportionately high rates of STIs in African Americans. First was that the structure of the population had a core-periphery sexual contact network, in which a small number of individuals acted as hubs in the network. Once these individuals contracted a disease, they would then spread it to many others. At the same time, these networks were found to be highly homophilous on race, also called assortative mating, which meant that African Americans within the population predominantly interacted with other African Americans. Taken together, these two factors meant that most African Americans in the community interacted with the same small number of highly connected actors. Once an infection entered the network, it quickly reached the hubs, and from there it reached everyone else.

A different network characteristic that can increase the diffusion rates of STIs is what Bearman et al. (2004) call spanning trees. Unlike a network with a few highly central hubs, these are networks in which people who have sexual contact with each other do not share any partners in common. In this kind of network, if Joe has six sexual contacts, then we can assume that each of those six contacts will each have six unique additional sexual contacts of their own, and, in turn, each of those contacts will also have six unique additional sexual contacts, and so on. In this kind of network, the number of people who can become infected from a single person, Joe, increases exponentially with each additional step. Only a few steps from Joe, hundreds of people become infected. And from there, it quickly grows to hundreds of thousands. Further studies, both theoretical and empirical, have also shown that these spreading dynamics of STIs are accelerated in networks in which individuals have concurrent sexual partnerships (Morris & Kretzschmar 1995, Morris et al. 2009, Rosenberg et al. 2012).

Beyond sexual contact, there are many other ways that pathogens can spread through social networks, some of them quite devious (Donker et al. 2010, Gardy et al. 2011, Meyers et al. 2005). For instance, even though the pathogen that causes dengue fever spreads via carrier mosquitos, the virus can nevertheless spread between people indirectly as a result of village-to-village movements of infected individuals. If an infected person visits a healthy village and is bitten by a local mosquito, then that mosquito can become a carrier for the virus. When that mosquito then subsequently bites healthy villagers, it can infect them with dengue. Subsequently, any mosquitos that bite those individuals will also become carriers for the virus. Those mosquitos can, in turn, spread the dengue virus by biting more people. Ultimately, this indirect social network of human-mosquito-human contact, stemming from a single infected visitor, can lead to an outbreak of dengue fever in the once-healthy village (Stoddard et al. 2013).

Recent data science approaches to understanding disease outbreaks have made progress in disease prevention by using large-scale network data sets to model the spreading dynamics of epidemics. Colizza et al. (2006) used data on global airline transportation networks in conjunction with the United States Census population data to develop a powerful mathematical model that was able to accurately forecast the emergence of an influenza outbreak. Developing a novel approach to studying flu outbreaks using wireless sensor technology, Salathé et al. (2010) were able to obtain high-resolution data of close contact interactions during a typical day at an American high school. Their analyses revealed a high-density network with small-world properties, showing a relatively homogeneous distribution of both interaction time and interaction partners among participants. Simulating the spread of the influenza virus on their reconstructed network, they were able to accurately account for the absentee data during the previous flu season.

Adopting a similar approach, Hornbeck et al. (2012) used sensor network technology to record contacts among health care workers and patients in an intensive care unit. Reconstructing the social networks, the researchers identified a small number of highly mobile, highly connected health care workers who had a disproportionately high level of contact with a large number of patients. These health care workers acted as hubs in the disease-transmission network. Even though the patients did not have direct contact with one another, if these highly connected health care workers did not properly sanitize themselves between each visit, they would act as vectors for the spread of hospital-generated (nosocomial) illnesses to a large number of patients.

One feature shared in common throughout all of these studies of social networks and the spread of pathogens is the formalization of disease as a simple contagion (Centola 2013, 2018; Centola & Macy 2007)—that is, a contagion that can be transmitted from a single contact between an infected individual and a susceptible one. While not every contact leads to transmission, every contact has a positive probability of transmission, and extended exposure to a single infected individual increases the probability of transmission. By contrast, most preventative health behaviors, particularly ones that are costly, difficult, or unfamiliar, are complex contagions—that is, they require social reinforcement from multiple sources before people will be willing to adopt them. One of the most notable consequences of complex contagions is the implication they have for diffusion through social networks. Although simple contagions spread rapidly through long-distance links across a social network—such as weak ties—complex contagions do not spread effectively. Even more striking, although highly connected actors, or hubs in a social network, can accelerate the spread of simple contagions, they can slow down the spread of complex contagions. More generally, most of the network properties that improve the spread of simple contagions wind up inhibiting the spread of complex contagions. In the section titled *New Directions* we show how these implications of complex contagions have given rise to exciting new approaches to studying health behavior and designing network-based health interventions. But, first, it is important to note that although diseases are typically simple contagions, there are also some interesting exceptions in which diseases spread as complex contagions.

Complex coinfections occur when patients contract simultaneous infections from multiple pathogens. This happens when infection with one pathogen increases a patient's susceptibility to other kinds of infections. For instance, infection with HIV increases susceptibility to many pathogens, especially syphilis and tuberculosis (Corbett et al. 2003). Similarly, upper respiratory infections such as tuberculosis increase the risk of infection with *Streptococcus pneumoniae*, a bacterium that causes pneumonia (Bogaert et al. 2004). While a single virus can efficiently use weak ties to spread across a network, coinfections from several viruses are typically adopted from different sources and thus cannot be easily transmitted the same way. Using simulation models, Hebert-Dufresne & Althouse (2015) showed that clustered social networks, which usually hinder the spread of pathogens, can speed up the spread of synergistic coinfections because they provide reinforcing contacts with multiple sources of coinfection.¹

¹This work is related to emerging research on syndemics in health (Singer et al. 2017), which emphasizes the interactions of two or more diseases or other health conditions on the dynamics of morbidity in a population. Earlier research identified several frequent co-occurrences of negative health conditions, such as drug use, intimate partner violence, childhood sexual abuse, depression, and AIDS on the individual level (Meyer et al. 2011, Parsons et al. 2012), and a few studies suggest the disruption of support social networks can contribute to syndemics (Singer et al. 2017). However, the question of what specific role contact networks play in shaping and influencing syndemic conditions is largely unstudied.

Contagion of Information and Beliefs

Information diffusion is one of the most established strategies for the promotion of preventive health behaviors—from hand washing to HIV prophylaxis. Regardless of whether health information is actively sought from others or is passively received from the media, public health officials strategically design health messages with the goal of helping people to navigate medical resources, manage health conditions, and form accurate beliefs about their health risks (Hornik et al. 2013, Rutten et al. 2006, Shim et al. 2006, Weaver et al. 2010). Despite significant governmental and organizational interest in spreading health information to every member of a society, there is a significant social stratification in the quantity and quality of the health information to which people are exposed (Southwell 2013). This knowledge gap in health information is in part a result of social networks.

The original work on the knowledge gap hypothesis found that people who already hold knowledge about a particular topic will be more likely to gather new information over time from various interpersonal and mediated sources (Viswanath & Finnegan 1996). This leads to compounding inequalities, as people who initially have more access to health information continue to gain additional access, while people who are initially deprived have increasingly less access to it (Langlie 1977). As expected, members of higher socioeconomic status groups are more likely to have extensive contact networks, which provide them with access to health information through personal ties, organizational memberships, and professional resources (Horvat et al. 2003).

One of the most important features of the spread of health information is that the way that information is received—that is, whether or not it is believed and propagated—is heavily influenced by the recipients' perceptions of its relevance and credibility (Eastin 2001, Pornpitakpan 2004). Information does not diffuse independently from opinions, which means that attitudes toward health information play a large part in how information spreads. Despite significant practical and scientific interest in the question of how health-related information diffuses through social networks, it was not until the recent availability of digital social network data that it was possible to identify the dynamics of this social spreading process. As a result of the meteoric rise of social media activity, a large number of studies have now examined how health information spreads in online social networks. The findings have identified both simple and complex contagion processes at work, depending on the kind of information and the topics that the study addresses (Lerman & Ghosh 2010, Leskovec et al. 2007, Weng et al. 2013).

Salathé et al. (2013) investigated the spread of health information about the influenza A (H1N1) vaccine on Twitter, following 318,379 tweets from their posters' Twitter networks. The researchers found that vaccination information was significantly more likely to spread between people with shared sentiments. Moreover, they found significant homophily among people who had similar sentiments toward vaccination. This study could not identify whether this homophily was induced through social influences among connected people or whether it was due to selection among people who already shared similar beliefs about vaccination. Regardless of how this pattern of association came to be, the researchers found that it had consequences both for the spread of health information and for the health behaviors that people exhibited. In the communities with positive sentiment, people were generally more likely to share information about vaccination, and vaccination rates were higher. In the communities with negative sentiments, vaccination information was less likely to spread, and overall vaccination rates were lower.

Another study by Surian et al. (2016) analyzed 285,417 tweets about human papillomavirus (HPV) vaccines from 101,519 users with more than 4 million social connections between them. They examined the alignment between local network community structures among the follower network of the Twitter users and the topics about which they posted. Combining community detection and topic modeling algorithms, they found that discussion topics in the different communities

focused on (a) vaccine harms/conspiracies, (b) medical evidence/advocacy, and (c) individual experiences. Members of communities *b* and *c* exhibited significant self-selection in their exposure to current health information, and members of community *a* were primarily exposed to tweets on the harms of HPV vaccines, which included links to specific antivaccine websites. These findings provide important observations suggesting people who share similar attitudes are selective in both their social connections and their informational exposures, both of which reinforce reduced contact with up-to-date health information.

Beyond exposure to health information, several studies have also explored the potential consequences of network disparities in informational access. Two studies (Campbell & Salathé 2013, Salathé & Bonhoeffer 2008) of the spread of antivaccination beliefs showed that these beliefs could spread through a social network, converting people to the so-called antivaxer position. The antivaxer movement was found to be a complex contagion, which could not spread in a weak tie network with many hubs but could spread very effectively in a clustered social network composed of overlapping residential neighborhoods. As the antivaxer movement spread, it effectively changed people's interest in health information, inoculating them from discovering new information about vaccine safety. As a result, the clustered, residential networks became widely populated with unvaccinated individuals, and therefore highly susceptible to triggering population-wide disease epidemics.

Similarly, Dunn et al.'s (2017) study showed that measures of information exposure from Twitter explained differences in actual vaccine coverage in states where vaccination rates could not be fully explained by socioeconomic factors. Vaccine coverage was lower in states where a higher proportion of tweets contained misinformation about vaccine safety and conspiracy theories about vaccination. These findings suggest that negative representations of vaccines on social media offer a useful indicator for offline access to health information and real world vaccination rates. For preventive health efforts, this work highlights the potential to use evidence from online information flow as a strategy for identifying relevant communities for targeted vaccination efforts. The results also suggest that belief change in these instances is likely a complex contagion, requiring social reinforcement for a change in sentiment, rather than a simple contagion requiring only exposure to new information.

Another important feature of social networks that affects the spread of both information and beliefs is the fact that individuals typically sample opinions locally, from their immediate peer group in the network, to infer what is believed globally in the population as a whole. Even individuals without strong reasons for having biased beliefs may nevertheless have a skewed view of available information because of the structure of their social networks.

One well-known network-based source of informational bias is the majority illusion. In social networks in which highly connected hubs have several times more contacts than most other people, the hubs' particular beliefs and informational biases will be well represented in a large number of people's social networks (Becker et al. 2017). The majority illusion suggests that under some conditions, individuals will overestimate popular agreement on incorrect beliefs (e.g., the safety of e-cigarettes) because of its prevalence among their immediate social contacts. Because high-degree nodes offer the same misinformation to many different people, they can create a skewed perception of the widespread belief in the information (Lerman et al. 2016).

Concerns about the majority illusion, and the accuracy of people's health-related beliefs, are directly connected to the process of network formation. As people make ties in a social network, people with extroverted personalities are naturally more active in the creation of social links (Wehrli 2008). More generally, the rich-get-richer model of social network formation has shown that once highly connected individuals emerge in a social network, the social dynamics tend to favor these individuals gathering still more connections (Barabási & Albert 1999). This network

formation dynamic can result in increasing inequality in network ties, which translates into further potential for misrepresentation and misinformation in the social network. For instance, recent work identifying a correlation between high network connectivity and excessive alcohol consumption suggests that network hubs may falsely inflate the normativity of excessive drinking behavior (Fairbairn et al. 2015). Closely related to these findings is work on the wisdom of crowds, which finds that highly centralized networks (with highly connected hubs) are more likely to lead to the spread of inaccurate information in the group, while decentralized networks, without any highly connected individuals, are more likely to lead to the spread of accurate information in the group (Becker et al. 2017, Guilbeault et al. 2018).

Contagion of Behaviors

Decades of research on health psychology have shown that health behavior changes are dependent upon individuals' perceptions of their risks, others' approval or disapproval of the behavior, how widely adopted the behavior is, and whether they believe the behavior is credible (Bicchieri 2017, Fishbein & Ajzen 2010). All of these factors are shaped by people's social networks.

The complexity of health-related behavioral contagions has been identified in numerous observational studies. For instance, examining contraception use among Cameroonian women, Valente et al. (1997) found that women who received reinforcing messages from many of their friends and relatives were much more likely to believe that contraception was acceptable and safe to use. Another study, examining the spread of smoking cessation in the Framingham Heart Study, showed that the likelihood of individuals quitting smoking increased significantly with exposure to multiple contacts who also attempted to quit, in part because smoking is often explicitly social and people are subject to normative pressure from others to quit (Christakis & Fowler 2008).

A related factor adding to the complexity of behavioral contagions is that health innovations (such as HIV prophylaxis) can run counter to entrenched social norms and cultural expectations. Two recent pre-exposure prophylaxis (PrEP) trials with women in sub-Saharan Africa (van der Straten et al. 2014a,b) were shown ineffective in preventing HIV, because very few participants adhered to taking the medication. One important barrier for these women was the social stigma: If they took the medication, people in their community would think they had HIV and discriminate against them. This stigma created resistance and impeded social communication about PrEP. Consequently, no one adopted the innovation because it was impossible for people to learn that others were taking it. This prevented the formation of reinforcing networks that might help to make the medication more acceptable in their community.

A similar kind of resistance to change can also emerge when there are competing social influences pulling people toward opposite behavior choices. In one study, Kuhlman et al. (2011) simulated the complex contagion dynamics of smoking under conditions where smokers could revert to smoking after quitting. Findings showed the presence of both pro- and antismoking norms increased individuals' dependence on reinforcement from peers. Individuals required increased contact with additional quitters in their social networks to successfully diffuse the quitting behavior. In another network simulation study, Zhang et al. (2015b) tested three strategies for diffusing physical activity behaviors among children. The results showed that targeting the groups of most sedentary children generated the biggest improvement in activity of all children, suggesting that reinforcing behavior changes within the social clusters composed of the most inactive children could spread outward, pulling the whole student population toward healthier behavior norms.

These theoretical findings found support in Centola's (2010) study of the spread of health behaviors through online social networks, in which he found that social networks that provided reinforcing social contact with multiple adopters significantly increased the speed at which the

behavioral contagions spread through the population. Centola (2011) showed that in addition to social reinforcement, homophily among network neighbors can also be a significant factor in the spread of behavioral contagions. Using an experimentally designed fitness community, this study showed that increasing the demographic similarity of online contacts directly increased the adoption of an online dieting tool among both healthy and obese members of the community.

Complementing these experimental findings, Aral & Nicolaides (2017) used large-scale behavior trace data to identify the role of normativity in daily exercise behaviors. They found the number of unconnected network components that exhibited exercising strongly predicted greater positive social contagion effects, suggesting that observing many different people adopting the same behavior can create a strong normative perception that everyone is doing it. However, supporting research shows that structural diversity will only be useful for establishing the normativity of a behavior when diverse signals come from relevant peers. This is because when it comes to decisions about health behavior, only relevant peers' choices are informative for helping individuals to judge the behavior's credibility, feasibility, and social desirability (Christensen et al. 2004, Cialdini 2007, Paluck et al. 2016, Paluck & Shepherd 2012). For instance, using data from the Chinese Longitudinal Healthy Longevity Survey, Li & Zhang (2015) found that although a diverse network was related to better subjective well-being, friendship networks of similar peers were more influential than extensive family networks in promoting physical health behaviors. Similarly, Huang et al. (2014) found that reinforcing signals from a diverse set of age-homophilous online peers were influential for the adoption of risky behaviors, indicating that reinforcing signals from relevant peers can be more influential than a diverse set of signals from siblings, teachers, and parents.

In light of these observational and experimental findings, it is useful to consider the social selection processes through which health networks form. Using a controlled study within an online health community, Centola & van de Rijt (2015) showed that people exhibited strong preference for connecting with peers who were homophilous on a small number of traits: age, gender, and body mass index (BMI). Centola (2018) shows that in other health contexts, choice homophily is likely to be governed by selection on other factors. For instance, in the online health community PatientsLikeMe (<https://www.patientslikeme.com>), which is dedicated to patients with rare diseases, social selection is based primarily on patients having similar ailments and symptoms, irrespective of age, gender, or BMI.

NEW DIRECTIONS

Recent advances point to three main directions for future research. The first concerns the study of how multiple contagions interact within the same social network and what their potential synergistic effects on health are. The second concerns the rise of online health networks and connections between online interactions and offline health. The third area concerns developing social network interventions for spreading health-related behavior change.

Multiple Contagions: Competition and Synergy

Theoretical research on contagions has recently begun to explore the complexities that arise when multiple contagions interact in the same network. These interaction dynamics can take several forms. In some cases, multiple contagions of the same kind may compete against each other, such as a competition in the diffusion of accurate health information versus misinformation. For instance, using an evolutionary game theoretic framework, Su et al. (2016) showed that informational contagions spreading through social networks can interact with each other much like organisms in a

population competing for survival. Strategic cooperation and competition could arise simultaneously, making the successful spread of particular informational messages a predictable feature of the number of competing messages in the same social network.

In other cases, multiple kinds of contagions interact with each other within a social network, such as the spread of a virus competing with the spread of vaccination behavior. In still other cases, multiple kinds of contagions are not competitive but rather are symbiotic, as the spread of one reinforces the spread of another. Taking a new approach to this phenomenon, Campbell & Salathé (2013) proposed a hybrid model in which the spread of complex contagions, such as antivaccination norms, can directly impact the subsequent spread of simple contagions, such as the viruses. They showed that the spread of antivaccination norms can unexpectedly transform networks that would otherwise be inoculated from epidemic outbreaks into communities that are highly susceptible to the spread of pathogenic contagions, such as the measles. The successful spread of antivaccination norms through local communities can create highly susceptible clusters in a network, which may not only be highly vulnerable to infection themselves but may also be large enough to eliminate herd immunity for the population as a whole—thereby rendering vaccination efforts less effective for the entire population. In a similar spirit, several scholars argued that the spread of misinformation contagions through social media could lead to outbreaks of diseases such as Ebola (Allgaier & Svalastog 2015) as well as the adoption of unhealthy behaviors such as vaping (Allem et al. 2017).

Zhang & Li (2017) proposed a different kind of hybrid model that showed how simple contagions could be used to spread complex contagions. This work found that if simple contagions, such as persuasive health messages, are used to target individuals' resistance to behavior change, then health messages can be used in concert with behavioral diffusion campaigns to facilitate the spread of health-promoting behavior change. These findings suggest that the spread of promotional messages through a social network can amplify the impact of peer-to-peer social influence.

Expanding on these ideas, a recent field experiment by Kim et al. (2015) identified how two different health behaviors—taking multivitamins and chlorinating water—spread as both simple and complex contagions through rural Honduran villages. They observed that while the spread of the relatively simple behavior, taking multivitamins, benefited from highly connected individuals with many weak ties, the more complex behavior of chlorinating water did not. Intuitively, this suggests that because of their differences in complexity, effectively spreading these two kinds of behaviors will require targeting two different kinds of social network structures (Centola 2018). However, a new direction in health promotion research has found that initiatives that target multiple behavioral changes (e.g., promoting physical activity and healthy eating together) can be a more effective approach than single-behavior interventions (Prochaska 2008, Wilson et al. 2015). It seems counterintuitive that a greater number of behavior changes would spread more effectively than a smaller number, but if each behavior change reinforces the other, then interventions that simultaneously spread these reinforcing behaviors may achieve greater uptake and maintenance than interventions that try to spread either one alone. This notion of synergistic complex contagions is a promising direction for future research on the conditions under which health contagions can work together to facilitate population-wide behavior change.

Online Networks, Offline Behaviors

The growing prevalence of online communities for people to interact and influence each other's health behaviors is an increasingly important domain for studying online social networks and their effects on health. Online health networks can be designed to fulfill a variety of functions that offline health networks cannot. For instance, online networks have the capacity to transcend

geographic boundaries, maintain different levels of anonymity (DeAndrea 2015), and at the same time, allow participants to connect with others who share similar characteristics and experiences (Naslund et al. 2016, Chung 2014, Tanis 2008). While Putnam (2000) argued that social life online lacks the stability and continuity to provide valuable forms of social capital, recent studies have expanded classic notions of social capital by examining the effects of online interaction networks on participants' giving and receiving of social support (Meng et al. 2016, Pan et al. 2017). For instance, Meng et al. (2016) found that the frequency of long-distance bridging ties in an online network predicted the amount of informational support that people received, whereas network closure (i.e., the frequency of clustered ties in which friends are connected to mutual friends) predicted the amount of emotional support and esteem building that people received. This suggests that classical theoretical approaches to understanding the relationships between social network characteristics and different types of social support may also be useful online.

Moreover, a growing number of innovative studies have begun to identify the link between online interactions and offline health. These studies are typically framed by an interest in determining whether and how online network interactions can generate observable offline behavior changes. For instance, Huang et al. (2014) analyzed 1,563 adolescents' online and offline network peers and found online friends' health risk behaviors were significantly correlated with adolescents' increased offline risk behaviors.

A methodological breakthrough in linking online interactions to offline behaviors comes with the use of mobile and wearable technologies to objectively track behaviors. For instance, Althoff et al. (2017) analyzed 791 million online and offline actions of 6 million users over the course of five years using data provided by a physical activity tracking application (app). The findings showed that the creation of new social connections increased user offline physical activity by 7% (about 400 steps per day). Importantly, the study found that homophilous social connections concerning gender and BMI further increased offline activities, which indicates homophilous online networks can improve real-world health outcomes. Taking a field experiment approach to this issue, two studies by Zhang et al. (2015a, 2016) demonstrated the causal impact of online interactions among strangers—embedded in homophilous, clustered social networks—on improving offline physical activity. Zhang et al. (2016) compared the effects of different online communities in which anonymous peers interacted in either a supportive online community or a competitive community. While the competitive community significantly increased offline physical activity levels, the supportive community actively suppressed physical activity—leading to less gym attendance than even the control group, who had no social network at all.

One important question that remains underexplored is whether, when people's offline social networks offer strong opposition to healthy behavior changes, online health connections can effectively overcome these offline influences. For stigmatized behaviors or contentious health choices such as HIV prophylaxis, contraception, and vaccination, people's local communities may impose strong normative regulations. A new direction for studies in this area is to explore the potential of online networks to interrupt these offline influences. One direction of particular importance for sexual and reproductive health is for researchers to design social networks for the members of at-risk groups to discuss stigmatized topics, such as HPV vaccination (Lyson et al. 2018) and contraception (Fox et al. 2017), in a safe setting without fear of stigmatization or reputation effects. Expanding on classical network concepts, online relationships offer the possibility of providing strong social reinforcement for behavior change while maintaining participants' anonymity—a property historically associated exclusively with weak ties (Centola 2018). Anonymity can be a valuable ally in these situations for providing social networks in which people at risk can discuss their concerns and receive helpful guidance. For some health issues, online networks may even offer a new kind of social environment for exploring and sustaining wellness.

Social Network Interventions

Translating network theories into effective social network interventions has been a slow process. A variety of approaches have been tested, including uses of opinion leaders, segmentation of communities, induction of new network connections and activities, and alteration of network structures (Valente 2012). Recent studies on network targeting have used the friendship paradox to recruit the friends of randomly chosen seed people, who on average will be of higher degree than the seeds. Kim et al. (2015) suggested this approach could be effective for disseminating simple health behaviors, while Chami et al. (2017) found that removing highly connected individuals from a network was an efficient way to fragment a network, thus inhibiting disease spread. Centola (2018) used a simulation approach to identify effective strategies for seeding behavioral interventions into the Add Health and Framingham Heart Study social networks. The study compared two types of intervention strategies, (*a*) increasing exposure for the intervention by randomly selecting seeds throughout the population and (*b*) clustering the seeds closely together to create small pockets of behavior change, to examine conditions in which the health behavior faced strong opposition from established social norms. The findings showed that the clustered seeding strategy produced successful diffusion of the health intervention, while the random seeding strategy failed because highly dispersed seeds were surrounded by strong countervailing influences from their neighbors.

These studies of offline behavioral interventions have recently been supplemented by social network interventions that use online networks to promote health. Online networks can be particularly useful for addressing behavior change topics that are taboo or embarrassing, such as potential HIV diagnoses, contraception, learning about STIs, and even smoking cessation. While these topics are difficult to address in face-to-face networks or within a person's network of strong ties and family associations, the anonymity offered by online networks has been found to be a valuable ally for designing health interventions. For these kinds of topics, online networks are increasingly being used to provide people with access to anonymous networks of peers who can offer access to new information and social reinforcement for behavior change (Centola 2013, Cobb et al. 2016, Fox et al. 2017, Lyson et al. 2018). For instance, Fox et al. (2017) constructed online discussion networks for women to discuss contraception including intrauterine devices (IUDs). In contrast to a control network with all non-IUD users, in structured networks with IUD users and non-IUD users, social influences from IUD users significantly increased the non-IUD users' understanding of all aspects of IUDs, which in turn increased their beliefs in the acceptability of IUDs.

Although a considerable number of online network-based health interventions have been published in the past decade, an important consideration for online interventions comes from recent meta-analyses indicating that they do not show consistent effects in improving health (Laranjo et al. 2014, Maher et al. 2014). One reason is that many of the interventions used social networking sites without giving proper attention to the theoretical properties of the social networks and their implications for behavioral influence. A common assumption is that providing people with an online platform to interact is sufficient to elicit social support or social influence. However, this approach understates the complexity of social influences and the ways in which the structure of a setting may determine how people engage in and benefit from online interactions. Notably, the online network interventions that have proven most successful have typically leveraged homophilous relationships and clustered social networks for inducing positive social influence (Graham et al. 2017, Patel et al. 2017, Young et al. 2014). For instance, examining the diffusion of a smoking cessation application through Facebook, Cobb et al.'s (2016) online experiment showed that when the app allowed participants to invite their friends, increasing participants' exposure to a greater diversity of shared content, the intervention reached the greatest diffusion rate (see also

Gremaud et al. 2018). These findings suggest that actively recruiting online peers to provide reinforcing support for an intervention can be an effective means for diffusing health-related behavior change.

METHODOLOGICAL CONCLUSION

The exciting growth of computational research on social networks and health over the past decade has given renewed life to understanding the causal processes through which social influences transform population health. The interdisciplinary work reviewed in this article highlights a particularly strong synergy between (a) large-scale observational data, (b) theoretical modeling, and (c) web-based experiments. New observational evidence has shown how previously unobserved network characteristics, such as structural diversity and the majority illusion, are linked to a variety of health determinants, morbidity, and mortality. Theoretical examinations that combine computational modeling with observational data have made great strides in understanding the causal mechanisms, such as the diffusion of simple and complex contagions, through which social networks affect health. Finally, web-based experiments have proven to be a powerful new strategy for testing these theoretical mechanisms and identifying the impact of network-based intervention strategies on health behaviors.

As social networks become increasingly diversified in the expanding ecology of social media applications, individuals' health and well-being will be shaped by a multitude of social forces, each of which can mediate different kinds of health contagion processes. In concert with these changes, intervention efforts can harness the growing prevalence of online communities in which patients exchange new health information and influence each other's health behaviors. These settings are an increasingly important domain for observational and experimental work on how social networks influence health outcomes. Altogether, these remarkable new synergies between observational, experimental, and theoretical network science point to an exciting next few years of research. The result will hopefully be a further integration of researchers working across sociology, communication, medicine, public health, and computer and information sciences to improve our collective understanding of the complex dynamics through which social contagions impact health.

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