



Regional contagion in health behaviors: evidence from COVID-19 vaccination modeling in England with social network theorem

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Abstract

Social contagion is a key mechanism that shapes health behaviors, but few studies have applied this approach at the regional level to examine how vaccination beliefs and rates vary and diffuse across geographic areas. Building upon the traditional SIR model, this paper addresses this gap by applying social network theory to a new compartmental model to simulate regional contagion in COVID-19 vaccination rates in England, using panel data of new and accumulated vaccination numbers from December 2020 to June 2022. This Social Network Vaccination Rate (SNVR) model estimates each region's initial and changing vaccination beliefs and their mutual influence on each other. The results reveal that remote regions had higher initial vaccination beliefs and stronger spillover effects on other regions such as London with more population diversity. The paper suggests that policies to increase vaccination rates should consider the heterogeneity and peer effects among regions that collectively affect vaccination beliefs. The paper also discusses the limitations of the network model and directions for future research.

Keywords COVID-19 · Vaccination · Social network · Forecast · Compartmental model · Social Network Vaccination Rate (SNVR) model

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Introduction

The SARS-CoV-2 (COVID-19) outbreak, which first appeared in Wuhan, China, at the end of 2019, has brought continuing transformation in people's lives and behaviors. The severe contagion of COVID-19 has led to significant morbidity and mortality, including long COVID-19 symptoms and 6.6 million cumulative deaths globally [41, 59]. The present evidence from experimental and real-world trials have demonstrated the effectiveness and safety of multiple COVID-19 vaccines against symptomatic infection, hospitalization, death, and the odds of developing long COVID-19 [4, 34, 43]. Following the emergency approval of multiple COVID-19 vaccines globally, countries have launched vaccination campaigns [8, 48].

Despite the efforts worldwide, only a relatively small proportion of the population is vaccinated in underdeveloped countries due to a lack of access to effective vaccines and vaccine hesitancy [45, 60, 66]. In many developed countries, including the US and UK, the vaccination rates have reached plateaus over the recent months, [13, 26, 36] and remained low among the underprivileged population and regions [1]. Extant studies have documented how the social determinants of health could lead to the regional clustering of diseases and health behaviors through contextual influences from cultural, geographical, and environmental factors alongside group influences arising from personal and peer interactions [22, 24, 30, 57]. The individual-level mechanisms behind geographic clustering in health behaviors and outcomes could be extended to understand the region-level variations in vaccination rates. Regions with lower average income and levels of education are more susceptible and often inundated with misinformation from social media and news outlets rather than public health campaigns, leading to lower regional intention to be vaccinated relative to other regions of the same country [15, 19, 29]. Some other studies on the social ecology of health promotions have also demonstrated the effectiveness of public health campaigns specifically based on regional environments and communities [3, 39, 46, 50].

Beyond the regional differences in health behaviors, there is no study to our knowledge that has examined the contagion of health behaviors between regions using the social network approach. The present study applies the social network approach in the regional vaccination data published by the UK government to propose a Social Network Vaccination Rate (SNVR) model, a new compartmental model that predicts the regional variations and contagion of COVID-19 vaccination behaviors. We argue that the regional health behaviors, in our case vaccination, might influence and be influenced by other neighboring regions for at least two reasons. First, internal migration within the country often means that the individuals living in the region may have and remain in frequent contact with many friends and families living in other regions who could share the benefits of vaccination [17, 38]. The vaccinated friends and families in other regions could also provide positive social contagions by creating social norms or even peer pressure to get vaccinated. Second, although the public perception of the COVID-19 severity may vary across different regions [31, 32], one region's success in managing the pandemic after achieving high vaccination rates may spread the behavioral contagion to people

in other regions to get vaccinated. Additionally, the extent of being influenced by the social contagion in vaccination (i.e., the recipient effect) may differ across regions. Regions with higher proportions of vulnerable populations or migrant laborers might be more accessible to spread social pressure to people of other regions that are more diverse [11, 37]. Conversely, regions with better economic development may be influenced by many other regions as economic diversity means having many network connections with regions, leading to becoming the recipient of regional impacts on health behaviors [33]. The findings of this study serve important purposes for public health policymakers and practitioners to accurately understand the extent of regional hemophilia in health behaviors that could contribute to health inequalities in COVID-19 and future epidemics.

Background

There has been broad academic interest in understanding the contagion of health in epidemics across multiple disciplines. The epidemiological work in public health has primarily focused on modeling the real-time transmission, infection, and hospital capacity needed during COVID-19 through clinical measures such as case reports and hospital records. Typically studies often adopt epidemiological models such as SIR/SEIR, which compartmentalizes people into one of the three categories: Susceptible, Exposed, Infectious, and Recovered with immunity [12, 56]. However, such models often fail to provide robust forecasting accuracy as their reliance on the strict assumptions in the epidemiological models makes it difficult to adjust for some realistic scenarios, such as the public's geographical mobility, the duration of vaccination-induced immunity, and the herd immunity threshold [6, 40]. Recently, other studies also adopted machine learning and deep learning algorithms as non-parametric approaches to predict health contagion [16, 63].

Beyond epidemiological approaches that primarily rely on clinical measures with potential measurement errors, medical sociologists and social epidemiologists attempted to understand the contagion of COVID-19 diseases and vaccination behaviors through social measures. Each individual's social behaviors are associated with not only the clinical contagion of virus pathogens from one individual to another but also complex diffusion in health information, sentiments, resources, and behaviors [9, 64]. The complex diffusion of health information requires multiple sources of social contagion reinforcing each other. Past studies widely revealed the presence of complex diffusion via digital traces when individuals interact with countless public health-related information on social media feeds, online news sites, and other digital platforms such as search engines [7, 44, 47]. For instance, Lam-sal et al. [27] applied sentiment-involved latent variable analysis on geographically-tagged Twitter conversations generated within Australia. The results suggest that the selected latent social media variables significantly improve Root Mean Square Error (RMSE) when predicting COVID-19 cases compared to the baseline model, which only regressed on the outcome. Jahanbin and Rahmanian [23] adopted a combination of tweets and online news articles to predict the COVID-19 outbreak globally.