

Network models of vaccine hesitancy on COVID-19 vaccines

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Abstract

The present study aims to analyze the process of diffusion of vaccine hesitancy through the computational analysis of different simulated scenarios. By harnessing data obtained from a pilot online survey and network analysis, which were specifically designed to investigate vaccine hesitancy among university students, the objective is to elucidate the impact of social structure, particularly the interconnections and positioning of social agents, in the dissemination of ideas that may potentially undermine disease control and prevention within our societies.

1. Introduction

The COVID-19 pandemic has emphasized the significance of human opinions and behaviors in disease development and spread. Vaccination decision-making processes greatly influence pandemic control [1,2]. To prevent disease contagion, vaccination coverage must exceed the herd immunity threshold [2]. Several determinants affect vaccination decisions, including perceived risk of disease infection [3], perceived safety and efficacy of vaccines regarding side effects [4], and economic costs associated with vaccines and disease infection [5]. However, besides these factors, structural determinants like the social dynamics of opinion contagion through social networks should also be considered [6]. Based on preliminary findings from the projects ACTION and DCODES, this work aims to analyze the process of diffusion of vaccine hesitancy through the computational analysis of different simulated scenarios. Using evidence from a pilot online survey and network data aimed at characterising vaccine hesitancy among university students, our study aims to answer two basic questions: (1) what are the main polarizing themes around the new COVID-19 vaccines; (2) how the structural positioning of initial hesitant nodes may affect the final composition of vaccine hesitancy in a network.

2. Methods

The present work combines survey data with agent-based simulation models.

2.1 Survey data

According to the survey data, we could observe that: a 45% of respondents were concerned about the adverse effects of COVID-19 vaccines; 22% of respondents did not consider vaccines necessary for diseases that were no longer common; 54% felt that the new COVID-19 (mRNA) vaccines carried more risk than the old vaccines; and 13% would not accept new doses of COVID-19 vaccines. These were the topics that produced higher polarisation among students. These values would later be used as values for the initialization of the vaccine hesitancy models.

2.2 Simulation models

The parameters and initialization values of the scale-free network simulation models are described in the Table 1:

Table 1: Initialization parameters

Three scenarios	Random	Marginal	Central
Num nodes	200	200	200
Num simulations	200	200	200
Time periods	30tp	30tp	30tp
Network type	SF	SF	SF
Adverse effects	45%	45%	45%
Perceived risks	54%	54%	54%
Necessity of vaccines	22%	22%	22%
Willing to accept new doses	13%	13%	13%

3. Results and discussion

3.1 Three scenarios

Figure 1 shows the three initialization scenarios of the simulation models used in this study: (A) random seeds where the initial seeds are randomly distributed in the network; (B)

central seeds that are positioned in nodes with a high centrality in the network; and (C) marginal seeds where the seeds start from isolated or peripheral nodes in the relationship structure.

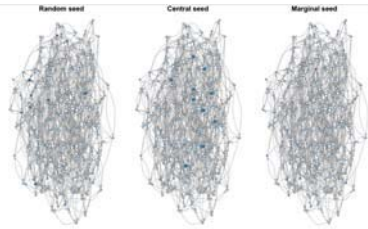


Figure 1: Initialization scenarios.

3.2 Susceptibility and infectivity

The susceptibility and infectivity of the different scenarios would also be analyzed to see which was the most favorable situation for the spread of vaccine hesitancy (i.e. the level of exposure in relation to contagiousness). In this case, it was observed that the scenario with central seeds was the most favorable in terms of infectivity-susceptibility (Figure 2).

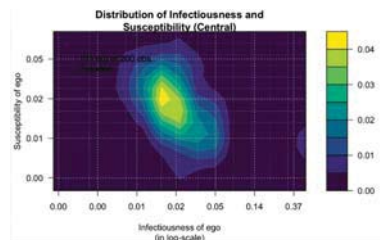


Figure 2: Distribution of infectiousness and susceptibility (central seeds scenario).

3.3 Vaccine hesitancy contagion

From these three initial scenarios, the parameter that would define the level of vaccine hesitancy in relation to the four topics that generated the greatest division among informants would be incorporated, which would offer us 12 different scenarios.

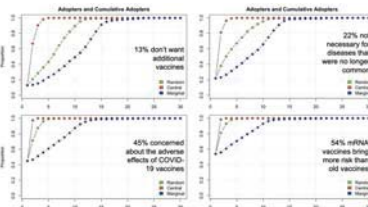


Figure 3: Distribution of adopters under specific vaccine hesitancy topics.

Figure 3 represents the spread of vaccine hesitancy on the four most divisive issues among the students who were interviewed (new vaccines: (1) have adverse health effects, (2) carry more risk than old vaccines, (3) are necessary in the current pandemic situation, and (4) willingness to get a new dose). The results show that the centrality of the person spreading vaccine hesitancy is even more relevant than the level of hesitancy that vaccines may generate among the population, indicating that even low levels of hesitancy (less than 10%) can easily spread if certain opinion leaders favor the spread of vaccine hesitancy.

To test this result, each of the simulation models were run 1000 times in order to verify our preliminary findings. The results of these simulations would confirm the relevance

of centrality in the propagation of vaccine hesitancy, as opposed to the peripheral and random positioning of the (mis)information spreaders (Figure 4).

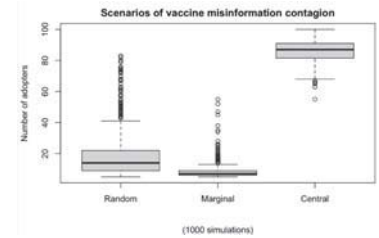


Figure 4: Results after 1000 simulations.

4. Conclusion

The present findings underscore the utmost importance of the social structure, specifically the connections and positions of social agents, in the dissemination of ideas that can potentially undermine disease control and prevention in our societies. These preliminary results hold substantial significance as they shed light on the pivotal role of social network structures in both the spread of vaccine hesitancy and the development of effective strategies to combat health misinformation. By understanding how social networks influence the diffusion of detrimental ideas, we can devise targeted interventions to foster accurate information dissemination and promote public health. Consequently, these findings contribute to the growing body of knowledge aimed at mitigating the negative impact of misinformation on disease control efforts.

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