Effects of a Vaccine-Adverse Minority on Vaccination Dynamics

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August 3, 2017

1 Abstract

Previous research has applied a game-theoretic model to a population's vaccination compliance when the population consists of subgroups with differing perceptions on vaccines (Cojocaru, Bauch, & Johnston, 2007) (Cojocaru & Bauch, 2009). This paper further analyzes the concept of a heterogeneous population by imposing a simplistic lattice neighborhood construction. When the vaccine-suspicious minority is small relative to the population, only a small proportion of that group cooperates. As the size of the minority increases, a larger percentage of the vaccine-suspicious are forced to cooperate in order to maintain an adequate level of herd immunity. In structured neighborhoods, vaccination rates are lower in general, as it becomes more difficult for individuals to become infected. By isolating the vaccine-adverse from the vaccine-friendly, we observe the minority group's negative influence on the vaccination habits of their peers.

2 Introduction

Epidemiological models show that the existence of an immunity-granting vaccine can limit the extent of a contagion, especially as a higher proportion of the population chooses to vaccinate. Paradoxically, as more people become immune and disease prevalence decreases as a result, there is less motivation for other population members to vaccinate. Instead, these free-riders choose to rely on the collective herd immunity of their peers as protection against the disease. However, accumulation of non-vaccinator strategy allows for a resurgence in a previously controlled disease, as was the concern for measles in the United Kingdom in the early 2000's (Jansen et al., 2003) (Bauch & Earn, 2004). Previous studies have shown that under voluntary vaccination policy, the cyclic nature of vaccination dynamics makes permanent disease eradication nigh impossible (Fu, Rosenbloom, Wang, & Nowak, 2011) (Cojocaru & Bauch, 2009).

There are two types of risk involved in the vaccine game. The decision to vaccinate incurs a guaranteed yet nominal cost. While deferment does not necessitate an initial expense, in the event of an outbreak unvaccinated individuals risk infection, which involves a relatively high cost to their physical well-being, finances, and personal time.

Not surprisingly, individuals of varying backgrounds and ideologies carry out different vaccination strategies. To reflect these social dynamics, this paper relaxes a typical assumption of vaccination models requiring a homogeneous population in favor of one that is heterogeneous with two subgroups. We investigate how the presence of a minority opinion affects the vaccination compliance of the overall population, and apply stochastic theory to cellular automaton to demonstrate the spread of contagion in structured neighborhoods, as well as observe the effect of peer networks on social learning.

3 The Vaccination Game

Initially, individuals form vaccination strategies based on a game-theoretic approach, with the goal of maximizing the payoff of their actions. In this section, the consequences of each strategy are considered and quantified to determine the optimal approach for each individual.

3.1 Assumptions

Before we move into the specifics of our game, we consider a number of assumptions that may or may not accurately reflect realistic societal dynamics.

1. The population is well-mixed.

   Each individual has an equal probability of interacting with any and every other person in the population. We will later remove this assumption in favor of structured neighborhoods, but for now we assume no social groupings. Members of both the majority and minority are dispersed evenly throughout the population.

2. The size of the population remains constant.

   While we make considerations for birth and death rates in the deterministic model, we assume for simplicity that population size does not fluctuate.

3. The vaccine grants cooperators perfect immunity against the disease.

   Vaccines that exist for many "childhood contagions" such as measles or pertussis are quite effective. After a second dose, the Measles-Mumps-Rubella (MMR) vaccine is estimated to be 97% effective against measles, the disease we considered in the creation of this model ("Measles Vaccination", 2017).

4. Individuals do not alter vaccination strategies in the midst of the epidemic.

   This is the least credible assumption of our model, and further research can improve on our results by introducing a parameter α that would represent the rate at which individuals change strategies, relative to the current state of the epidemic in the population.

3.2 Game Setup

In the vaccination game, those who vaccinate and contribute to the herd immunity of the whole population are considered to be cooperators, and those who forgo vaccination are defectors. Let a finite population of individuals be categorized into either a "vaccine-friendly" majority group G_1 or a "vaccine-suspicious" minority group G_2. Individuals within the same group share similar beliefs about vaccination, but these views differ between the two groups.

The anticipated vaccination cost for members of G_1 is r_{v1}, and is significantly lower than r_{v2}, the perceived vaccination cost of G_2. Both groups share similar beliefs about the risks and consequences of illness, π and r_s. The ratio r_i represents each group's perceived cost of vaccination relative to the cost of infection, i.e. $r_i = \frac{r_{vi}}{r_s}$. Trivially, we assume r_v to be less than r_s, because if a vaccination is seen to be more costly than the disease it prevents, it is in the individuals' best interest to never vaccinate. Since members of G_2 tend be more hostile towards vaccines, r_{v2} is relatively large, and thus $r_1 < r_2$.

The proportion of the population that belongs to G_1 is denoted by a.

3.3 Optimal Outcome

As each individual deliberates whether to vaccinate, she must consider the expected outcomes associated with her decision, as visualized in Figure 1. Potential costs of vaccination include the money or time taken to acquire the vaccine, as well as any real or perceived side effects from its administration. If enough of the population gets vaccinated, π decreases, and a non-vaccinator is more likely to escape the epidemic uninfected and free from cost obligation. Ultimately, such free-riding is the optimal outcome because it results in the best payoff. However, free-riding attemptees risk infection if not enough of their counterparts vaccinate. The costs of sickness include physical discomfort, doctor visits, and potential morbidity, and are much higher than those of vaccination; for this reason, contracting the illness is the least favorable outcome.

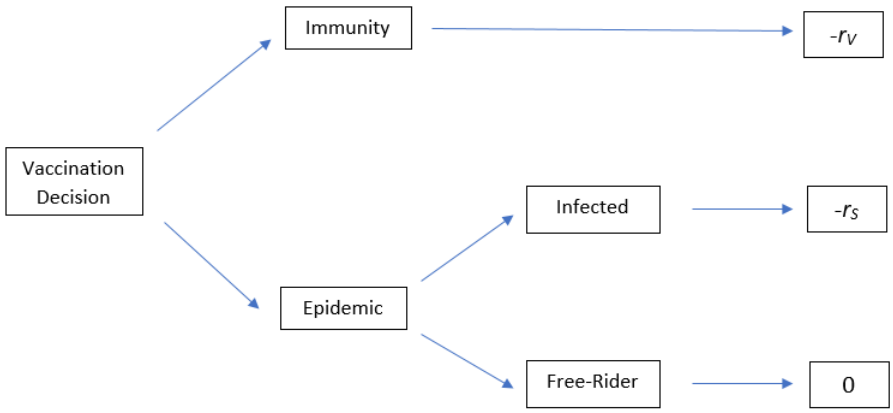

Figure 1: The flowchart demonstrates the potential outcomes of the vaccination game. If an individual chooses to immunize, her outcome will be a payoff of $-r_v$. If she chooses to forgo vaccination, her outcome will be either a contracted illness or a successful evasion of the epidemic, will incur costs $-r_s$ and 0, respectively.

Symbolically, the expected payoffs of vaccinating (V) and not vaccinating (NV) are as follows:

$$\begin{aligned} \mathrm{E(V}_i) &= -r_{vi} \\ \mathrm{E(NV)} &= \pi \times -\mathrm{r}_s + (1-\pi) \times 0 \end{aligned}$$

As the two groups vary in their perceptions of r_v, their expected vaccination payoffs also differ. Thus, what passes as an ideal strategy for one group may not appear so favorable for the other.

Now we calculate the Nash Equilibrium x^* of this game. In this context, the Nash Equilibrium is an individual's probability to choose a vaccinator strategy, in which increasing or decreasing this probability unilaterally would lower the individual's expected payoff. Let x_i be the probability that G_i vaccinates, and x be the proportion of the whole population that vaccinates. To find the Nash Equilibrium, we set the expected payoffs of each strategy equal, and solve for x_i (Fu et al., 2011).

$$-\mathrm{r}_{vi} = \pi \times -\mathrm{r}_s$$

Divide each side of the equality by -r_s:

$$r_i = \pi$$

From (Fu et al., 2011), we have $\pi = 1 - e^{-R_0 R(\infty)}$, where R_0 is the disease's basic reproductive ratio. (For our disease, we choose R_0 to be 18 ("Measles Vaccination", 2017)).

Now we have

$$r_i = 1 - e^{-R_0 R(\infty)}$$

To find the value of $R(\infty)$, we recall that at any time t, the proportion of susceptible, infected, and recovered individuals must be equal to the proportion of the population that did not vaccinate, and thus must fall into one of these three categories.

$$S(t) + I(t) + R(t) = 1 - x$$

At $t = \infty$, the disease eventually reaches a state of equilibrium, and the proportion of recovered individuals is equal to the proportion of unvaccinated individuals times the probability that unvaccinated individuals become infected.

$$R(\infty) = (1 - x)\pi = (1 - x)(1 - e^{-R_)R(\infty)} = (1 - x)r_i$$

We see also from (Fu et al., 2011) that $R(\infty) = -\frac{log(1-r_i)}{R_0}$.
We rearrange and solve for x to obtain the Nash Equilibrium:

$$x_i{}^* = 1 + \frac{log(1 - r_i)}{R_0 r_i}$$

The Nash Equilibrium depends on an individual's vaccination-to-sickness cost ratio and thus the will vary between G_1 and G_2. We calculate x as a weighted average of the vaccination strategies of each group. Note that $x < 1$ because when vaccination rates reach a critical level $p_{crit} = 1 - \frac{1}{R_0} < 1$, the disease is effectively eradicated (i.e., $\pi = 0$). Without the threat of infection, individuals cease vaccinating. Unfortunately, as x approaches p_{crit}, and π decreases, fewer individuals are motivated to vaccinate. This leads x to consistently fall short of the level needed to eradicate the disease (Fu et al., 2011) (Cojocaru & Bauch, 2009).

4 Deterministic Model

In this section, we define the methods and parameters used in the creation of our deterministic model. We apply theory from the previous section to determine individuals' initial vaccination decisions, and then incorporate epidemic dynamics to observe how this alters our population's likelihood to vaccinate.

4.1 Initial Conditions

We set the cost of sickness for both groups to be 1. The cost of vaccination for G_1 to be $\frac{1}{100}$, i.e., members of Group 1 view the disease to be 100 times as dangerous as the vaccine that prevents it. Members of Group 2 view vaccines to be five times more dangerous than Group 1, so that $r_{v2} = \frac{1}{20}$. We will vary the value of a to investigate the effect that the size of the minority group has on population vaccination adherence.

4.2 SIR Model

Let the disease in question have a vaccine that is administered to children in the early stages of their lives, such as measles, whose MMR vaccine is recommended for children aged 6-12 months ("Measles Vaccination", 2017). We implement a modification of the Kermack-McKendrick SIR model to this scenario, which represents individuals as either Susceptible, Infected, or Removed (Kermack & McKendrick, 1927). Note that in this case, individuals who are immune to the disease due to natural recovery or immunization belong to the Removed category.

The epidemic dynamics can be deterministically represented using a system of ordinary differential equations. The parameters β, γ, and μ represent the average rates of infection, recovery, and generational turnover, respectively.

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI + \mu(1-x) - \mu S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I + \mu x - \mu R \end{aligned}$$

As disease spreads, new members enter the population according to the birth rate, and vaccinate at a rate relative the actual disease occurrence in the population. Again, this rate differs between those of G_1 and G_2, and can be modeled with first-order differential equations.

$$\frac{dV_i}{dt} = V_1(1-V_1)(-r_{vi} + r_s I)$$

Or, equivalently:

$$\frac{dV_i}{dt} = V_1(1-V_1)(-r_i + I)$$

Vaccination increases if disease incidence exceeds the vaccination cost, and decreases when infection prevalence is low. We ran this simulation at different values of a for 100 iterations. The results are analyzed in the discussion section.

5 Stochastic Theory and Application

Our first model works under the assumption that the average infection, recovery, and birth/death rates accurately represent the progression of individuals through each of the S, I, and R, states. However, individual experiences with illness differ, and average rates do not account for the randomness typical of biological processes. To counter this, we apply stochastic theory, which converts the rates into probabilities that determine which events occur and the time that they occur.

5.1 Gillespie Algorithm

Here we outline the Gillespie Algorithm (Regoes & Schafroth, n.d.), and how it can be implemented to create a stochastic model.

1. Initialization

   In this stage, we determine the probabilities governing our model, the initial conditions, and the time t_{final} when we will commence the model. Rates can be converted to probabilities using the formula $1 - e^{-rate}$.

2. Determine the time for the next event.

   The Gillespie Algorithm operates with the idea that we can divide our continuous time frame into intervals so small that only one event occurs at each interval. However, we have no way of choosing these ideal intervals that would contain exactly one event, so we pick a random number from an exponential distribution to represent the time change between events, δt. The time at the next event will be the current time added to δt.

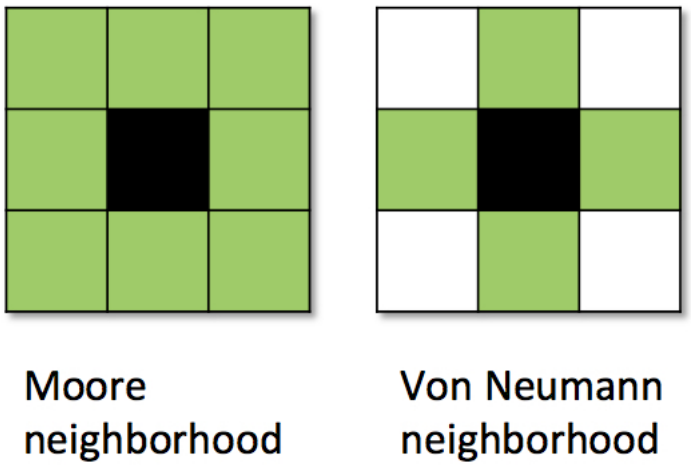

Figure 2: The figure shows two possible neighborhood constructions to a Cellular Automaton model. For this research, we choose to utilize the Von Neumann setup.

3. Determine which event occurs.

   We sum the probabilities of each event and scale the sum so that it is equal to one, and the probability of each event corresponds to some interval between zero and one. To choose which event will take place during the next time interval, we pick a random number from a uniform distribution. The event interval that contains this chosen number is the one selected to occur.

4. Repeat steps 2 and 3 until $t + \delta t$ exceeds t_{final}.

As each event occurs, an individual exits one stage and enters another. The Gillespie Algorithm can be applied to a SIR simulation and is a more accurate representation of the biological processes relating to infection and recovery.

5.2 Application to Cellular Automaton

We apply this probabilistic approach to two-dimensional cellular automaton to visualize infection spread among neighbors in structured networks. Cellular automaton represent a population as a grid-like structure in which every cell represents an individual and the value associated with each cell at time t indicates its current state (Wolfram, 1983).

There are multiple structures that can be used to represent neighborhoods in cellular automaton; here we use the Von Neumann neighborhood (see Figure 2). This setup violates the "well-mixed" assumption we made in regards to our deterministic model. In the present case, each individual only has access to their neighbors. One can imagine folding the planar grid into a torus shape so that even individuals on the "edge" of the grid interact with exactly four others. Neighbors facilitate the spread of disease and act as role models in the vaccination decision process.

The model we present consists of two stages. In the first stage, individuals form vaccination strategies, and in the second stage, we introduce an epidemic. After each epidemic stage, individuals reevaluate their strategies by comparing their payoff from the previous round with the payoffs of their neighbors. Individuals will switch to their neighbor's strategy with probability

$$1 - \frac{1}{1 + e^{-k(f_n - f_m)}}$$

where f_n is the payoff of the neighbor and f_m is the fitness of the individual. The parameter k is the strength of selection constant. Here, we choose k to be one, although for higher values of k, one is more likely to switch to a neighbor's strategy (Fu et al., 2011).

We simulate two versions of this cellular automaton problem: one where the members of G_1 and G_2 are evenly and randomly dispersed, and another where the member of G_2 are kept relatively isolated from the rest of the population. The results of each simulation are discussed in the next section.

6 Results

We ran simulations of both the deterministic and stochastic models at different values of a to observe how the size of the vaccine-suspicious minority affected the compliance of the overall population.

As could be expected, increasing the proportion of the population belonging to G_2 had a negative effect on population vaccination rates (Figure 3). However, compliance rates of G_1 tended to increase, perhaps in an attempt to compensate for the dropping level of community immunity. When a was larger than 0.7, individuals belonging to G_2 vaccinated with a probability near zero, choosing to rely on the vaccination protection by members of G_1 instead. At smaller values of a, the herd immunity created by G_1 was not sufficient to diminish the spread of disease, and individuals of G_2 began to view the risk of infection as more costly than the vaccine, leading to higher vaccination levels among G_2.

The stochastic cellular automaton model places emphasis on the spread of biological contagion and public opinion through a population. The first set-up assumes a starting population in which members of the majority and minority groups are distributed randomly. The vaccination compliance according to this model was much lower than we had observed with the deterministic model, and is likely the result of the "negative influence" that successful free-riding has on would-be vaccinators (Figure 4,5).

Conversely, when we separate the members of G_2 from the rest of the population, we observe much higher vaccination levels among G_1. This was accomplished by segregating all G_2 members into the upper right hand corner of the cellular automaton as the initial state. Among members of G_1, there is little attempted free-riding from the first iteration of the simulation. Those who do not vaccinate free-ride successfully, but few neighbors switch to this strategy because of both the scarcity of the free-riders and the relatively little incentive G_1 members face by choosing to not vaccinate.

The pocket of G_2 members encounter a different experience. More individuals of this group attempt to free-ride, and occasionally do so successfully if the initial inoculum (whose position is determined randomly) happens to be concentrated heavily among the highly vaccinated G_1. When individuals do free-ride successfully, their neighbors are very likely to switch to that strategy on the next round, leading to a large drop in vaccination. However, this means that the subsequent epidemic is likely to be quite severe, leading individuals to imitate those few who had stuck to a vaccinator strategy. As a result, the vaccination rates for G_2 oscillate wildly. The overall population vaccination rate tends to be very high in comparison to the even dispersal model, although it tends to be higher with smaller values of a (Figures 6,7).

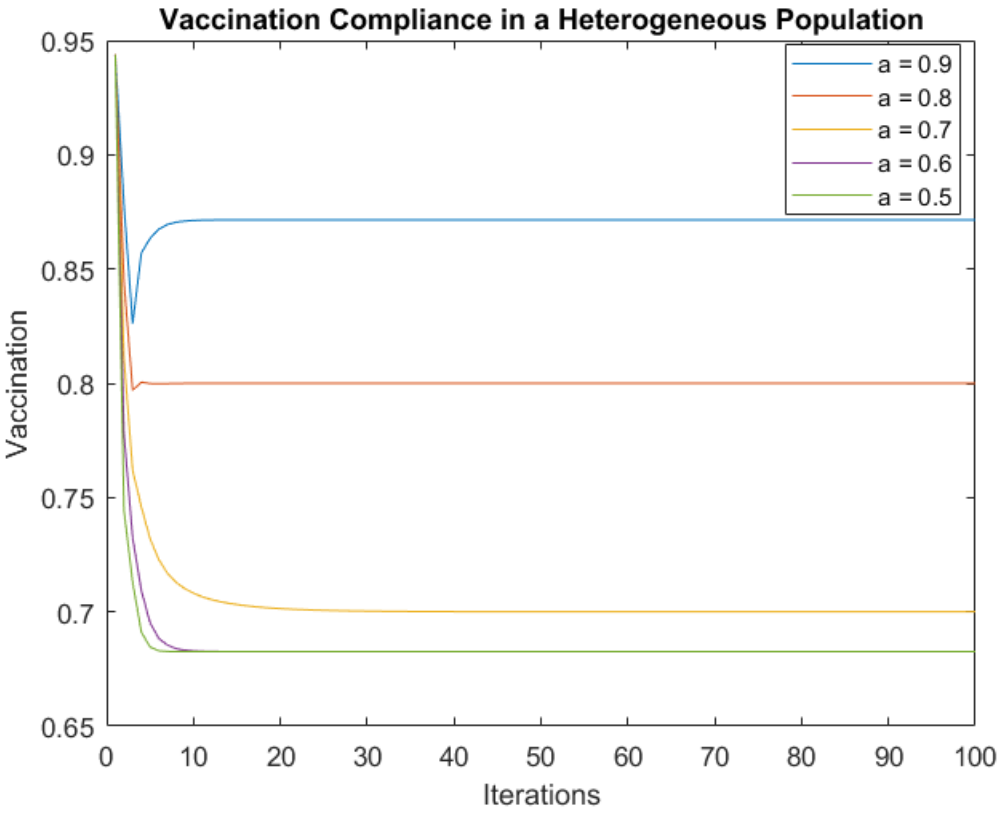

Figure 3: The graph shows the population vaccination rates after 100 iterations of the model and varying values of a. While the population rates decreased with a, the compliance rates of G_2 increased as the minority group took up a larger portion of the population.

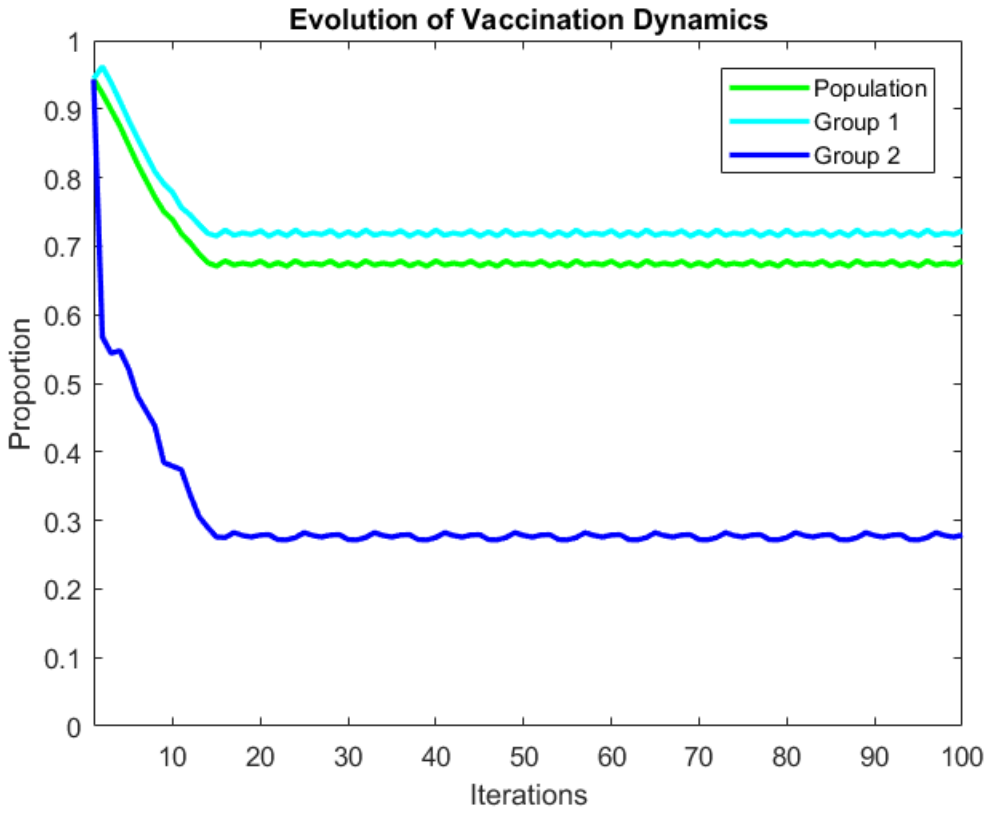

Figure 4: Vaccine compliance rates of the population and each subgroup at $a = 0.90$

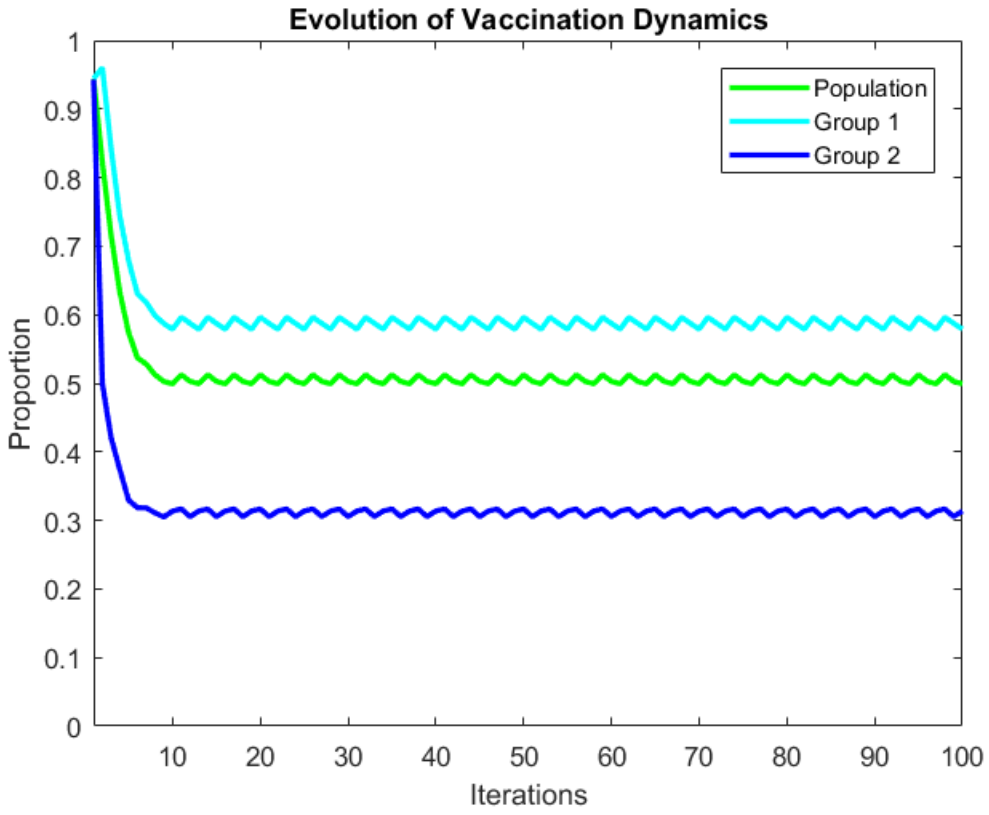

Figure 5: Vaccine compliance rates of the population and each subgroup at $a = 0.70$

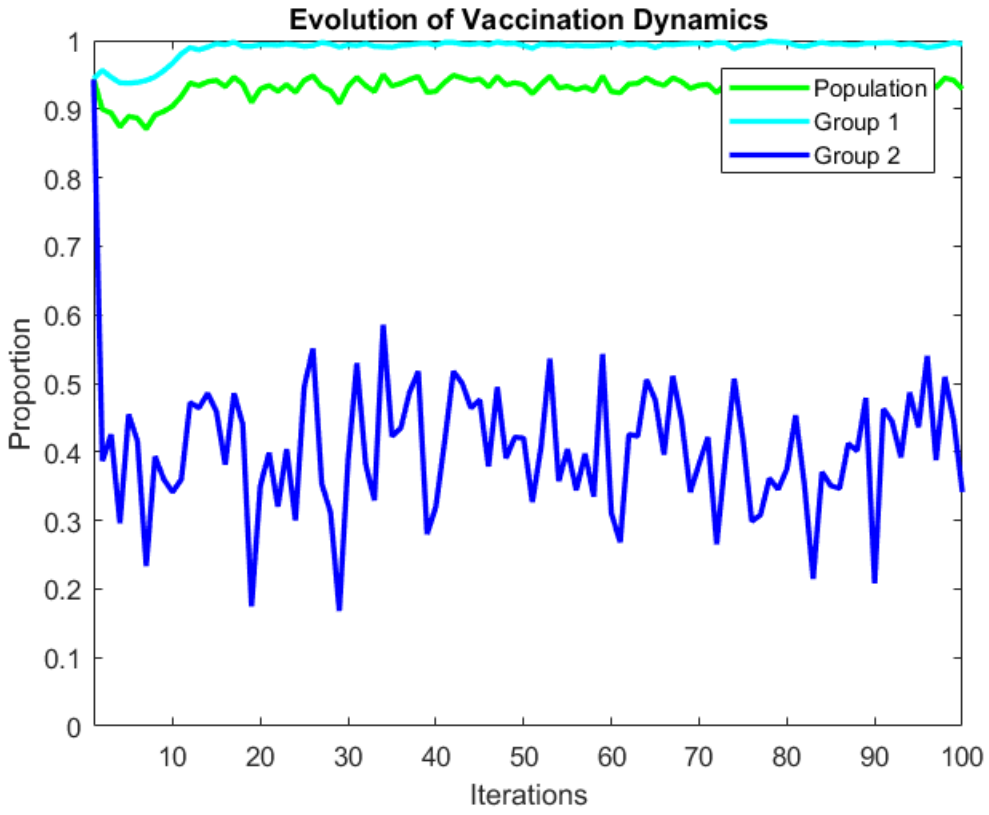

Figure 6: Vaccine compliance rates of the population and each subgroup with structured social networks at $a = 0.90$

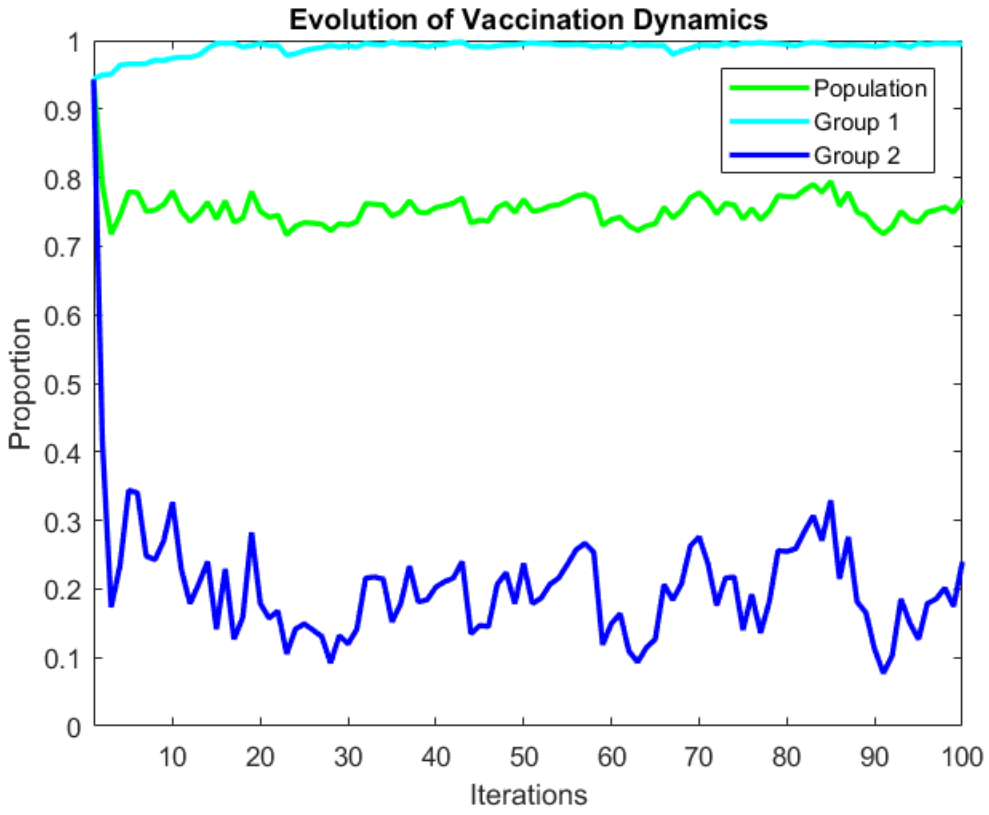

Figure 7: Vaccine compliance rates of the population and each subgroup with structured social networks at $a = 0.70$

7 Discussion

This paper suggests the scope of influence that a vaccine-adverse minority wields, but these results are by no means exhaustive. Other studies have examined how these results change when the two subgroups differ in both the perceived cost of infection and expected probability of illness, citing polls that suggest a correlation between vaccine distrust and underestimated infection risk (Cojocaru et al., 2007) (Cojocaru & Bauch, 2009). Similarly, the practicality of our model would be much improved if we allowed individuals to alter their vaccination strategies during an epidemic (Fu et al., 2011). Other areas of interest include vaccines that grant imperfect immunity (Weinberg & Szilagyi, 2010), different neighborhood structures (Fu et al., 2011), or multiple opinion groups (Cojocaru & Bauch, 2009).

Despite any shortcomings of the simplistic models discussed in this paper, we can conclude that the existence of a minority group such as G_2 can negatively impact the vaccine compliance of a population. These individuals are more likely to forgo vaccination, which can compromise the herd immunity that is necessary to protect those too young to become vaccinated and those who must forgo vaccination due to medical reasons. Furthermore, as seen in our stochastic cellular automaton model, these people also act as negative influences on those who would otherwise be likely to vaccinate.

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