Bull Math Biol
DOI 10.1007/s11538-011-9646-4

ORIGINAL ARTICLE

Impact of Imitation Processes on the Effectiveness of Ring Vaccination

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Received: 3 September 2010 / Accepted: 18 February 2011

Abstract Ring vaccination can be a highly effective control strategy for an emerging disease or in the final phase of disease eradication, as witnessed in the eradication of smallpox. However, the impact of behavioural dynamics on the effectiveness of ring vaccination has not been explored in mathematical models. Here, we analyze a series of stochastic models of voluntary ring vaccination. Contacts of an index case base vaccinating decisions on their own individual payoffs to vaccinate or not vaccinate, and they can also imitate the behaviour of other contacts of the index case. We find that including imitation changes the probability of containment through ring vaccination considerably. Imitation can cause a strong majority of contacts to choose vaccination in some cases, or to choose non-vaccination in other cases—even when the equivalent solution under perfectly rational (non-imitative) behaviour yields mixed choices. Moreover, imitation processes can result in very different outcomes in different stochastic realizations sampled from the same parameter distributions, by magnifying moderate tendencies toward one behaviour or the other: in some realizations, imitation causes a strong majority of contacts not to vaccinate, while in others, imitation promotes vaccination and reduces the number of secondary infections. Hence, the effectiveness of ring vaccination can depend significantly and unpredictably on imitation processes. Therefore, our results suggest that risk communi-

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Published online: 16 March 2011

cation efforts should be initiated early in an outbreak when ring vaccination is to be applied, especially among subpopulations that are heavily influenced by peer opinions.

Keywords Ring vaccination · Vaccinating behaviour · Imitation · Networks · Modelling

1 Introduction

Mass vaccination has historically been the dominant means of reducing morbidity and mortality due to vaccine-preventable infectious diseases (Bonanni 1998). However, in some contexts, other strategies such as ring vaccination are preferable. Ring vaccination involves identifying infectious index cases and vaccinating their close contacts to prevent them from being infected (Greenhalgh 1986; Muller et al. 2000). Ring vaccination tends to be more efficient and more effective than UMV for preventing outbreaks when (1) outbreaks are localized, (2) infected individuals and their exposed contacts can be rapidly identified, and (3) the vaccine induces an immune response rapidly enough for contacts to be protected before they can become infected.

Ring vaccination has been applied to outbreak control for hepatitis A (Diel et al. 2000), foot-and-mouth disease in cattle (Toma et al. 2002; Keeling et al. 2003) and smallpox (Fenner et al. 1988). Ring vaccination was credited as the strategy that culminated the eradication of smallpox (Hopkins 1988). One of the earliest applications of ring vaccination was in Nigeria, when a smallpox outbreak developed among a religious sect. Faced with limited resources and vaccine supplies, staff learned to isolate infected individuals and identify and vaccinate their contacts, leading to successful containment of the outbreak (Hopkins 1988; Strassburg 1982). In the case of smallpox, the vaccine can prevent both infection and disease in persons who have already been infected, meaning that ring vaccination could be particularly effective despite delays in identifying index cases. For pandemics of novel emerging pathogens, ring vaccination may likewise be an optimal strategy if there are not sufficient vaccine supplies to mount mass vaccination campaigns.

Because ring vaccination involves reaching a relatively small number of individuals, the success or failure of ring vaccination can depend strongly on stochastic effects. The debate about whether to include stochastic effects in infection transmission models is long-running (Lloyd-Smith et al. 2005). Often the average of many realizations of a stochastic model is identical to what would be predicted from a deterministic model, in which case the primary advantage of the stochastic model is to provide an estimate of variability. However, in other situations the average of many stochastic realizations may differ from the prediction of the equivalent deterministic model or there may be other important qualitative differences. For instance, if the number of secondary infections per index case is modelled as a negative binomial distribution, a stochastic modelling approach can predict more frequent extinctions, and rarer but more severe outbreaks, than a deterministic modelling approach (Lloyd-Smith et al. 2005). Similarly, network models have been

used to demonstrate that a wide range of outbreak sizes and outbreak probabilities caused by severe acute respiratory syndrome (SARS) are possible even for the same R_0, highlighting the role of underlying contact networks (Meyers et al. 2005).

In a separate but related vein, models have been used to explore the interaction between disease transmission and individual vaccinating behaviour (Brito et al. 1991; Bauch and Earn 2004; Bauch 2005, Klein et al. 2007; Reluga et al. 2006; Galvani et al. 2007; Chane and Cottrell 2009) and how model dynamics change if transmission is modelled as occurring on a network instead of through homogeneous mixing (Salathe and Bonhoeffer 2008, Perisic and Bauch 2009a, 2009b, Funk et al. 2009). Conversely, there have been a number of mathematical models of ring vaccination that do not explicitly incorporate behaviour considerations (Greenhalgh 1986; Muller et al. 2000; Kretzschmar et al. 2004; Kaplan 2004). However, relatively little work has focussed on behavioural effects and ring vaccination per se (Perisic and Bauch 2009a, 2009b).

Some of these previous models have assumed that individuals adopt new strategies through an imitation process, where individuals base their vaccinating decisions partly on the experiences or opinions of other individuals in the population. Empirical studies confirm the common knowledge that the opinion of the healthcare provider is important determinant of vaccine uptake (Smith et al. 2006). However, empirical studies also find that peer opinion has a very large influence on individual vaccinating decisions (Merrill et al. 1958; Streefland et al. 1999; Sturm et al. 2005; Rao et al. 2007). For example, Merrill et al. (1958) found that vaccinating decisions of mothers in California were influenced by their peer groups. Sturm et al. (2005) review Merrill et al. (1958) and other more recent publications documenting the strong roles of peer group opinion and social norms in vaccinating decisions. An empirical study analyzing perceptions of vaccination on real-world social networks likewise found that peer opinion is an important determinant of perceive value of vaccination and vaccinating behaviour, to the point that "students coordinate their vaccinating decisions with their friends" (Rao et al. 2007). Hence, imitation processes appear to be an important mechanism in individual vaccination decisions.

Here, we evaluate the impact of imitation dynamics on the success of voluntary ring vaccination. We develop a series of simple stochastic models in which individuals can choose whether or not to vaccinate based on the benefits (to themselves) of vaccinating versus the benefits of not vaccinating. Moreover, in some versions of the model the individual decision whether or not to vaccinate is influenced by the decisions of other contacts of the index case. We incorporate stochasticity since stochastic effects can be important determinants the success or failure of ring vaccination. The vaccinating choices of the index case's contacts therefore determine whether or not ring vaccination will be successful. The particular question of interest is whether models that include stochastic effects and imitation processes have qualitatively different predictions from a model that is deterministic, and/or does not include imitation processes.

2 Models

We describe three models in this subsection. In the "simple stochastic model", we employ a stochastic model of vaccine decision-making among the contacts of an index case, where the payoffs of vaccinating versus not vaccinating are the same for all contacts of the index case. We analyze this model to generate expressions for the probability of outbreak control and the expected number of secondary infections created by the index case. In the "distributed stochastic model", this stochastic model is further extended by drawing parameters for vaccine and disease risks for each individual from probability distributions, meaning that contacts of the index case can have different payoff functions, leading to different decisions. Finally, for "the distributed stochastic model with imitation", the distributed stochastic model is extended by including an imitation process between contacts of the index case. All three models are also simulated for a range of parameter values to gain insights into impact of imitation behaviour in the context of voluntary ring vaccination.

2.1 Simple Stochastic Model

We suppose the index case has Q contacts, each contact is initially susceptible, and there is a daily probability p of transmitting infection to a given contact. We assume that the infection has an incubation period of ω days, an infectious period of δ days, and a latent period of σ days. Likewise, we assume that the time between the decision to vaccinate and attainment of protective immunity (where individuals do not develop disease and do not transmit further) is λ days, as a result of either logistic delays and/or the time required for the immune system to mount a fully protective response. The vaccine efficacy is ε. Parameter values and definitions appear in Table 1.

We will derive P_{control}, defined as the probability that there is no secondary transmission, as well as R_{control}, the expected number of secondary infections produced by the index case if some of the contacts have the option to vaccinate and thereby reduce secondary transmission. We assume that the payoff of vaccinating as soon as the index case exhibits symptoms is P_V, the payoff of not vaccinating is P_N, the baseline payoff is L, the cost of vaccinating is r_{vac}, and the cost of infection is r_{inf}. We assume that, if individuals decide to vaccinate at all, they decide to do so as soon as the index case exhibits symptoms. If they wait to vaccinate, then they incur the same cost of vaccinating as if they decided to vaccinate right away, but incur additional costs due to the possibility of exposure because of their delay. Therefore, rational individuals either vaccinate as soon as the index case exhibits symptoms, or not at all, depending on conditions.

We restrict attention to the case $\omega \geq \sigma$ since $\omega < \sigma$ is not biologically plausible. This is further broken down into two cases:

Case 1: *Vaccine does not work in time*, $\lambda + \omega \geq \delta + \sigma$

In this case, the vaccine does not provide protective immunity in contacts until after the index case has recovered and, therefore, does not provide any benefit in the current outbreak. Hence, we assume that no one will vaccinate and from basic probability

Table 1 Parameter definitions and baseline values

Parameter	Definition	Baseline values
Q	Number of contacts of index case	100 or 1000
p	Transmission probability per edge per day	0.05 per day
ω	Incubation period	5 days
δ	Infectious period	5 days
σ	Latent period	4 days
λ	Time between decision to vaccinate and attainment of protective immunity	1 day
ε	Vaccine efficacy	0.95
r_{vac}	Penalty due to being vaccinated (e.g. adverse events, potential monetary cost)	0.001
r_{inf}	Penalty due to being infected (e.g. disease complications)	0.3
L	Baseline payoff	1
P_V	Payoff to vaccinate as soon as index case exhibits symptoms	
P_N	Payoff not to vaccinate	

Fig. 1 Timeline when $\lambda + \omega < \delta + \sigma$

theory we have that

$$P_{\text{cont}} = (1-\zeta)^Q, \tag{1}$$

$$R_{\text{cont}} = \sum_{k=0}^{Q} k \binom{Q}{k} \zeta^k (1-\zeta)^{Q-k}, \tag{2}$$

where

$$\zeta = 1 - (1-p)^\delta \tag{3}$$

is the probability that a given neighbour who remains susceptible is infected by the index case before the index case recovers.

Case 2: *Vaccine may work in time to prevent infection*, $\lambda + \omega < \delta + \sigma$

In this case (Fig. 1), we derive the payoff to vaccinate immediately and the payoff not to vaccinate, and we assume that a contact vaccinates if

$$P_V > P_N. \tag{4}$$

The payoff not to vaccinate is given by

$$P_N = (L - r_{\text{inf}})\zeta + L(1-\zeta), \tag{5}$$

where the first term of the equation represents the outcome in which the unvaccinated contact is infected by the index case, and the second terms represent the outcome in which the unvaccinated contact is not infected by the index case. The payoff to vaccinate is given by

$$\begin{aligned} P_V = {} & (L - r_{\text{vac}} - r_{\text{inf}})\left\{\left[1 - (1-p)^{\lambda+\omega-\delta}\right]\right. \\ & \left. + \left[(1-\varepsilon)(1-p)^{\lambda+\omega-\delta}\left(1 - (1-p)^{\delta-(\lambda+\omega-\sigma)}\right)\right]\right\} \\ & + (L - r_{\text{vac}})\left\{\left[\varepsilon(1-p)^{\lambda+\omega-\delta}\left(1 - (1-p)^{\delta-(\lambda+\omega-\sigma)}\right)\right] + [1-p]^{\delta}\right\}. \end{aligned} \tag{6}$$

Details of the derivation are given in Appendix A. The expression in the first square brackets of the top line of (6) represents the outcome where an individual chooses to vaccinate but makes an effective contact before vaccine-derived protective immunity is developed (and is thus infected). The expression in the second square bracket of the top line represents the outcome where the individual chooses to vaccinate, makes an effective contact after the time required for protective immunity to develop but is still infected because of ineffective vaccination. The expression in the first square bracket of the bottom line represents the outcome where the individual choose to vaccinate, makes an effective contact after the time required for protective immunity to develop but is not infected because the vaccine was efficacious. The expression in the second square bracket of the bottom line represents the outcome where the individual vaccinates but is never challenged because an effective contact is never made.

When $P_N \geq P_V$, there is no incentive for any of the contacts of the index case to vaccinate and so P_{cont} and R_{cont} are given by (1) and (2). However, when $P_N < P_V$, every contact of the index case vaccinates as soon as the index case exhibits symptoms, and we have

$$P_{\text{cont}} = (1-\xi)^{Q}, \tag{7}$$

$$R_{\text{cont}} = \sum_{k=0}^{Q} k \binom{Q}{k} \xi^{k} (1-\xi)^{Q-k}, \tag{8}$$

where

$$\xi = 1 - \left\{(1-p)^{\lambda+\omega-\sigma}\left(1 - p[1-\varepsilon]\right)^{\delta-(\lambda+\omega-\sigma)}\right\} \tag{9}$$

is the probability that a given neighbour who decides to vaccinate as soon as the index case exhibits symptoms is infected by the index case. Together, (1)–(9) under the various cases for parameter values determine the probability P_{cont} that an outbreak is controlled through ring vaccination as well as the average number of secondary infections R_{cont} produced by the index case.

The simple stochastic model was simulated in Matlab version 7.6.0. The algorithm used for the simulation appears in Appendix B.

2.2 Distributed Stochastic Model

In the distributed stochastic model, the parameters values for the infectious period δ, latent period σ, vaccine efficacy ε, cost of infection r_{inf}, cost of vaccination r_{vac},

time to protective immunity λ, incubation period ω, and transmission probability p are sampled from a lognormal distribution for each individual. The resulting variation between individuals can be conceived of either as real or perceived differences. This model was likewise simulated in Matlab version 7.6.0.

2.3 Distributed Stochastic Model with Imitation

The distributed stochastic model with imitation is identical to the distributed stochastic model except for the imitation-based decision making process used by contacts of the index case. On the first day that the index case is symptomatic, we determine P_V and P_N as before from (5) and (6). We let V denote the number of individuals for whom $P_V > P_N$ (hence, Q-V is the number for whom $P_V \leq P_N$). Each individual chooses to vaccinate with probability ν, where

$$\nu = (1 - \kappa)H(P_V - P_N) + \kappa g(V), \tag{10}$$

and where $H()$ is the Heaviside function, $g(V)$ is a function of V describing how individuals tend to imitate the most prevalent strategy among the contacts, and κ is a parameter governing the relative importance to an individual's decision making process of imitation processes versus weighing the individual's own values of P_V and P_N. The function $g(V)$ is an increasing function of V, indicating a higher probability that the individual vaccinates if vaccinating is also favourable for the majority of other contacts. We explore cases where $g(V)$ is a hyperbolic tangent function or a step function. With ν thus calculated for each individual, we determine whether individuals vaccinate by sampling a random number between 0 and 1.

2.4 Simulation Design

For each parameter set analyzed, we ran 2,500 realizations, computing the mean and standard deviation of the average number of secondary infections R across all realizations. We explored R as it depended on parameters governing natural disease history and imitation behaviours. We also plotted the frequency distribution of the number of secondary infections and the number of vaccinators for certain scenarios of the distributed stochastic model in the presence of imitation.

3 Results

The mean and standard deviation of R across all 2,500 realizations were calculated as a function of cost of infection r_{inf}, cost of vaccination r_{vac}, vaccine efficacy ε, and incubation period ω for all three models. The standard deviation for these realizations is large since the neighbourhood size Q is approximately 10. However, the mean value of R varies within certain parameter regimes, as described below.

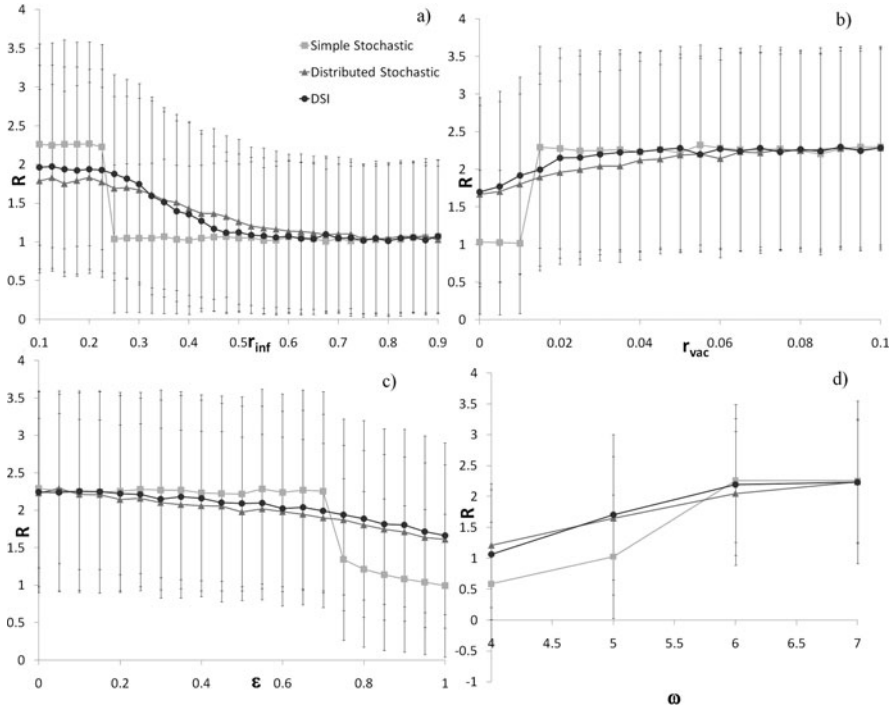


Fig. 2 Mean and $+/-$ the standard deviation of values of R versus r_{inf}, r_{vac}, ε, ω with all other parameter values fixed at values in Table 1. "DSI" indicates the distributed stochastic model with imitation

3.1 Simple Stochastic Model

In the simple stochastic model, all individuals make the same decision: all individuals either vaccinate or do not vaccinate at a given set of parameter values, because the payoff function and its constituent parameter values are the same for all contacts of the index case. Hence, the value of R can change suddenly as certain threshold parameter values are surpassed (Fig. 2). For instance, for low infection risk, none of the contacts of the index case vaccinate since $P_V < P_N$, and thus the average value of R is 2.3. However, for the cost of infection $r_{\text{inf}} > 0.25$, $P_V > P_N$, all of the contacts vaccinate and the mean value of R becomes approximately 1 (Fig. 2a). A similar effect appears in the plot of R versus r_{vac}, cost of vaccination, (Fig. 2b) and ε, vaccine efficacy, (Fig. 2c). The mean value of R is constant on either side of these thresholds for the plots of mean R versus r_{inf} and r_{vac} because these parameters influence vaccinating behaviour but not the probability that a susceptible or vaccinated person becomes infected. However, the mean value of R declines with increasing ε beyond the threshold in ε because beyond this threshold, all contacts vaccinate, and ring vaccination is more successful at higher vaccine efficacy.

Although a threshold is not observed in the plot of mean R versus the incubation period ω at the parameter values tested, the mean value of R increases as ω increases because contacts are exposed to infection for a longer period before symptoms appear in the index case, giving contacts the first opportunity to vaccinate (Fig. 2d).

The deterministic predictions from (2) in the case of no vaccination and (8) in the case of vaccination agree with the mean values of the realizations of the simple stochastic case (results not shown).

3.2 Distributed Stochastic Model

In the distributed stochastic model, each individual is assigned a parameter value for: time to protective immunity λ, latent period σ, infectious period δ, incubation period ω, vaccine efficacy ε, cost of vaccination r_{vac}, cost of infection r_{inf}, and transmission probability p. The values are drawn from a lognormal distribution with the same mean value as in the simple stochastic model (see values in Table 1). The distributed stochastic model is otherwise identical to the simple stochastic model. The resulting mean value of R is plotted against the mean parameter values for $r_{\text{inf}}, r_{\text{vac}}, \varepsilon$, and ω from the lognormal distribution (Fig. 2). The model predictions are qualitatively different from the simple stochastic model. Primarily, the thresholds in $r_{\text{vac}}, r_{\text{inf}}$, and ε appear to be "smeared out" relative to the simple stochastic model, because heterogeneity in the sampled parameter values means that the payoff functions for individuals are also variable. Therefore, in general there is no parameter value for which either $P_V > P_N$ or $P_V < P_N$ is true for all individuals. In general, for any given mean parameter value, $P_V > P_N$ will hold for some individuals and $P_V < P_N$ will hold for others. However, as the mean parameter values change, so does the mean behaviour: the mean value of R increases for increasing r_{vac} and ω, because vaccination becomes less favourable as the perceived vaccine risk and the incubation period increase (Fig. 2b, d). In contrast, the mean value of R decreases for increasing r_{inf} and ε, because vaccination becomes more favourable as the disease risk and vaccine efficacy increase.

3.3 Distributed Stochastic Model with Imitation

In the imitation model, individuals consider both their own values of P_V and P_N as well as the inclination of other contacts (as measured by whether $P_V > P_N$ or $P_V < P_N$) in making their decision about whether or not to vaccinate, as specified in (10). We use the stepwise functional form for $g(V)$ for our analyses, except where noted otherwise, because the impact of imitation is most clear with this functional form.

In the presence of imitation, the mean value of R (the average number of secondary infections) appears to be roughly the same as the mean value of R in the distributed stochastic model without imitation, for a broad range of parameters**,** including the lack of a threshold (Fig. 2). Moreover, the mean value of R does not change across a wide range of values of the imitation strength κ, under three different functional forms for the function $g(V)$ (Fig. 3). We attribute this to the fact that imitation does not have a bias: individuals tend to imitate whichever strategy appears to be favoured.

However, if we examine how the values of R are distributed across the stochastic realizations, some interesting differences emerge. The distribution of R, and also of the number of individuals are who vaccinated, changes as the imitation strength κ

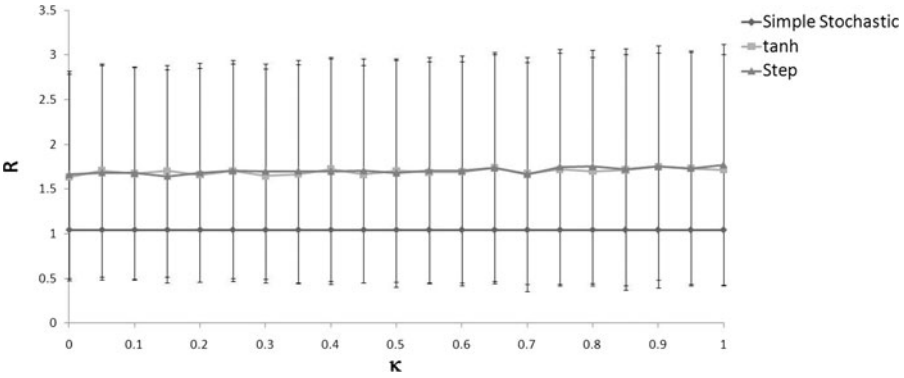


Fig. 3 Mean and $+/-$ the standard deviation of values of R versus imitation strength κ for three different functional forms for $g(V)$, with all of the other parameter values fixed at values in Table 1

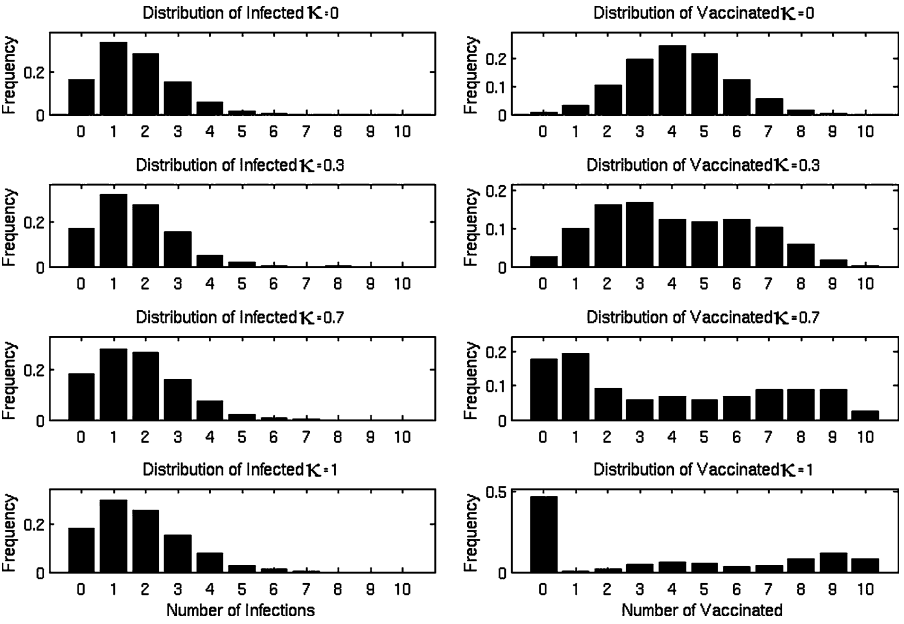


Fig. 4 The distribution of the number of secondary infections (*left*) and number of vaccinators (*right*) for the case of $Q = 10$ neighbours for different values of imitation strength κ and other parameter values as in Table 1

increases (Fig. 4). For low values of κ, both distributions are unimodal and clustered around the same mean value as for the distributed stochastic model without imitation. However, as κ increases, the distribution of the number of vaccinated individuals becomes bimodal: for some parameter sets, vaccination is the favoured strategy in terms of what the payoff functions indicate for most individuals, and thus a strong majority of contacts opt for vaccination; for other parameter sets, non-vaccination is the favoured strategy and most contacts refuse vaccination (even those for whom the

payoff to vaccinate exceeds the payoff not to vaccinate). This bimodal effect occurs at parameter values such that, on average, neither vaccination nor non-vaccination are favoured by a strong majority of contacts. (We note that the special case $\kappa = 0$ recovers the case of the distributed stochastic model without imitation, and simulations of the distributed stochastic model without imitation at the same parameter values fail to show bimodality (results not shown).)

Interestingly, at the same parameter values where the number of contacts who vaccinate is bimodal, the distribution of secondary infections appears to remain relatively unimodal (Fig. 4). This is partly because imitation has larger impact on the first order effect of distribution of vaccinators than on the second order effect of the distribution of secondary infections. However, this is also because a relatively low number of contacts ($Q = 10$) does not provide sufficient resolution to distinguish two close peaks. Indeed, when the number of neighbours is increased to $Q = 100$ and parameter values are otherwise unchanged, clear bimodality in the distribution of secondary infections emerges as κ increases (Fig. 5, $p = 0.05$ results). Bimodality in the number of vaccinators remains dominant (in fact, with some appearance of trimodality) (Fig. 5, $p = 0.05$ results). The stronger unimodality in the distribution of the number of secondary infections compared to the distribution of the number of vaccinators also explains why the variance in the average number of secondary infections R is so similar for the distributed stochastic models with and without imitation (Fig. 2), despite the fact that the parameter ranges covered in Fig. 2 include baseline parameter values where the number of vaccinators is known to be bimodal for the model with imitation.

For all values of the imitation strength κ, the peaks in the distribution of secondary infections shift to higher values (i.e., more simulations with a large number of secondary infections) when the transmission p is increased from the baseline value $p = 0.05$ to a higher rate $p = 0.2$ (Fig. 5). This effect is not surprising because a higher transmission rate implies a greater number of secondary transmissions, even when vaccination is taken up and provides some reduction in secondary cases. However, what is more interesting is that the relative magnitude of the two peaks in the distribution of number vaccinated changes as p is increased: when $p = 0.05$ most individuals do not vaccinate, whereas when $p = 0.2$, most of them do (i.e., the relative size of the two peaks in the distribution of vaccinators is switched in the case for $p = 0.05$ compared to $p = 0.2$). An increase in p increases the probability of eventually becoming infected and thus experiencing disease penalties, hence vaccination becomes attractive for higher p, at least at these parameter values. This switch is again observed in the distribution of the number of secondary infections: when $p = 0.05$, the peak corresponding to more secondary infections (i.e., less vaccination) is larger, indicating that in most realizations, the majority of contacts do not vaccinate and the number of secondary infections increases. By comparison when $p = 0.2$, the peak corresponding to fewer secondary infections (i.e., more vaccination) is larger, indicating that in most realizations, the majority of contacts vaccinate.

As noted above, we used a step function to represent our imitation function $g(V)$ in the case of distributed stochasticity with imitation (Figs. 4–5). However , we also explored these results for a hyperbolic tangent function (results not shown) and found that instead of obtaining a bimodal distribution, we obtained a distribution that resembled a skewed normal distribution. This effect occurs because for most parameter

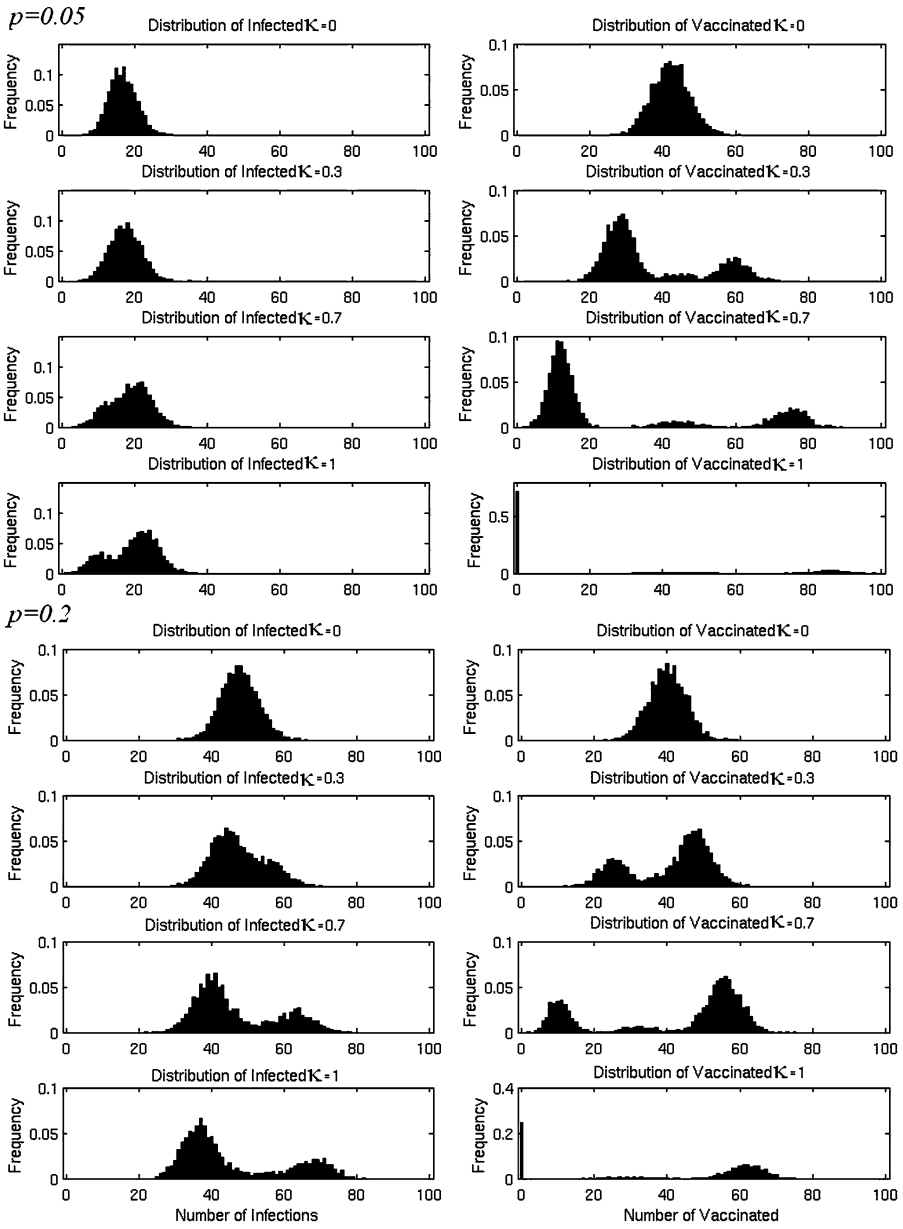


Fig. 5 The distribution of the number of secondary infections (*left*) and number of vaccinators (*right*) for the case of $Q = 100$ neighbours for different values of imitation strength κ and other parameter values as in Table 1

values, the switch between favouring vaccination versus favouring non-vaccination is much sharper at the origin for the step function than for *tanh* under most parameter choices.

These results imply a fully-connected network where each contact of the index case is connected to—and exchanges information with—every other contact of the index case. To understand the impact of this assumption, we also explored the semi-connected case where individuals can only imitate the nearest plus or minus n neighbours in the ring. The introduction of semi-connectedness can change the results significantly for certain values of connectedness. For the special case of no connectedness ($n = 0$), the case of the distribution stochastic model without imitation is recovered and distributions are unimodal (results not shown). For $n = 3$, there was likewise little impact and the distributions remained unimodal (results not shown). For cases of intermediate connectedness ($n = 12$ and $n = 25$), the results change significantly (Fig. 6). The distribution of the number of vaccinators is no longer bimodal but becomes a highly skewed unimodal distribution with a high variance. The variance increases as the strength of imitation κ increases. This spreading effect occurs because in the semi-connected case, individuals are sampling a small proportion of the total number of contacts of the index case and, therefore, the average attractiveness of vaccinating versus not vaccinating is more highly variable than in the fully connected case, giving rise to greater variation in the level of vaccine adherence overall. Although the bimodality disappears, the greater variance still supports the conclusion that adding imitation can increase the variability in the predicted vaccine adherence, relative to the case of the distribution stochastic model without imitation. For the case $n = 50$, the fully-connected case is recovered, including bimodality (results not shown).

The emergence of bimodality occurs for parameter sets such that the payoff to vaccinate is close to the payoff not to vaccinate. In such situations, individual variability in model parameters means that for some stochastic realizations, the payoff to vaccinate will be higher for the majority of contacts and hence vaccination tends to dominate. For other stochastic realizations, however, the payoff not to vaccinate will be higher and hence non-vaccination will dominate for the same mean parameter values. Moving away from this parameter regime sufficiently far means that either vaccination or non-vaccination will be favoured for all stochastic realizations, and imitation will only strengthen this tendency. This should cause a unimodal distribution of the number of secondary infections and the number of vaccinators.

This effect is seen in the distribution of secondary infections (Fig. 7) and vaccinators (Fig. 8) for a range of possible values for eight of the model parameters: $\lambda, \varepsilon, \omega, r_{\text{vac}}, \delta, \sigma, p, r_{\text{inf}}$. For most parameters, moving away from the baseline values collapses, the bimodal distribution function into a unimodal function that represents either dominant vaccination or dominant non-vaccination, depending on whether there has been an increase or a decrease relative to the baseline parameter value (Figs. 7 and 8). For instance, increasing the cost of vaccination r_{vac} above the baseline value makes vaccination unattractive, collapsing the bimodal distribution to a unimodal distribution that represents dominant non-vaccination behaviour. In contrast, decreasing r_{vac} below the baseline value creates a unimodal distribution representing dominant vaccinating behaviour. However, for the transmission probability

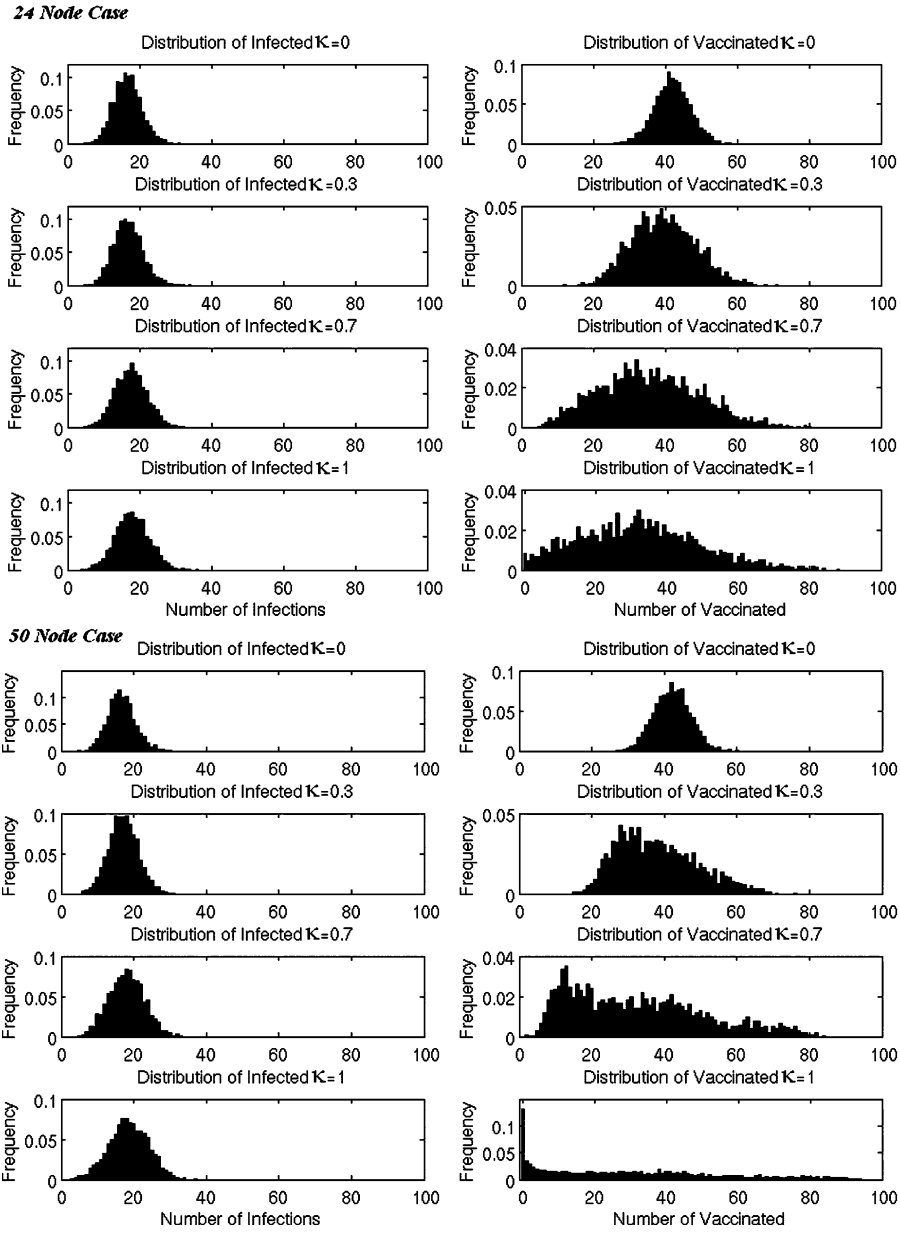


Fig. 6 The distribution of the number of secondary infections (*left*) and number of vaccinators (*right*) for the case of $Q = 100$ neighbours, who are imitating n neighbours to the *right* and n neighbours to the *left*, for different values of imitation strength κ and other parameter values as in Table 1. The values of n are $n = 24$ (*top half of panels*) and $n = 50$ (*bottom half of panels*)

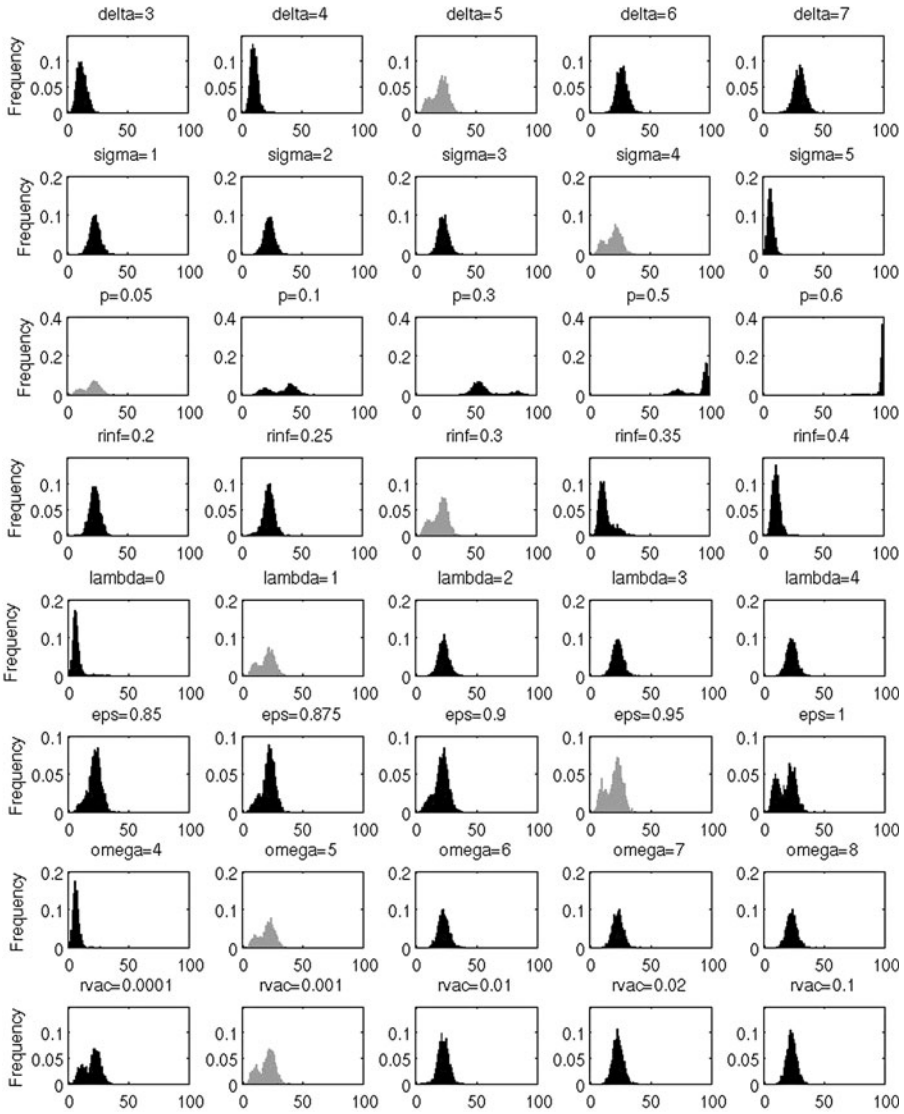


Fig. 7 The distribution of the infected individuals under full imitation for the case of $Q = 100$ for the parameters $\lambda, \varepsilon, \omega, r_{\text{vac}}, r_{\text{inf}}, p, \sigma, \delta$. The baseline parameter values are used to generate the gray distributions and black distributions represent variations from baseline

p, the distribution remains bimodal across a broad range of parameter values before collapsing to a unimodal distribution. This is because p appears in both the payoff to vaccinate and the payoff not to vaccinate ((5) and (6)). Increasing p decreases both payoffs because the individual is more likely to get infected for higher values of p, thus the relative size of P_V versus P_N does not change as much. Therefore, the distribution of secondary infections and vaccinators remains bimodal for a range of values of p.

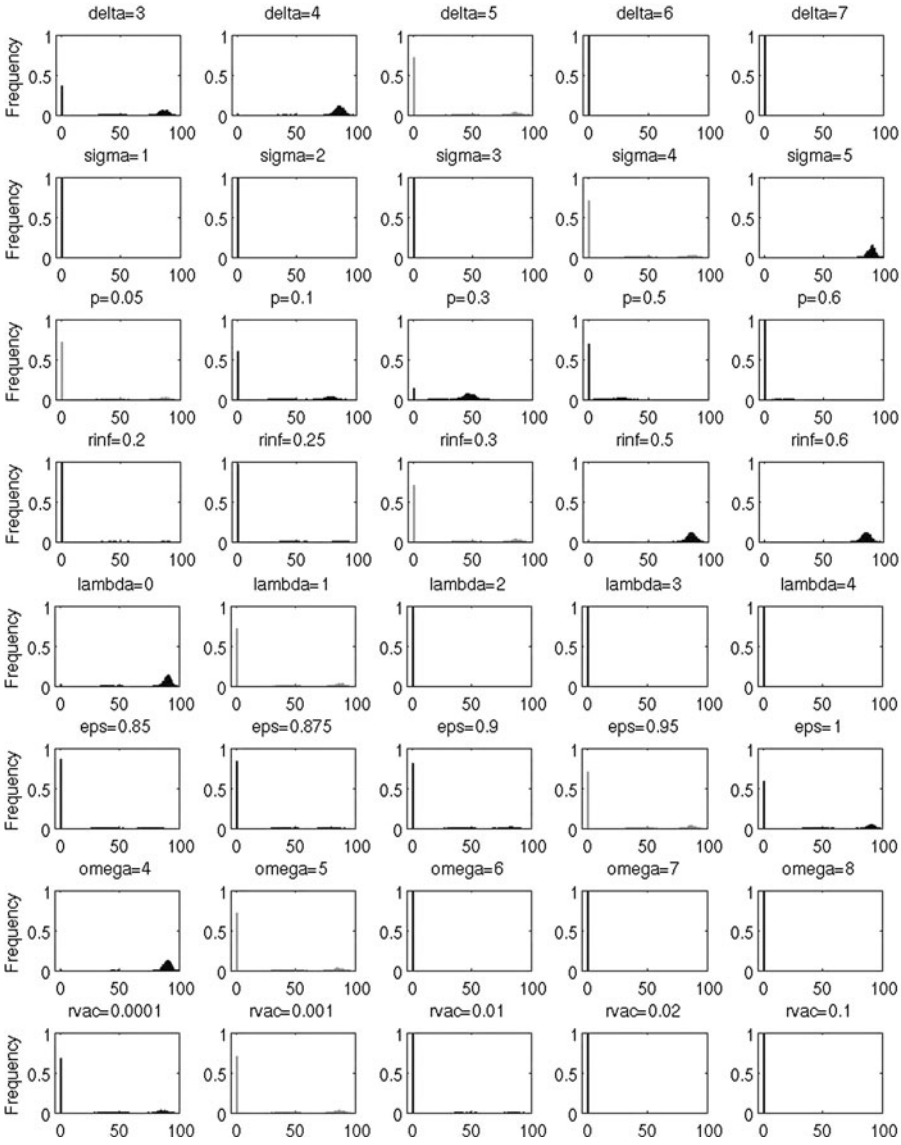


Fig. 8 The distribution of the vaccinated individuals under full imitation for the case of $Q = 100$ for the parameters $\lambda, \varepsilon, \omega, r_{\text{vac}}, r_{\text{inf}}, p, \sigma, \delta$. The baseline parameter values are used to generate the gray distributions and black distributions represent variations from baseline

4 Discussion

In this paper, we developed three models of ring vaccination where individual contacts of the index case choose whether or not to vaccinate according to payoffs for vaccinating versus not vaccinating. These payoffs depend on disease and vaccine risks. We considered a simple stochastic model that permitted us to derive expres-

sions for the probability of no secondary cases P_{control} and the expected number of secondary infections R. In the distributed stochastic model, we also developed an extension where the parameter values constituting the payoff functions were sampled from a lognormal distribution for each individual, resulting in heterogeneous payoff functions. This was further extended in the distributed stochastic model with imitation, where the individual vaccine decision-making process was partly determined by imitating the vaccinating decisions to which the majority of contacts are inclined.

In the simple stochastic model, all contacts are assigned the same parameter values, and hence all contacts either vaccinate or do not vaccinate depending on the parameter values that influence the payoff functions. As a result, there are threshold parameter values at which all contacts of the index case switch from vaccinator to non-vaccinator or vice versa. The effect of sampling parameter values from lognormal distributions for each individual (i.e., the distributed stochastic model) is to moderate this effect and remove the thresholds, since each individual can have a different payoff. Consequently, mixed outcomes are possible where some contacts vaccinate and some do not. Adding imitation to the model has little effect on the mean and variability of the number of secondary infections at the parameter values tested. However, even when the mean and variability do not change very much, the distribution of the number of secondary infections and number of vaccinators can become bimodal at certain parameter values when imitation is strong (for the assumption of fully connected contacts of the index case). This occurs because individuals adopt whichever strategy appears to be favourable to the majority. For some stochastic realizations the apparently favourable strategy is vaccinating, whereas for others it is not vaccinating. The consequence is that ring vaccination can be highly successful under some realizations (when imitation causes most contacts to vaccinate), but can completely fail under other realizations of the same parameter values (when imitation causes most contacts not to vaccinate), resulting in failure to contain the outbreak. This occurs despite the average outcome being the same as for the model without imitation. If the contacts are semi-connected instead of fully connected, the distribution of the number of vaccinators is no longer bimodal but it remains very broad, with many possible outcomes for the same mean parameter values.

Previous work has analyzed how the predictions of models that include stochastic effects or contact structure differ qualitatively from the predictions of models that do not include such effects (Lloyd-Smith et al. 2005; Meyers et al. 2005). Similarly, it has been shown how opinion formation in social networks can lead to pockets of susceptibility, ensuring the persistence of infection despite high vaccine coverage even when homogeneous mixing models predict that the infection should already be eliminated (Salathe and Bonhoeffer 2008). Here, we have shown how imitation behaviours can exacerbate such differences in situations where ring vaccination is employed, by making the contacts of an index tend to behave in similar ways. As a result, there is a parameter regime where, for approximately the same input parameter values, vaccinating is a dominant strategy in some realizations and non-vaccinating is a dominant strategy in others. Even for parameter regimes where either vaccinating or non-vaccinating is always favoured, imitation has the role of ensuring greater homogeneity in vaccination decisions than would occur under purely rational behaviour.

Given that social contact networks tend to be highly clustered, especially for close contact infections, the contacts of an index case are likely to know one another. Moreover, imitating the decisions of others in one's peer group is often an important factor in vaccine decision-making (Merrill et al. 1958; Dempsey et al. 2006). Therefore the results of our model suggest that imitation effects may have an important additional role in determining the success or failure of ring vaccination strategies for many infectious diseases where vaccination is voluntary or where a mandatory policy is not enforceable.

Network models are a natural way to describe infection transmission through a social contact network and the effects of ring vaccination, although they tend to be difficult to analyze (Perisic and Bauch 2009a, 2009b). Here, we opted for a simpler approach that did not model the full network but rather just the contacts of the index case. This model has the advantage of being much easier to analyze than network models; it has the disadvantage of not capturing the full network—this is relevant to imitation processes in ring vaccination since contacts of the index case may imitate individuals who are not contacts of the index case. One rationale for only modelling the contacts of the immediate case is that if ring vaccination fails for the contacts of a single index case, it will likely fail in more complex situations where the infection has already started to spread through the social contact network. However, this may not be the case in clustered networks where the possibility of containment is determined not only by edge-wise transmissibility but also by the structure of the emerging cluster of infections (Keeling 1999; Bauch 2005). Thus, an important limitation of our model is that it does not describe the links between contacts of the index case. We also did not capture changes in the contact structure in response to the appearance of symptoms in the index case (Zanette and Gusman 2008) or other interventions such as antiviral drugs.

Mathematical models have often suggested that early intervention is valuable for controlling an outbreak, because the effectiveness of early intervention is disproportionately higher than the impact of later intervention (Moghadas et al. 2008; Zivkovic Gojovic et al. 2009; Ferguson et al. 2005). Typically, these models have considered interventions such as vaccination, contact precautions, and antiviral drugs and have implicitly assumed that the uptake of these interventions can be set at any level desired. Our model shows that the success of containment through ring vaccination can be highly variable in cases where the uptake cannot be guaranteed by the public health authorities, such as when the contacts of the index case are free to choose whether or not to vaccinate and in cases where contacts also tend to be influenced by the vaccination decisions of other contacts. Under some circumstances, these imitation processes can lead to a failure of ring vaccination. Therefore, early action to counter the possible emergence of vaccine exemption in epidemiologically important peer groups during an outbreak may be warranted. Our findings suggests that risk communication should also be thought of as an important public health intervention during a disease outbreak and that it should be likewise be applied in a timely fashion at the start of an outbreak.

Acknowledgements C.R.W. was supported by an Ontario Graduate Scholarship in Science and Technology scholarship.

C.T.B. was supported by a Discovery Grant from the Natural Sciences and Engineering Research Council of Canada.

A.P.G. and L.A.M. were supported by NIH MIDAS grant 5U01GM087719.

J.M.T. was supported through a postdoctoral appointment funded by a grant from the Ontario Ministry of Research and Innovation awarded to CTB.

Appendix A: Derivation of the Payoff Functions

Let Q be the number of neighbours and ε the vaccine efficacy. We want to derive conservative estimate for outbreak control.

Let q_i be the probability of not infecting neighbour i during the infectious period, q_{tot} the probability of not infecting any neighbour. Thus, the probability of not infecting anyone is

$$q_{\text{tot}} = \prod_{i=1}^{Q} q_i = q_1 \cdot q_2 \cdot q_3 \cdots q_Q.$$

For identical neighbours, $q_{\text{tot}} = q^Q$. Let $q_{i,j}$ be the probability of no transmission to neighbour i on day j. Thus,

$$q_i = q_{i,1} \cdot q_{i,2} \cdot q_{i,3} \cdots q_{i,\delta} = \prod_{k=1}^{\delta} q_{i,k},$$

where $\delta$is the duration of infection in days (integer). So, what is $q_{i,j}$?

Let τ be the time required for vaccine to mount a protective immune response, and $\delta$the duration of infection. If $\tau > \delta$, then, assume no one will vaccinate. On the contrary if $\tau < \delta$, then some or all would vaccinate.

B1: *Case where* $\tau > \delta$

Under assumption of identical neighbours, $q_{i,j} = 1 - p$ where p is the *per day* transmission probability. So,

$$q_i = q_{i,1} \cdot q_{i,2} \cdot q_{i,3} \cdots = (1-p)^\delta = q \Rightarrow q_{\text{tot}} = q_1 \cdot q_2 \cdot q_3 \cdots q_Q = q^Q = (1-p)^{\delta Q}.$$

B1: *Case where* $\tau < \delta$

In this case, some may vaccinate since the vaccine may protect before the individual is infected by the index case. Let

$P_V(t)$ be the payoff to vaccinate on day t where $t = 1$ is the day that the index case is infectious and starts showing symptoms.
P_N is the payoff not to vaccinate at all.
r_{vacc} the penalty to vaccinate, i.e., the risk of adverse events.
r_{inf} the penalty due to being infected, i.e., the disease complication risk.
L is the payoff before penalties, i.e., the number of life years if never vaccinated and never infected.

Assume

$$P_V(1) < P_N \quad \Rightarrow \quad P_V(t) \begin{cases} P_V(t) < P_V(1), \\ P_V(t) < P_N(t), \end{cases} \quad \forall t.$$

Since a person who waits several days to vaccinate accepts the same vaccine penalty as the individual who immediately vaccinates, $P_V(1)$, say, but also accepts a greater probability of infection since the individual may be infected during the time the individual waited (waiting time), the two possible outcomes are:

$P_V(1) < P_N \quad \Rightarrow$ never vaccinate (same q_{tot} as in the case B1 above).

$P_V(1) > P_N \quad \Rightarrow$ vaccinate as soon as a neighbour exhibits symptoms. But what are the explicit expressions for $P_V(1)$ and P_N?

Now let $\rho(t)$ be the probability of infection on day t (and not before), p the transmission probability per day. Thus,

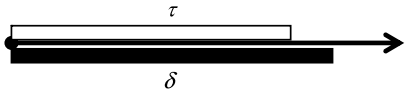
$$\begin{aligned} P_N &= \rho(1)(L - r_{\text{inf}}) + \rho(2)(L - r_{\text{inf}}) + \cdots + \rho(\delta)(L - r_{\text{inf}}) \\ &\quad + \big(1 - \rho(1) - \rho(2) - \cdots - \rho(\delta)\big)L \\ &= p(L - r_{\text{inf}})\big\{1 + (1-p) + (1-P)^2 + \cdots + (1-p)^{\delta-1}\big\} \\ &\quad + L\big\{1 - p\big[1 + (1-p) + \cdots + (1-p)^{\delta-1}\big]\big\}. \end{aligned}$$

Using Taylor series expansion of the functions $\frac{1}{1-x}$, we have $\frac{1-x^n}{1-x} = 1 + x + x^2 + \cdots + x^{n-1}$. Therefore, the above expression for P_N simplifies to

$$P_N = (L - r_{\text{inf}})\big[1 - (1-p)^{\delta}\big] + L(1-p)^{\delta}. \tag{11}$$

A.1 Payoff to Vaccinate Immediately

This involves the following scenarios: $t < \tau$, $t > \tau$ but vaccine failed ($t < \delta$), $t > \tau$ and vaccine worked and $t > \delta$ (not infected).



$$\begin{aligned} P_V(1) &= \big[\rho(1) + \rho(2) + \cdots + \rho(\tau)\big](L - r_{\text{vac}} - r_{\text{inf}}) \quad t < \tau \\ &\quad + (L - r_{\text{vac}} - r_{\text{inf}})(1-\varepsilon)\big[\rho(\tau+1) + \rho(\tau+2) + \cdots + \rho(\delta)\big] \quad t > \tau \end{aligned}$$

but vaccine failed ($t < \delta$)

$$\begin{aligned} &+ \varepsilon(L - r_{\text{vac}})\big[\rho(\tau+1) + \rho(\tau+2) + \cdots + \rho(\delta)\big] \quad t > \tau \text{ and vaccine worked} \\ &+ (L - r_{\text{vac}})\big[1 - \rho(1) - \rho(2) - \cdots - \rho(\delta)\big] \quad t > \delta \text{ (not infected)} \\ &= +(L - r_{\text{vac}} - r_{\text{inf}})\big[p + p(1-p) + p(1-p)^2 + \cdots + p(1-p)^{\tau-1}\big] \end{aligned}$$

$$+ (L - r_{\text{vac}} - r_{\text{inf}})(1-\varepsilon)\big[p(1-p)^{\tau} + p(1-p)^{\tau+1} + \cdots + p(1-p)^{\delta-1}\big]$$
$$+ \varepsilon(L - r_{\text{vac}})\big[p(1-p)^{\tau} + p(1-p)^{\tau+1} + \cdots + p(1-p)^{\delta-1}\big]$$
$$+ (L - r_{\text{vac}})\big[1 - p - p(1-p) - p(1-p)^2 - \cdots - p(1-p)^{\delta-1}\big].$$

The terms in the square brackets are geometric series and can simply be written as

$$P_V(1) = (L - r_{\text{vac}} - r_{\text{inf}})\big\{\big[1-(1-p)^{\tau-1}\big] + (1-\varepsilon)(1-p)^{\tau}\big[1-(1-p)^{\delta-\tau-1}\big]\big\}$$
$$+ (L - r_{\text{vac}})\big\{\varepsilon(1-p)^{\tau}\big[1-(1-p)^{\delta-\tau-1}\big] + \big[1-\big(1-(1-p)^{\delta-1}\big)\big]\big\}.$$

After some rearrangements, we have

$$P_V(1) = (L - r_{\text{vac}} - r_{\text{inf}})\big\{\big[1-(1-p)^{\tau-1}\big] + (1-\varepsilon)(1-p)^{\tau}\big[1-(1-p)^{\delta-\tau-1}\big]\big\}$$
$$+ (L - r_{\text{vac}})\big\{\varepsilon(1-p)^{\tau}\big[1-(1-p)^{\delta-\tau-1}\big] + (1-p)^{\delta-1}\big\}. \tag{12}$$

Therefore, the two subclasses under B1 are:

C1: Case where $P_V(1) < P_N$ with payoffs $P_V(1)$ and P_N given by (11) and (12).

$$q_{\text{tot}} = (1-p)^{\delta Q}.$$

C2: Case where $P_V(1) > P_N$. Hence, individuals vaccinate immediately. Thus, $q_{i,j} \equiv \widetilde{q}_j$ under assumption of identical neighbours, where $\widetilde{q}_1$is the probability of no transmission on day 1, that is, $\widetilde{q}_j = 1 - p$. Similarly,

$$\widetilde{q}_2 = 1 - p,$$
$$\vdots$$
$$\widetilde{q}_{\tau-1} = 1 - p \quad \text{(probability of no transmission on day } \tau - 1),$$
$$\widetilde{q}_{\tau} = 1 - p(1-\varepsilon),$$
$$\widetilde{q}_{\tau+1} = 1 - p(1-\varepsilon),$$
$$\vdots$$
$$\widetilde{q}_{\delta-1} = 1 - p(1-\varepsilon),$$
$$\widetilde{q}_{\delta} = 1 - p(1-\varepsilon).$$

Therefore, $\widetilde{q}_{\text{tot}} = \widetilde{q}^{Q}$ where $\widetilde{q}$ is the probability that the neighbour never gets infected. Thus,

$$\widetilde{q} = \widetilde{q}_1 \cdot \widetilde{q}_2 \cdots \widetilde{q}_{\delta} = (1-p)^{\tau-1}\big[1-p(1-\varepsilon)\big]^{\delta-\tau+1}.$$

Thus,

$$\widetilde{q}_{\text{tot}} = \big\{(1-p)^{\tau-1}\big[1-p(1-\varepsilon)\big]^{\delta-\tau+1}\big\}^{Q}.$$

A.2 Summary OR Results

B1: $\tau > \delta$, no one vaccinates, $q_{\text{tot}} = (1-p)^{\delta Q}$ (probability of no secondary transmission)
B2: $\tau < \delta$, some may vaccinate
- *Subcase* C1: $P_V(1) \leq P_N$, no one vaccinates and $q_{\text{tot}} = (1-p)^{\delta Q}$.
- *Subcase* C2: $P_V(1) > P_N$, all neighbours vaccinate, $\widetilde{q}_{\text{tot}} = \{(1-p)^{\tau-1}[1-p(1-\varepsilon)]^{\delta-\tau+1}\}^{Q}$.

D: $\varepsilon = 1$, then

$$P_V(1) = (L - r_{\text{vac}} - r_{\text{inf}})\left[1-(1-p)^{\tau-1}\right] + (L - r_{\text{vac}})(1-p)^{\tau},$$
$$P_N = (L - r_{\text{inf}})\left[1-(1-p)^{\delta}\right] + L(1-p)^{\delta}.$$

E: $r_{\text{vac}} \ll r_{\text{inf}} \Rightarrow L - r_{\text{vac}} - r_{\text{inf}} \cong L - r_{\text{inf}}$ and $L - r_{\text{vac}} \cong L$. Thus,

$$P_V(1) = (L - r_{\text{inf}})\left[1-(1-p)^{\tau-1}\right] + L(1-p)^{\tau} \quad \text{and}$$
$$P_N = (L - r_{\text{inf}})\left[1-(1-p)^{\delta}\right] + L(1-p)^{\delta}.$$

A.3 Generalization

Let ω be the incubation period, τ the time required for the vaccine to provide protection, σ the latent period and $\delta$the infectious period.

Case 1: $\omega < \sigma$ this is not biologically relevant.
Case 2: $\omega \geq \sigma$.
Scenario 1: $\tau + \omega > \delta + \sigma \Rightarrow$ no one vaccinates and

$$q_{\text{tot}} = (1-p)^{\delta Q}$$

Scenario 2: $\tau + \omega < \delta + \sigma$
- $P_V(1) \leq P_N$, no one vaccinates, thus, $q_{\text{tot}} = (1-p)^{\delta Q}$.
- $P_V(1) > P_N$ all neighbours vaccinate

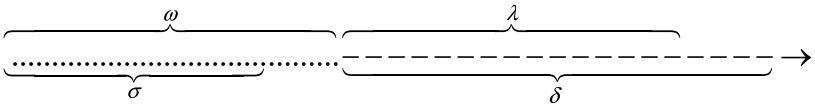
$$\widetilde{q}_{\text{tot}} = \Big\{ \underbrace{(1-p)^{\tau+(\omega-\sigma)}}_{\substack{\text{No infection before vaccine}\\ \text{starts to work}}} \underbrace{[1-p(1-\varepsilon)]^{\delta+\sigma-(\omega+\tau)}}_{\substack{\text{No infection after vaccine}\\ \text{should have started to work}}} \Big\}^{Q},$$

$$P_N = \underbrace{(L - r_{\text{inf}})\left[1-(1-p)^{\delta}\right]}_{\text{Infected}} + \underbrace{L(1-p)^{\delta}}_{\text{Not infected}},$$

$P_V(1)$ is the payoff to vaccinate as soon as index case symptoms show,

$$
\begin{aligned}
P_V(1) = (L - r_{\text{vac}} - r_{\text{inf}})\Big\{ & \underbrace{1 - (1-p)^{\tau+\omega-\sigma}}_{a} \\
& + \underbrace{(1-\varepsilon)(1-p)^{\tau+\omega-\sigma}\left[1 - (1-p)^{\delta+\sigma-\omega-\tau}\right]}_{b}\Big\} \\
& + (L - r_{\text{vac}})\Big\{\underbrace{\varepsilon(1-p)^{\tau}\left[1 - (1-p)^{\delta-\tau-1}\right]}_{c} + \underbrace{(1-p)^{\delta-1}}_{d}\Big\}.
\end{aligned}
$$

(a) Those infected before vaccine could start working.
(b) Those infected after vaccine started working plus infected due to ineffective dose.
(c) Those infected after vaccine started working plus not infected due effective dose.
(d) Those never infected.



Appendix B: Simulation algorithm

In the simulation, the following algorithm was used for each day

1. Determine if it is the first day that symptoms show in the index case. If it is the first day that symptoms show and $P_V > P_N$ (where P_V and P_N comes from (5) and (6)), then all contacts of the index case will vaccinate.
2. To determine which contacts are successfully vaccinated one samples Q random numbers between 0 and 1. The individuals for whom the random sample is less than or equal to ε are considered to have been successfully vaccinated (although it will still require a time λ before they are protected).
3. Determine if the index case is still infectious. If so, then determine which susceptible individuals are infected. Sampling random numbers from 0 to 1 for each susceptible individual, the individuals whose sample is less than or equal to p become infected.

Steps 1 and 2 are repeated until either the maximum simulation time is exceeded or the infectious period of the index case ends. After each day, individual states are updated as well as the counter for days remaining in each state. The natural history assumptions are as given in the first part of this subsection: individuals who have been vaccinated but are not yet immune remain fully susceptible to infection because the vaccine has yet to take full effect; when a susceptible contact becomes infected they enter the latent stage. Recall that payoffs are such that vaccination can only occur once for each individual, on the first day that symptoms appear in the index case.

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