Technical appendix

We constructed a simple Susceptible-Infectious-Removed model of a respiratory viral disease, as in (1). The model was subdivided into two connected sub-populations: vaccinated individuals and unvaccinated individuals. A schematic "stock and flow" diagram of the model is presented below. The model is a closed system without births or deaths. Individuals are susceptible (S), infectious (I) or immune (R), and are assigned to a vaccinated or unvaccinated subpopulation, denoted by subscript "v" or "u", respectively. Subpopulation sizes are denoted N. Force of infection is defined by mixing within and between groups under varying assumptions about assortativity. Here β represents the product of contact rate in a group times infection probability following effective contact. The fraction of contacts among individuals in the ith group (e.g., vaccinated or unvaccinated), with those in the jth group is denoted f_{ij}. The rate of recovery is denoted γ. The model assumes durable immunity.
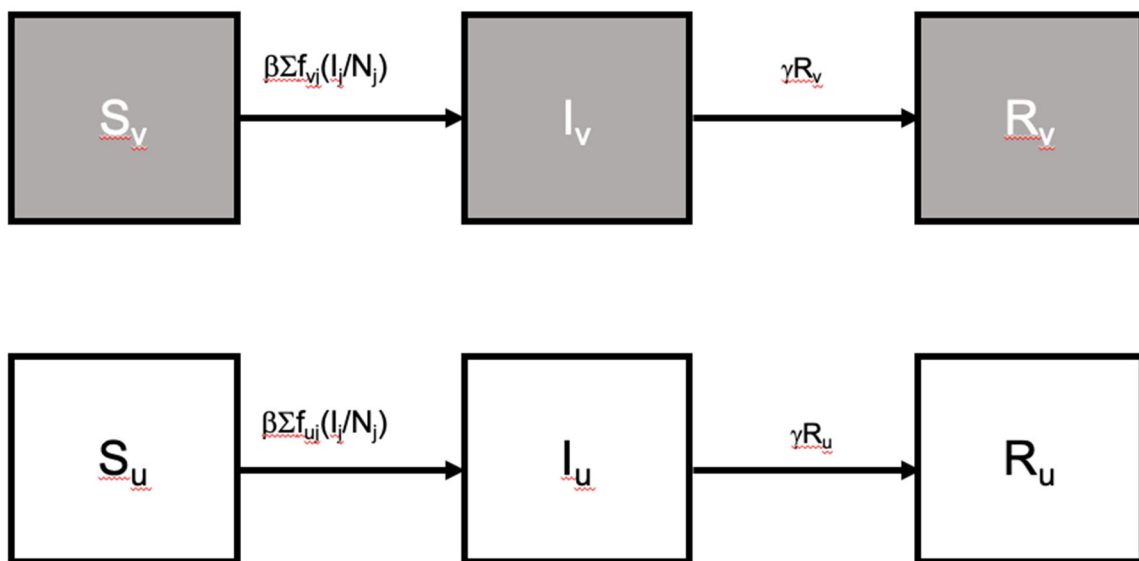
The model is governed by the following ordinary differential equations, where i represents the vaccination status of the group, and j represents vaccination status of contacts.

$$dS_i/dt = -\beta\Sigma f_{ij}(I_j/N_j) \tag{1}$$

$$dI_i/dt = \beta\Sigma f_{ij}(I_j/N_j) - \gamma I_i \tag{2}$$

$$dR_i/dt = \gamma I_i \tag{3}$$

Here β represents the product of contacts per unit time and probability of transmission per contact, which is considered equivalent in vaccinated and unvaccinated individuals, and estimated as R_o/D, where D is the duration of infectivity and R_o is the basic reproduction number. In order to capture non-random mixing between vaccinated and unvaccinated sub-populations, we modeled frequency-dependent transmission, with assortativity modeled using the approach described by Garnett and Anderson (2), which is based on earlier work by Blower and McLean (3), and Gupta et al. (4), and which Blower and McLean refer to as "process models", to denote the preference inherent in this approach.

Under an assumption of random mixing, the probability of interactions between individuals in different population groups are proportionate to the product of group sizes; if 10% of the population is unvaccinated, under an assumption of random mixing, we would expect 1% of all interactions in the population to involve contacts between unvaccinated individuals (i.e., 0.10 x 0.10 = 0.01). By contrast, we could construct a mixing matrix to describe complete assortativity, in which individuals only interacted with those within their own group; the trace of such a matrix would sum to 1, while the anti-trace would have a sum of zero, as there are no interactions with individuals from other groups. To refer to the example above, under complete assortativity, 10% of all interactions would be interactions of unvaccinated individuals with other unvaccinated individuals, and 90% of interactions would be between vaccinated

individuals. The trace of this matrix (which is an identity matrix) would sum to 1 (i.e., 0.9 + 0.1 = 1).

The method described by Garnett and Anderson takes complete assortativity as a starting point, such that the probability of contact between individuals in different groups is represented by the trace of the identity matrix, and the fraction of interactions that occur within the ith group would simply be the fraction of individuals in the ith group (e.g., 10% or 90%, in the example above. Garnett and Anderson denote this probability δ_{ij}. In other words, the probability of within group mixing under complete assortativity is:

$$f_{ij} = \delta_{ij} \tag{4}$$

They then redistribute contacts from within-group to between-group contacts based on the propensity towards random mixing in the population, which we denote in our model as η. When we have a matrix of proportions that sum to 1, with p_i representing the proportion of individuals in the ith group, and p_j (or $1-p_i$ if there are only 2 groups, as here) representing the proportion of contacts in in the jth group, the trace of the matrix is simply Σp_{ij}. Our contact patterns are now characterized as:

$$f_{ij} = (1-\eta)\delta_{ij} + \eta p_{ij} \tag{5}$$

When η is closer to 0 mixing is closer to random, while values closer to 1 represent extreme assortativity. This approach ensures symmetry in contact matrices, such that the number of contacts between vaccinated and unvaccinated individuals is the same, regardless of directionality of contact.

References

1.   Tuite AR, Fisman DN, Greer AL. Mathematical modelling of COVID-19 transmission and mitigation strategies in the population of Ontario, Canada. CMAJ. 2020;192(19):E497-E505.

2.   Garnett GP, Anderson RM. Sexually Transmitted Diseases And Sexual Behavior: Insights From Mathematical Models. The Journal of Infectious Diseases. 1996;174(Supplement_2):S150-S61.

3.   Blower SM, McLean AR. Mixing ecology and epidemiology. Proc Biol Sci. 1991;245(1314):187-92.

4.   Gupta S, Anderson RM, May RM. Networks of sexual contacts: implications for the pattern of spread of HIV. AIDS. 1989;3(12):807-17.