

Optimal Distribution of Vaccinations (improvement necessary)

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Abstract

Description

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1 Rule-based modeling

In the proposed model the compartments are Susceptible (S), Infectious (I), Recovered and Dead (D). Individuals either live in area one (a_1) or area two (a_2). They are non-vaccinated (v_0), vaccinated with vaccine one (v_1) or vaccinated with vaccine two (v_2). Since we are dealing with two virus variants, the wild type w and the mutant m , we account for this by introducing the feature c_j with $j \in \{w, m\}$ that indicates the type of virus we are referring to.

We use the set notation of [Waites et al. \(2021\)](#) to address certain subsets of the population. $\mathcal{P}()$ means all individuals. $\mathcal{P}(x_u)$ denotes all individuals from compartment $u \in \{S, I, R, D\}$, $\mathcal{P}(a_l)$ denotes all individuals from area $l \in \{1, 2\}$, $\mathcal{P}(v_i)$ are all individuals with vaccination status $i \in \{0, 1, 2\}$, where zero indicates non-vaccinated, and $\mathcal{P}(c_j)$ are all individuals that currently have or had an infection with virus $j \in \{w, m\}$. With this notation we can pick desired subsets of the population by combining the appropriate features. All individuals from area one that are infected with the wild type are addressed by $\mathcal{P}(x_I, c_m)$. If we only want the unvaccinated individuals of them we use $\mathcal{P}(x_I, c_m, v_0)$. The usual set operators, like \cup . Using these operators allows us to address even more specific subsets like the set of all vaccinated individuals $\mathcal{P}(v_1) \cup \mathcal{P}(v_2)$. The set $\mathcal{P}()$ is defined as the whole population. The cardinality $|\cdot|$ is used to address the respective number of individuals in a set, e.g. $|\mathcal{P}(x_S, a_1)|$ equals the number of all susceptible individuals in area one. *include symptomatic*

In more specific cases it might be more comprehensive to replace the index numbers by meaningful abbreviations.

1.1 Model

The following list gives a brief description of the parameters used to describe the model.

Parameter

- $\nu_j \in (0, 1)$ for $j = 1, 2$: vaccination rate of vaccine j
- $\alpha_i \in (0, 1)$ for $i = b, m$: infection rate of virus i
- $\delta_i \in (0, 1)$ for $i = b, m$: death rate of unvaccinated individuals that are infected with virus i

- $\beta_i \in (0, 1)$ for $i = b, m$: recover rate of unvaccinated individuals that are infected with virus i
- $\omega_{i,j} \in (0, 1)$ for $i = b, m$ and $j = 1, 2$: how much percent of the people that are vaccinated with vaccine i die less due to virus j .
- $f_{i,j} \in (0, \infty)$ for $i, j = 1, 2$: average number of people meeting between area a_i and area a_j . It should hold that $f_{i,j} = f_{j,i}$ and $f_{i,i} > f_{i,j}$ for all $i \neq j$.
- $\gamma \in (0, 1)$: inverse proportion of immunity that remains after vaccination ($\gamma = 0$ means vaccine makes 100% immune)

Assumptions so far:

- no distinction between symptomatic and asymptomatic infected cases
- no vaccination during infection [see here](#) (US Center for Disease Control)
- no births and other deaths
- no reinfection
- vaccination decreases infection rate by $\gamma \in (0, 1)$ and is the same for both vaccines across both viruses

1.2 Transition Rates

Vaccination

For $j \in \{1, 2\}$

$$\begin{aligned} \mathcal{P}(x_S, v_0, a_1) &\xrightarrow{\nu_j(t-k)} \mathcal{P}(x_S, v_j, a_1) \\ \mathcal{P}(x_R, v_0, c_w, a_1) &\xrightarrow{\nu_j(t-k)} \mathcal{P}(x_R, v_j, c_w, a_1) \end{aligned}$$

Susceptible to Infectious

To facilitate notation, we distinguish between individuals that are alive and those that are dead. We exclude all dead individuals by using prime notation to only address all living individuals, e.g. $\mathcal{P}'(a_l) = \mathcal{P}(x_S, a_l) \cup \mathcal{P}(x_I, a_l) \cup \mathcal{P}(x_R, a_l)$. We define $N_l(t) = |\mathcal{P}'(a_l)|$ as

the number of living individuals in area l at time t . For specifying the transition rates we need to specify the probabilities that two individuals of a certain type meet. We do so by using the relative frequencies and adjust for cross-area meetings. The probability of an individual $i \in \mathcal{P}()$ to be in a particular subset is approximated by the relative frequencies. For example, the (time dependent) probability that a randomly drawn living individual is from area l is $\mathbb{P}(i \in \mathcal{P}'(a_l)) = \frac{N_l(t)}{N_1(t) + N_2(t)}$. To compute the probability that an individual is susceptible, conditioned that it is from area l , we can use Bayes' formula

$$\mathbb{P}(i \in \mathcal{P}(x_S) | i \in \mathcal{P}'(a_l)) = \frac{\mathbb{P}(i \in \mathcal{P}(x_S, a_l))}{\mathbb{P}(i \in \mathcal{P}'(a_l))} = \frac{|\mathcal{P}(x_S, a_l)|}{|\mathcal{P}'(a_l)|} = \frac{|\mathcal{P}(x_S, a_l)|}{N_l(t)}. \quad (1)$$

We are interested in how many individuals are on average infected by an infected individual. To facilitate notation we assume that the infected individual lives in area one and is infected with the wild type w . The average number of infected individuals is a composition of the infection rate that is dependent on the virus type, the average number of contacts per infected individual and unit of time and the share of susceptible individuals that can be infected. We start with the baseline case of two unvaccinated individuals and first define the transition for susceptible individuals from area two.

Let $i_1 \in \mathcal{P}(x_I, v_0, c_w, a_1)$ and $i_2 \in \mathcal{P}()$. We fix the location, vaccination status and compartment of individual one and allow individual two to potentially be from both areas and every compartment. We need to define $\mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0, a_2) | i_1 \in \mathcal{P}(x_I, v_0, c_w, a_1))$, the probability that the individual that can be infected is susceptible, unvaccinated and from area two given that individual one is infected with the wild type, unvaccinated and from area one. We assume that only the area has an influence on the probability of meeting an individual. The problem facilitates to finding $\mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0, a_2) | i_1 \in \mathcal{P}(a_1))$ or equivalently $\mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0) \wedge i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1))$. Using Bayes' formula we can rewrite this as

$$\begin{aligned} \mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0) \wedge i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1)) &= \mathbb{P}(i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1)) \\ &\quad \cdot \mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0) | i_1 \in \mathcal{P}(a_1), i_2 \in \mathcal{P}(a_2)) \\ &= \mathbb{P}(i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1)) \\ &\quad \cdot \mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0)) \end{aligned}$$

We first specify the probability $\mathbb{P}(i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1))$, which is to say, the probability that i_2 is from area two. We cannot use the relative frequency of the number of individuals $\frac{N_2(t)}{N_1(t) + N_2(t)}$ as probability since this would not take into account that individuals meet more often within one region. We therefore add a penalty term $b(d(a_1, a_2))$ that accounts for the

distance between the areas

$$\mathbb{P}(i_2 \in \mathcal{P}(a_2) | i_1 \in \mathcal{P}(a_1)) = \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2)).$$

$b(y) \in [0, 1]$, $b(0) = 1$ and $\lim_{y \rightarrow \infty} b(y) = 0$. *idea for* $b(y) = \frac{1}{1+by}$. The probability of individual two to be unvaccinated and susceptible, conditioned that it is from area two, is taken to be the relative frequency of unvaccinated, susceptible individuals from area two

$$\mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0)) = \frac{|\mathcal{P}(x_S, v_0, a_2)|}{N_2(t)}$$

Combining both results yields

$$\mathbb{P}(i_2 \in \mathcal{P}(x_S, v_0, a_2) | i_1 \in \mathcal{P}(x_I, v_0, c_w, a_1)) = \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2)) \cdot \frac{|\mathcal{P}(x_S, v_0, a_2)|}{N_2(t)}$$

Hence, i_1 meets on average $c \cdot \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2)) \cdot \frac{|\mathcal{P}(x_S, v_0, a_2)|}{N_2(t)}$ unvaccinated susceptible individuals from area two. At this meetings, α individuals become infected. This probability changes if we condition on the mutant. i_1 infects on average $\alpha \cdot c \cdot \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2)) \cdot \frac{|\mathcal{P}(x_S, v_0, a_2)|}{N_2(t)}$ individuals. This is done by $|\mathcal{P}(x_I, v_0, a_1)|$ individuals from area one and therefore we get the transitions

$$\alpha \cdot c \cdot \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2)) \cdot \frac{|\mathcal{P}(x_S, v_0, a_2)|}{N_2(t)} |\mathcal{P}(x_I, v_0, a_1)|$$

Using rule-based notation we write this as

$$P(x_I, v_0, c_w, a_1), P(x_S, v_0, a_2) \xrightarrow{\frac{\alpha \cdot c \cdot b(d(a_1, a_2))}{N_1(t) + N_2(t)}} P(x_I, v_0, c_w, a_1), P(x_I, v_0, c_w, a_2)$$

Same but for unvaccinated from same area (*we ignore minus one*)

$$P(x_I, v_0, c_w, a_1), P(x_S, v_0, a_1) \xrightarrow{\frac{\alpha \cdot c}{N_1(t)} \cdot \left[1 - \frac{N_2(t)}{N_1(t) + N_2(t)} \cdot b(d(a_1, a_2))\right]} P(x_I, v_0, c_w, a_1), P(x_I, v_0, c_w, a_1)$$

define $m_{k,l}$ as meeting probs and shorten notation with that. Write down for other cases (vaccines)

Infectious to Recovered/Death

non-vaccinated

$$\begin{aligned}\mathcal{P}(x_I, v_0, c_w, a_1) &\xrightarrow{p\lambda} \mathcal{P}(x_D, v_0, c_w, a_1) \\ \mathcal{P}(x_I, v_0, c_w, a_1) &\xrightarrow{q(1-p)\lambda} \mathcal{P}(x_R, v_0, c_w, a_1, S_y) \\ \mathcal{P}(x_I, v_0, c_w, a_1) &\xrightarrow{(1-q)(1-p)\lambda} \mathcal{P}(x_R, v_0, c_w, a_1, S_n)\end{aligned}$$

vaccinated. for $i \in \{1, 2\}$

$$\begin{aligned}\mathcal{P}(x_I, v_i, c_w, a_1) &\xrightarrow{\omega_{i,w}p\lambda} \mathcal{P}(x_D, v_i, c_w, a_1) \\ \mathcal{P}(x_I, v_i, c_w, a_1) &\xrightarrow{q(1-\omega_{i,w}p)\lambda} \mathcal{P}(x_R, v_i, c_w, a_1, S_y) \\ \mathcal{P}(x_I, v_i, c_w, a_1) &\xrightarrow{(1-q)(1-\omega_{i,w}p)\lambda} \mathcal{P}(x_R, v_i, c_w, a_1, S_n)\end{aligned}$$

To-do: write mutant and write that everything applies for area 2 as well, graph, explain everything (what do q,p, etc. do)

1.3 Rules

The rules are written down using the P -notation. For the transition from non-vaccinated individuals to recovered or dead individuals, we need two rules that are dependent on the virus type. For $i = b, m$

$$\begin{aligned}P(x_{I_i}, v_0) &\xrightarrow{\delta_i} P(x_{D_i}, v_0) \\ P(x_{I_i}, v_0) &\xrightarrow{\beta_i} P(x_{R_i}, v_0).\end{aligned}\tag{2}$$

The vaccination can be described by two rules. *For the purpose of the analysis we should think of making ν_1 and ν_2 time-dependent.*

$$\begin{aligned}P(S, v_0) &\xrightarrow{\nu_1} P(S, v_1) \\ P(S, v_0) &\xrightarrow{\nu_2} P(S, v_2).\end{aligned}\tag{3}$$

For the transition from vaccinated individuals to recovered or dead individuals, we need two rules that are dependent on the virus type and the type of vaccination. For $i = b, m$ For $i = b, m$ and $s = 1, 2$. *Using $(2 - \omega_{i,1})$ has the advantage that we need to define less parameters. However, I would program it as single parameter and then change it accordingly*

during the parameter specification.

$$\begin{aligned} P(x_{I_i}, v_s) &\xrightarrow{\omega_{i,s}\delta_i} P(x_{D_i}, v_s) \\ P(x_{I_i}, v_s) &\xrightarrow{(2-\omega_{i,s})\beta_i} P(x_{R_i}, v_s) \end{aligned} \quad (4)$$

For the transitions from susceptible to infectious we need to distinguish in between meetings of individuals from the same area and in between vaccination types. We write down the rules for Susceptible individuals from area one. The same logic with slightly different indices applies for area two. For $l = 1, 2$ and $i = b, m$ the infection of unvaccinated individuals can be described by

$$\begin{aligned} P(x_{I_i}, a_l, v_0), P(x_S, a_1, v_0) &\xrightarrow{\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_0), P(x_{I_i}, a_1, v_0) \\ P(x_{I_i}, a_l, v_1), P(x_S, a_1, v_0) &\xrightarrow{\gamma \alpha_i f_{l,1}} P(x_{I_i}, a_l, v_1), P(x_{I_i}, a_1, v_0) \\ P(x_{I_i}, a_l, v_2), P(x_S, a_1, v_0) &\xrightarrow{\gamma \alpha_i f_{l,1}} P(x_{I_i}, a_l, v_2), P(x_{I_i}, a_1, v_0). \end{aligned} \quad (5)$$

We need similar rules for the infection of individuals vaccinated with vaccine one. Their average number of infection is lowered by $\sigma_{i,1}$, yielding for $l = 1, 2$ and $i = b, m$ the rules

$$\begin{aligned} P(x_{I_i}, a_l, v_0), P(x_S, a_1, v_1) &\xrightarrow{\sigma_{i,1}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_0), P(x_{I_i}, a_1, v_1) \\ P(x_{I_i}, a_l, v_1), P(x_S, a_1, v_1) &\xrightarrow{\gamma \sigma_{i,1}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_1), P(x_{I_i}, a_1, v_1) \\ P(x_{I_i}, a_l, v_2), P(x_S, a_1, v_1) &\xrightarrow{\gamma \sigma_{i,1}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_2), P(x_{I_i}, a_1, v_1) \end{aligned} \quad (6)$$

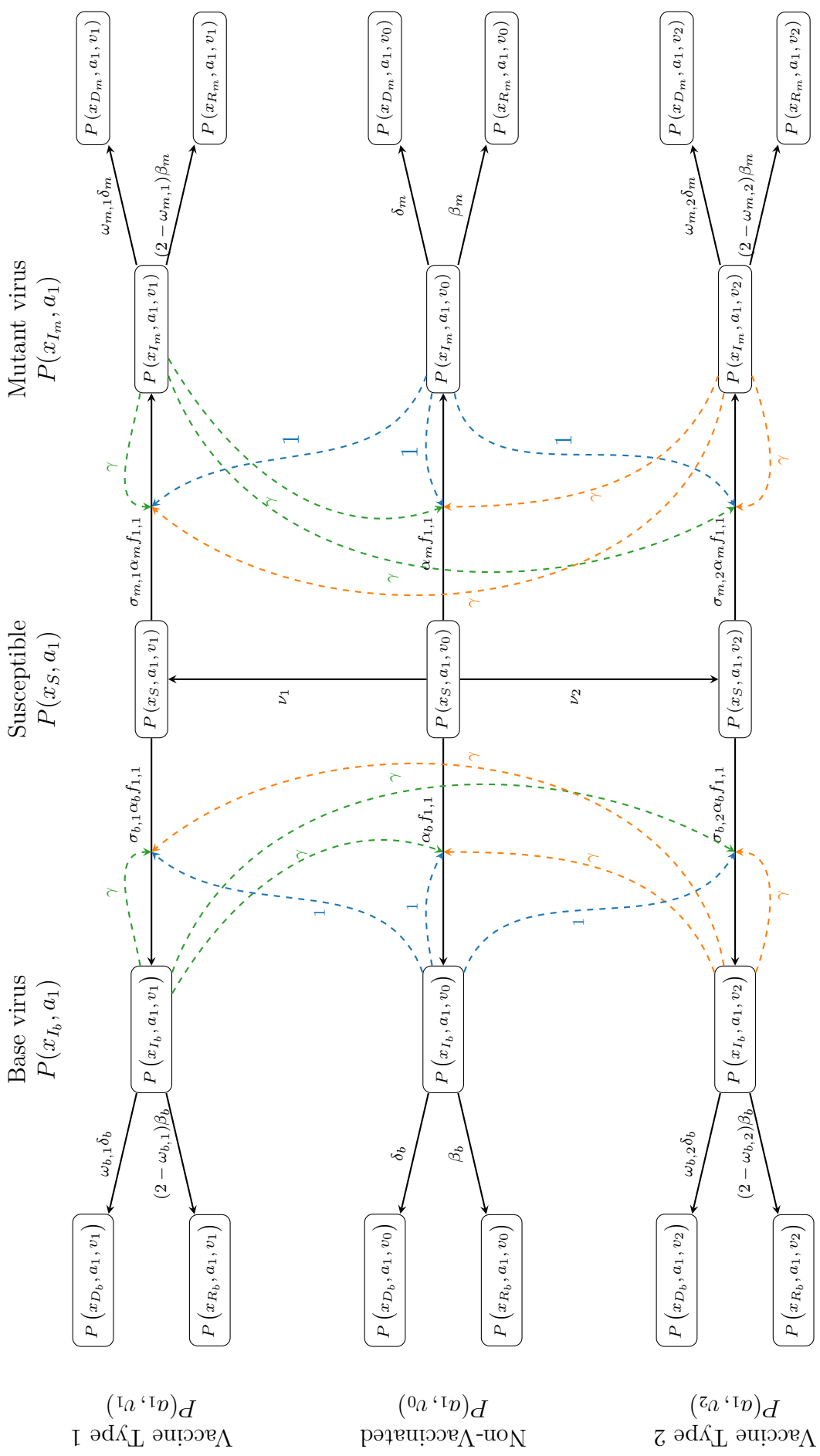
Analogously, we can define the infection of individuals vaccinated with vaccine two using $\sigma_{i,2}$. The rules are for $l = 1, 2$ and $i = b, m$.

$$\begin{aligned} P(x_{I_i}, a_l, v_0), P(x_S, a_1, v_2) &\xrightarrow{\sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_0), P(x_{I_i}, a_1, v_2) \\ P(x_{I_i}, a_l, v_1), P(x_S, a_1, v_2) &\xrightarrow{\gamma \sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_1), P(x_{I_i}, a_1, v_2) \\ P(x_{I_i}, a_l, v_2), P(x_S, a_1, v_2) &\xrightarrow{\gamma \sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_2), P(x_{I_i}, a_1, v_2) \end{aligned} \quad (7)$$

1.4 Graphical model description

On the next page you find a graphical representation of the model using tikz. I have omitted the second region and cross-border infections from the graph to increase readability.

Area one (a_1)



References

Waites, W., Cavaliere, M., Manheim, D., Panovska-Griffiths, J., and Danos, V. (2021). Rule-based epidemic models. *arXiv Working Paper*.