Optimal Distribution of Vaccinations (improvement necessary)

Manuel Huth*

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Abstract

Description

Keywords: ...

*University of Bonn, e-mail: *s6mahuth@uni-bonn.de*

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 refering 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 cardinalty $|\cdot|$ is used to addres 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.

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

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

Susceptible to Infectious

We define $N_l(t) = |\mathcal{P}(x_S, a_l) \cup \mathcal{P}(x_I, a_l) \cup \mathcal{P}(x_R, a_l)|$ as the number of living individuals in area l.

From $\mathcal{P}(x_S, v_0, a_1)$ to $\mathcal{P}(x_I, v_0, c_w, a_1)$ (*do not forget to multiply by* $|\mathcal{P}(x_S, v_0, a_1)|$)

$$rate(v_0) = \alpha b \left[\frac{p_m}{N_1(t) + N_2(t)} \left(|\mathcal{P}(x_I, v_0, c_w, a_1)| + \gamma |\mathcal{P}(x_I, v_1, c_w, a_1) \cup \mathcal{P}(x_I, v_2, c_w, a_1)| \right) \right.$$
$$\left. + \frac{(1 - p_m)N_1(t) + N_2(t)}{N_1(t) + N_2(t))N_2(t)} \left(|\mathcal{P}(x_I, v_0, c_w, a_2)| + \gamma |\mathcal{P}(x_I, v_1, c_w, a_2) \cup \mathcal{P}(x_I, v_2, c_w, a_2)| \right) \right]$$

The rule is defined by

$$\mathcal{P}(x_S, v_0, a_1) \xrightarrow{rate(v_0)} \mathcal{P}(x_I, v_0, c_w, a_1)$$

From $\mathcal{P}(x_S, v_i, a_1)$ to $\mathcal{P}(x_I, v_i, c_w, a_1)$ for $i \in \{1, 2\}$. (*do not forget to multiply by* $|\mathcal{P}(x_S, v_i, a_1)|$)

$$\mathcal{P}(x_S, v_0, a_1) \xrightarrow{\rho_{i,w} \cdot rate(v_0, c_1)} \mathcal{P}(x_I, v_0, c_w, a_1)$$

Infectious to Recovered/Death

non-vaccinated

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

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

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

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 $i = b, m$

$$\begin{aligned} P(x_{I_i}, v_0) &\xrightarrow{\delta_i} P(x_{D_i}, v_0) \\ P(x_{I_i}, v_0) &\xrightarrow{\beta_i} P(x_{R_i}, v_0). \end{aligned} \tag{1}$$

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.*

$$\begin{aligned} P(S, v_0) &\xrightarrow{\nu_1} P(S, v_1) \\ P(S, v_0) &\xrightarrow{\nu_2} P(S, v_2). \end{aligned} \tag{2}$$

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.*

$$\begin{aligned} P(x_{I_i}, v_s) &\xrightarrow{\omega_{i,s}\delta_i} P(x_{D_i}, v_s) \\ P(x_{I_i}, v_s) &\xrightarrow{(2-\omega_{i,s})\beta_i} P(x_{R_i}, v_s) \end{aligned} \tag{3}$$

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

$$\begin{aligned} P(x_{I_i}, a_l, v_0), P(x_S, a_1, v_0) &\xrightarrow{\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_0), P(x_{I_i}, a_1, v_0) \\ P(x_{I_i}, a_l, v_1), P(x_S, a_1, v_0) &\xrightarrow{\gamma\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_1), P(x_{I_i}, a_1, v_0) \\ P(x_{I_i}, a_l, v_2), P(x_S, a_1, v_0) &\xrightarrow{\gamma\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_2), P(x_{I_i}, a_1, v_0). \end{aligned} \tag{4}$$

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

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

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

$$\begin{aligned} P(x_{I_i}, a_l, v_0), P(x_S, a_1, v_2) &\xrightarrow{\sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_0), P(x_{I_i}, a_1, v_2) \\ P(x_{I_i}, a_l, v_1), P(x_S, a_1, v_2) &\xrightarrow{\gamma\sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_1), P(x_{I_i}, a_1, v_2) \\ P(x_{I_i}, a_l, v_2), P(x_S, a_1, v_2) &\xrightarrow{\gamma\sigma_{i,2}\alpha_i f_{l,1}} P(x_{I_i}, a_l, v_2), P(x_{I_i}, a_1, v_2) \end{aligned} \tag{6}$$

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)
Base virus
$P(x_{I_b}, a_1)$
Susceptible
$P(x_S, a_1)$
Mutant virus
$P(x_{I_m}, a_1)$
Vaccine Type 1
$P(a_1, v_1)$
Non-Vaccinated
$P(a_1, v_0)$
Vaccine Type 2
$P(a_1, v_2)$
$P(x_{D_b}, a_1, v_1)$
$P(x_{R_b}, a_1, v_1)$
$P(x_{I_b}, a_1, v_1)$
$P(x_S, a_1, v_1)$
$P(x_{I_m}, a_1, v_1)$
$P(x_{D_m}, a_1, v_1)$
$P(x_{R_m}, a_1, v_1)$
$P(x_{D_b}, a_1, v_0)$
$P(x_{R_b}, a_1, v_0)$
$P(x_{I_b}, a_1, v_0)$
$P(x_S, a_1, v_0)$
$P(x_{I_m}, a_1, v_0)$
$P(x_{D_m}, a_1, v_0)$
$P(x_{R_m}, a_1, v_0)$
$P(x_{D_b}, a_1, v_2)$
$P(x_{R_b}, a_1, v_2)$
$P(x_{I_b}, a_1, v_2)$
$P(x_S, a_1, v_2)$
$P(x_{I_m}, a_1, v_2)$
$P(x_{D_m}, a_1, v_2)$
$P(x_{R_m}, a_1, v_2)$
$\omega_{b,1}\delta_b$
$(2-\omega_{b,1})\beta_b$
$\sigma_{b,1}\alpha_b f_{1,1}$
$\alpha_b f_{1,1}$
$\sigma_{b,2}\alpha_b f_{1,1}$
$\omega_{b,2}\delta_b$
$(2-\omega_{b,2})\beta_b$
δ_b
β_b
$\omega_{m,1}\delta_m$
$(2-\omega_{m,1})\beta_m$
$\sigma_{m,1}\alpha_m f_{1,1}$
$\alpha_m f_{1,1}$
$\sigma_{m,2}\alpha_m f_{1,1}$
$\omega_{m,2}\delta_m$
$(2-\omega_{m,2})\beta_m$
δ_m
β_m
ν_1
ν_2
1
γ

References

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