A structural epidemiological model for the optimal allocation of vaccines across countries

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1 Introduction

Up to July 2021, the outbreak of the COVID-19 pandemic, with the first registered case in December 2019 in Wuhan, China (Hui et al., 2020), has globally caused around 187 million reported infections following around 4 million deaths (ECDC, 2021a). Infections are estimated to be even higher due to asymptomatic unregistered cases (Byambasuren et al., 2020). Policymakers have responded to the outbreak of the pandemic with non-pharmaceutical interventions, such as minimizing the contact numbers of individuals, to reduce the spread of the virus (Gabler et al., 2021). Economists have tried to quantify the costs of these containment measures. Miles et al. (2020) have estimated the costs of the lock down in the United Kingdom from March 2020 to beginning of June 2020 to be between 100 and 200 billion pounds, which is 5-10% of the UKs GDP. Deb et al. (2020) use world-wide data and estimate a 15% loss in industrial production up to 30 days after the implementation of containment measures.

Since the outbreak, more infectious virus mutants have spread increasing the physical and social costs even more. The European Centre for Disease Prevention and Control (ECDC) classifies the virus types into three categories. For (1) *variants of concern* there is already clear evidence of a significant impact on infections or severity of the disease. For (2) *variants of interest*, these evidence is still preliminary and (3) *variants under monitoring* have been detected to potentially have the aforementioned impacts (ECDC, 2021c).

Despite non-pharmaceutical measures and tests yielded desired reductions in infections (Gabler et al., 2021), the high physical and economical costs have raised the need for vaccinations that provide immunity. In September 2020 more than 100 vaccines against COVID-19 where in the development phase (Mullard, 2020). In late 2020, the first vaccines have become approved. As of July 2021, four vaccines are approved within the European Union (EU) and two are in the development phase (European Commission, 2021b). In mid July 2021, around 65% of adults within the European Economic Area have at least received one shot and about half of the adult population have received full vaccination (ECDC, 2021a). With the agreement of all member states, the European Commission and a Joint Negotiation team represented by seven member states, have taken on negotiations with the vaccine suppliers representing the member states. Countries indicate during the negotiation phase with a

manufacturer if they are interested in the respective vaccine. Vaccine doses are subsequently allocated between the interested member states according to their relative population size (European Commission, 2021a).

Our research raises the question whether the European Union could allocate the purchased vaccines more efficiently by more flexible vaccination strategies than constant rates. Attempting to answer this question, we develop a deterministic Susceptible, Infectious, Recovered, Deceased (SIRD) model with two countries, two vaccines, and two virus types and calibrate it using parameters from the literature. We utilize the real-world vaccine purchase numbers of the EU as exogenous vaccine inflow and scale it down to the population size of our two-country model. Vaccines in our model have varying efficacies with respect to the variants. Variants are distributed heterogeneously across countries. We use piecewise constant functions and logistically transformed cubic Hermite splines as vaccination channels that determine the fractions of the vaccine doses each country receives. Both channels allow the fraction to be non-constant over the time course of the pandemic yielding potentially more complex vaccination strategies. We minimize the number of deaths by optimizing over the parameters of the channel functions, once with additional Pareto constraints and once without the additional constraints. Subsequently, we benchmark the results against the current population size based strategy. We further validate our deterministically derived optimal strategies within a stochastic model.

Closest to our research is the work of Bertsimas et al. (2020). They use a one-country DELPHI model, an extension to the SEIR model, with different regions of the United States to quantify the effects of vaccinations and demographics within one country. Matrajt et al. (2021) examine the optimal vaccination strategy with respect to the prioritization of groups within one country. Tuite et al. (2021) aim to find an optimal policy that allocates vaccines efficiently among first and second vaccine shots.

Our work extends existing research by exploring if knowledge about the spread of virus types and the respective vaccine efficacies against different types can be used to minimize the number of deceased individuals. We place focus on the importance of policy-wise implementable strategies, such as Pareto improvements with respect to previously applied strate-

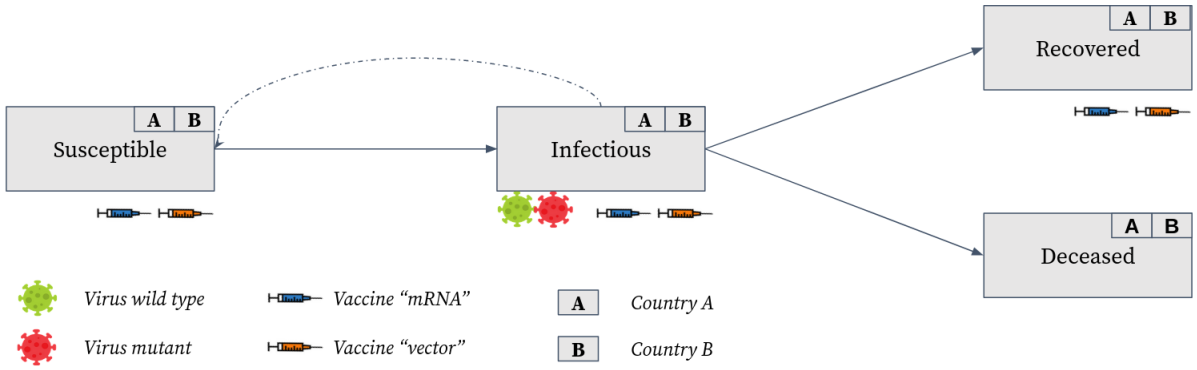
gies.

We structure the paper as follows. In Section 2 we introduce our deterministic and stochastic SIRD models, review how the system of differential equations can be derived from modeling the transitions as chemical reactions, and specify the corresponding reactions. In Section 3, we introduce the two vaccination channels and specify the optimization problem for the deterministic model. Section 4, elaborates on the calibration of our model and presents the results. Section 5 concludes.

2 Model

We subdivide the classic SIRD compartments, Susceptible (S), Infectious (I), Recovered (R) and Deceased (D), with sub-compartments allowing for heterogeneous areas of residence and vaccination states as well as infections by different virus types. Figure 1 illustrates the general model. Individuals either live in country A or country B. They are non-vaccinated U_0, vaccinated with vaccine one U_1 or vaccinated with vaccine two U_2. Vaccine U_1 represents the messenger ribonucleic acid (mRNA) vaccines and vaccine U_2 represents the vector vaccines. We assume that one vaccination shot is sufficient to get the full protection of vaccine U_l. We introduce two virus types. A wild type W that serves as baseline variant and a more infectious mutant variant M.

To describe our model we denote every sub-group of individuals by a set $\mathcal{C}_t(F_n)$, where F_n is a placeholder for features that the individuals (elements) within the set $\mathcal{C}_t$ share and t denotes the time at which the set is evaluated. We illustrate the features F_n in the following with examples. Let X_i for $i \in \{S, I, R, D\}$ indicate to which general compartment an individual belongs, then, $\mathcal{C}_t(X_S)$ is the set of all susceptible individuals and $\mathcal{C}_t(X_I)$ is the set of all infectious individuals at t. If we want to distinguish not only between general compartments but additionally between countries of residence, we use the feature C_j for $j \in \{A, B\}$ to indicate that the country of residence is j. $\mathcal{C}_t(X_S, C_A)$ is the set of all susceptible individuals of country A and $\mathcal{C}_t(X_S, C_B)$ of country B. Analogously, $\mathcal{C}_t(V_k)$ is the set of all individuals infected with virus k and $\mathcal{C}_t(U_l)$ is the set of all individuals with vaccination status l.



Note: Solid lines indicate transition paths and dashed lines indicate infections. Shots below a compartment indicate that individuals from this compartment are vaccinated. Viruses below a compartment indicate that this compartment is infectious. Each compartment is subdivided according to country of residence and vaccination status.

Figure 1: Model structure

We can link sets with the common set operators, e.g. $\mathcal{C}_t(X_S, C_A) \cup \mathcal{C}_t(X_S, C_B) = \mathcal{C}_t(x_S)$ or $\mathcal{C}_t(X_S) \cap \mathcal{C}_t(X_I) = \emptyset$. The negation operator $\neg$ is used to indicate that a certain feature applies for all but the specified compartment, e.g. $\mathcal{C}_t(\neg X_D)$ is the set of all alive individuals. The cardinality $|\cdot|$ represents the respective number of individuals in a set, e.g. $|\mathcal{C}_t(X_S)|$ equals the number of all susceptible individuals. To shorthand notation, we define $y_t(F_n) = |\mathcal{C}_t(F_n)|$ as the number of individuals within the set $\mathcal{C}_t(F_n)$. By definition $\mathcal{C}_t() = \cup_{i \in \{S,I,R,D\}} \mathcal{C}_t(X_i)$ is the set of all individuals. An overview of all features is given in Table 1.

We impose a set of assumptions to the compartments to rule out undesired cases within the model

Assumption 1. *For all* $t, r \in \mathbb{R}_+$, $k \in \{W, M\}$ *and* $s \in [-t, \infty)$ *let*

$$\mathcal{C}_t(X_I, V_k) \cap \mathcal{C}_{t+r}(X_S) = \emptyset \tag{1.1}$$

$$\mathcal{C}_t(U_1) \cap \mathcal{C}_{t+s}(U_2) = \emptyset \tag{1.2}$$

$$\mathcal{C}_t(C_A) \cap \mathcal{C}_{t+s}(C_B) = \emptyset \tag{1.3}$$

$$\mathcal{C}_t(X_S, V_k) = \emptyset. \tag{1.4}$$

Assumption 1.1 rules out reinfections such that an individual that has been infected once cannot become reinfected after it had recovered. According to Roy (2020), there is evidence

Table 1: Notation

Feature	Code	Indices	Explanation
General compartment	X_i	$i \in \{S, I, R, D\}$	Individuals can either be Susceptible (S), Infectious (I), Recovered (R) or Deceased (D).
Country of residence	C_j	$j \in \{A, B\}$	Individuals can either live in country A or country B.
Virus Type	V_k	$k \in \{W, M\}$	An infection can either be caused by the wild type (W) or the mutant (M) virus. This feature has to be understood, depending on X_i, as *is* or *has been* infected with type k. For example an individual of $\mathcal{C}_t(X_I, V_k)$ *is* currently infected and an individual of $\mathcal{C}_t(X_R, V_k)$ *has been* infected.
Vaccine Type	U_l	$l \in \{0, 1, 2\}$	An individual can either be vaccinated with vaccine 1 or 2 or being unvaccinated (U_0).
Placeholder	F_n	$n \in \mathbb{N}$	A placeholder that is used to address an arbitrary combination of features. $\mathcal{C}_t(F_n)$ should be read as the set of a fixed but arbitrary compartment. If we need to distinguish between two arbitrary compartments, we use F_1 and F_2.

that recovered individuals cannot become reinfected but reinfections cannot be ruled out fully. However, the number of reinfected individuals might be negligible, therefore, we do not incorporate reinfections to keep our model parsimonious. Assumption 1.2 implies that an individual only receives one type of vaccine. Receiving one vaccination shot in our model implies that an individual is fully protected according to the vaccine properties making it needless to assign a second shot to the same individual. Assumption 1.3 rules out permanent cross-country movements of individuals. We do so since permanent movements should not be a main driver of the pandemic but would require to incorporate more compartments. We refrain from incorporating permanent cross-country movements to keep our model parsimonious. We incorporate cross-border infections by assigning a fraction of infections to be cross-border infections. Assumption 1.4 ensures that susceptible individuals cannot be associated with any type of virus, since they have not been infected yet.

2.1 Deterministic model

We use a compartment SIRD model, based on a system of ordinary differential equations (ODEs), to simulate the pandemic. We see every subcompartment as its own chemical species and each transmission, e.g. vaccinations, infections, recoveries, and deaths, as a chemical reaction. Thus, our system becomes a chemical reaction network. To make this

thesis self-contained, we explain how the dynamics of a chemical reaction network are modeled using ODEs. We can limit ourselves to the case of irreversible reactions since recovered and deceased individuals cannot become infectious again and infectious individuals become recovered but not susceptible.

Let $\mathcal{C}_t(F_1), \ldots, \mathcal{C}_t(F_n)$ be n pairwise disjoint sets and $\cup_{i=1}^{n} \mathcal{C}_t(F_i) = \mathcal{C}_t()$. Every irreversible reaction R_j, for $j = 1, \ldots, m$, can be expressed as reaction of all compartments

$$\underbrace{\nu_{1j} y_t(F_1) + \ldots + \nu_{nj} y_t(F_n)}_{Reactants} \longrightarrow \underbrace{\mu_{1j} y_t(F_1) + \ldots + \mu_{nj} y_t(F_n)}_{Products}, \tag{1}$$

where $\nu_{ij} \in \mathbb{N}_0$ and $\mu_{ij} \in \mathbb{N}_0$ are called stoichiometric coefficients. If a compartment $\mathcal{C}_t(F_i)$ is not a reactant or product within reaction, R_j the respective stoichiometric coefficients ν_{ij}, μ_{ij} are set to zero. ν_{ij} describes how much of species $\mathcal{C}_t(F_i)$ is consumed and μ_{ij} how much is produced within reaction R_j. The difference $\mu_{ij} - \nu_{ij}$ is the total change of $y_t(F_i)$ due to one reaction R_j.

We are not only interested in how one reaction (e.g. one infection, one vaccination, etc.) influences the state of the system but rather how often this happens within an interval $[t, t + \tau]$, for $\tau \in \mathbb{R}_+$. If we restrict us to the case $\tau = 1$, the latter is described according to the law of mass action by

$$v_{t,j} = r_j \prod_{i=1}^{n} y_t(F_i)^{\mu_{ij}}, \tag{2}$$

where r_j is a reaction-specific constant. The product is the number of combinations to assign individuals from different compartments, that have $\mu_{ij} \neq 0$, together.

The change in the magnitude of $y_t(F_i)$ within the interval $[t, t + \tau]$ is given by the sum of the influences of all m reactions

$$y_{t+\tau}(F_i) - y_t(F_i) = \sum_{j=1}^{m} (\mu_{ij} - \nu_{ij}) v_{t,j} \tau. \tag{3}$$

$(\mu_{ij} - \nu_{ij})$ is, as outlined above, the stoichiometry that specifies how one reaction influences the system, $v_{t,j}\tau$ is the number of times reaction R_j happens within the interval $[t, t + \tau]$,

and therefore the product is the influence of R_j on $y_t(F_i)$ within $[t, t+\tau]$. Summed over all reactions yields the change of $y_t(F_i)$ within the system.

We divide both sides of (3) by τ, let $\tau \to 0$ and plugin (2) to obtain the ordinary differential equation

$$\dot{y}_t(F_i) = \sum_{j=1}^{m} \left[(\mu_{ij} - \nu_{ij}) \underbrace{r_j \prod_{i=1}^{n} y_t(F_i)^{\mu_{ij}}}_{v_{t,j}} \right]. \tag{4}$$

We write down the equations for all compartments in matrix form to obtain the system of ODEs, which we use subsequently to ease notation

$$\underbrace{\begin{pmatrix} \dot{y}_t(F_1) \\ \vdots \\ \dot{y}_t(F_n) \end{pmatrix}}_{\dot{Y}(t)} = \underbrace{\begin{pmatrix} \mu_{11} - \nu_{11} & \dots & \mu_{1m} - \nu_{1m} \\ \vdots & \vdots & \vdots \\ \mu_{n1} - \nu_{n1} & \dots & \mu_{nm} - \nu_{nm} \end{pmatrix}}_{\mathbf{S}} \cdot \underbrace{\begin{pmatrix} v_{t,1} \\ \vdots \\ v_{t,m} \end{pmatrix}}_{v_t} \tag{5}$$

If we additionally fix the initial condition $Y(0) = Y_0$, the problem becomes an initial value problem. We use AMICI (Fröhlich et al., 2021) to solve the initial value problem via simulations. AMICI provides the Python interface to interact with the SUNDIALS (Hindmarsh et al., 2005) solvers. We choose the Backward Differentiation Formulas (BDF) methods implemented in SUNDIALS for our implementation of the initial value problem. The BDF, as all numerical solvers we are aware of, discretizes the ODE system to simulate it. Let $\tau_t \in \mathbb{R}_+$ be a varying step-size and $q \in \mathbb{N}$ be the order of the BDF. For coefficients $a_k \in \mathbb{R}$ and $b \in \mathbb{R}_+$, the BDF-q is

$$Y(t) = \sum_{k=1}^{q} a_{t,k} Y(t - \sum_{i=1}^{k} \tau_{t-i}) + \tau_t b_t \underbrace{\dot{Y}(t)}_{=\mathbf{S}v_t} \tag{6}$$

The function value $Y(t)$ is a linear combination of the last q simulated function values and its derivative. In Equation (3), the baseline function value to determine the next value is the previous function value. In Equation (6), the baseline function value is the weighted sum of the previous q function values. To account for this, the increase of the tangent $\tau_t \dot{Y}(t)$ is corrected by a factor b that accounts for the incorporation of the q last function values.

Since V_t depends on Y_t, Equation (6) defines $Y(t)$ implicitly. Thus, it cannot be simulated directly from Equation (6) and numerical methods must be applied. SUNDIALS offers several nonlinear solver choices, such as Newton iteration, to solve this numerical problem. For more details on the implementation of the BDF and the nonlinear solvers see Hindmarsh et al. (2021).

2.2 Stochastic model

We use the stochastic equivalent of our model to test how the derived strategies perform under uncertainty. (Gillespie, 1977) proposed an algorithm modeling the duration between reactions as random variables that are dependent on the system's state. After one reaction fired, the state is updated and the time to the next period is drawn from the random variable. Hence, every probability distribution is based on the latest state of the system and the algorithm is therefore classified as *exact* SSA. On the contrary, approximate algorithms, like $\tau - leaping$ (Gillespie, 2001), group reactions together and use the number of times a reaction happens within one interval as random variable. However, the reactions within one interval almost surely do not happen at the exact same time. Therefore, the true probability distributions of the second and subsequent reactions, within the interval, must change with respect to the outcome of the first reaction. By simulating all reactions at once, approximate algorithms do not account for this update of the probability distributions and are therefore classified as *approximate*. The drawback of approximation can be justified by a speed-up of approximation methods that are due to fewer function evaluations. Since our model includes a large number of reactions, we decided to use the approximate method. We subsequently dive into the math of it (Gillespie, 2001).

We impose an arbitrary order on all subcompartments. We do so by expressing all compartments by n features $F_1, \dots F_n$ yielding the necessary conditions that $\cup_{i=1}^{n} \mathcal{C}_t(F_i) = \mathcal{C}_t()$ and $\mathcal{C}_t(F_1), \dots, \mathcal{C}_t(F_n)$ are mutually disjoint. We specify the state of the system in terms of the compartments $Y(t) = \begin{pmatrix} y_t(F_1) & y_t(F_2) & \dots & y_t(F_n) \end{pmatrix}'$. Recall that $\mathbf{S} \in \mathbb{R}^{n \times m}$ is the stoichiometric matrix, as defined in (5), with coefficients s_{ij} and columns $s_{.j}$. R_j, for $j = 1, \dots, m$, is the j-th reaction. Let $V_{t,j}$ be the random variable counting the number of times R_j will fire within the interval $[t, t + \tau)$, for $\tau \in \mathbb{R}_+$. We denote by V_t the random

vector collecting the random variables $V_{t,1}, \ldots, V_{t,m}$. Dividing the whole period of interest $[0, T]$ in intervals of length τ, the algorithm is an iterative update of the discretized system's state

$$Y(t + \tau) = Y(t) + \mathbf{S}V_t. \tag{7}$$

Equation (7) is the equivalent of equation (3), with the only difference that the number of reactions within a given interval are random in Equation (7). Making use of the latter equation, the change in the system's state $\Delta Y(t) = Y(t + \tau) - Y(t) = \mathbf{S}V_t$ can be expressed in terms of a linear combination of the columns of $\mathbf{S}$ with random scalars $K_{t,j}$

$$\Delta Y(t) = \sum_{j=1}^{m} K_{t,j} \cdot s_{\cdot j}. \tag{8}$$

$s_{\cdot j}$ consists of the stoichiometry for each compartment i according to reaction R_j and therefore indicates how the state of the system changes if reaction R_j happens. $K_{t,j}$ is the number of occurrences of reaction R_j. Thus, the product is the system's change due to R_j. Aggregating over all reactions yields the total change of the system R_j, similar to the deterministic equation (3).

So far, we have not specified the distribution of K_t. We are interested in the conditional joint probability distribution $\mathbb{P}_t(K_{t,1} = k_{t,1}, \ldots, K_{t,m} = k_{t,m}|\tau)$ of the random vector $K_t = \Big(K_{t,1}, \ldots, K_{t,m}\Big)'$ conditioned on the state of the system and a fixed interval size τ. Recall that we have defined $\mathbb{P}_t$ to be the conditional probability with respect to the state of the system and, therefore, we omit to write the condition explicitly within as condition statement. We simplify the problem to specifying the marginal distributions by assuming independence of all $K_{t,1}, \ldots, K_{t,m}$. Let $a_j(y) = \mathbb{P}_t(K_{t,j} = 1|\tau = 1)$ be the propensity function of the j-th reaction with respect to the state of the system $Y(t) = y$. We assume that for infinitesimal small dt

$$\mathbb{P}_t(K_{t,j} = 1|\tau = dt) = a_j(y) \cdot dt, \tag{9}$$

is the probability that R_j fires once within the interval $[t, t + dt)$ and $(K_{t,j}|Y(t), \tau = dt)$ is

Bernoulli $\text{Ber}(a_j(y) \cdot dt)$ distributed. The Bernoulli assumption is justified by choosing dt infinitesimal small, such that R_j fires at most once almost surely.

For simplicity we assume that $\frac{\tau}{dt}$ is an integer. If we assume that $a_j(y)$ is constant within $[t, t+\tau)$, we can partition the interval in $\frac{\tau}{dt}$ subintervals with length dt. In each of these subintervals the conditional random variable is Bernoulli distributed $(K_{t+s\cdot dt,j}|Y(t), \tau = dt) \sim \text{Ber}(a_j(y) \cdot dt)$ for $s = 0, 1, \ldots, \frac{\tau}{dt} - 1$. Thus, the sum

$$\sum_{s=0}^{\frac{\tau}{dt}-1} (K_{t+s\cdot dt,j}|Y(t), \tau = dt) \sim \text{B}\left(\frac{\tau}{dt}, a_j(y) \cdot dt\right) \tag{10}$$

follows a binomial distribution. The practical problem of this Binomial distribution is that sampling from it requires to define a value for dt. By definition, dt is infinitesimally small, such that we aim for $dt \to 0$. Fortunately, $dt \to 0$ leads to a Poisson random variable that can be specified by the known τ and $a_j(y)$ such that we can sample from it.

Theorem 1. *$B\left(\frac{\tau}{dt}, a_j(y) \cdot dt\right) \xrightarrow{d} Po(a_j(y) \cdot \tau)$ if $dt \to 0$.*

Proof. The proof is moved to Appendix A.2.3 □

Armed with the probability distribution of the reactions and an update rule for the states in Equation (7), we can write down the algorithm explicitly.

Algorithm 1: τ-leaping

Result: $Y(t) \quad \forall t \in [0, T]$

Initialize $Y(0) = Y_0, t = 0$, and set fixed $\tau, \mathbf{S}$;

while $t < T$ **do**

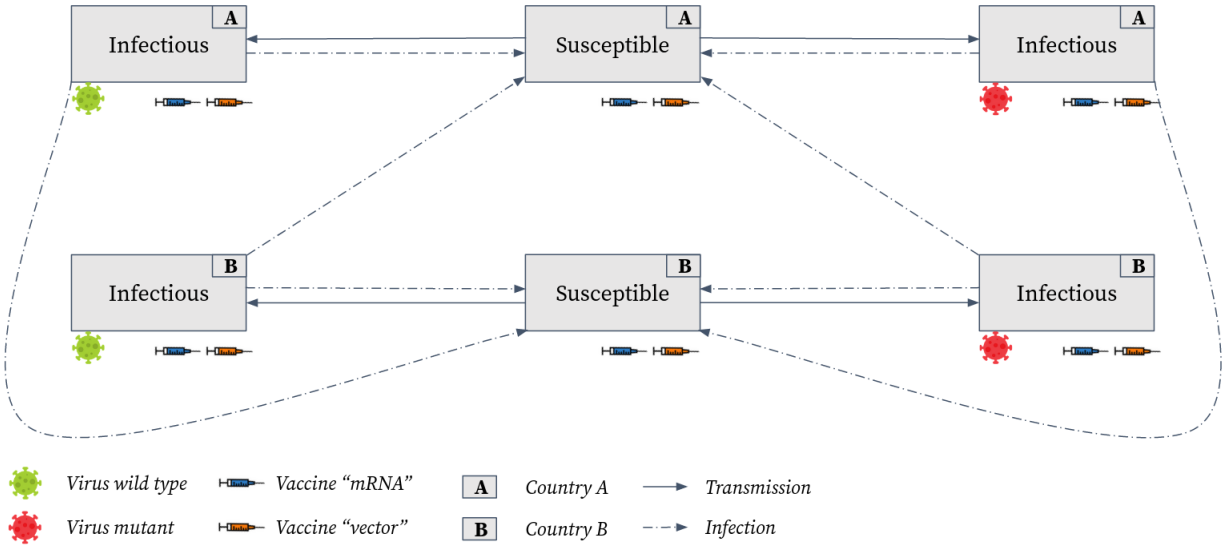
- Set y = Y(t);
- Update $a_j = a_j(y)$ for all $j = 1, \ldots, m$;
- Draw $K_{t,j} \sim \text{Po}(a_j \tau)$ for all $j = 1, \ldots, m$;
- Compute $Y(t+\tau) = Y(t) + \mathbf{S}K_t$;
- Store $Y(t+\tau)$;
- Update $t = t + \tau$;

end

2.3 Reactions

From a chemical reaction network's point of view, our model can be divided into four major groups of reactions: 1. Infections, 2. Recoveries and Deaths and 3. Vaccinations. We group recoveries and deaths, since their reactions have the same structure. We subsequently state the general and explicit reactions. We define the reactants, products, stoichiometric coefficients and reaction constants, such that that the ODE system (5) is determined. We emphasize on the reaction constants since they incorporate most of the parameterization of our model.

2.3.1 Infections



Note: Solid lines indicate transition paths and dashed lines indicate infections. Shots below a compartment indicate that individuals from this compartment can be vaccinated. Viruses below a compartment indicate that this compartment is infectious with the respective virus type. The letters in the top right corner of each compartment indicate the country of residence of individuals within the compartment.

Figure 2: Infection structure

Figure 2 depicts the structure of the transmissions from the susceptible to the infectious compartments. Every infectious individual $i_1 \in \mathcal{C}_t(x_I)$ can infect a susceptible individual $i_2 \in \mathcal{C}_t(x_S)$ regardless of their countries of residence. However, we account for the higher chance of becoming infected due to an individual from the same country by shrinking the influence of the infectious compartments from another country via the reaction constants.

In chemical terms, one infectious and one susceptible compartment serve as reactants and yield two infectious compartments that might be subdivided by further features as products

$$y_t(x_I, F_1) + y_t(x_S, F_2) \longrightarrow y_t(X_I, F_1) + y_t(X_I, F_2). \tag{11}$$

We use F_1, F_2 to indicate that the reactions differ with respect to not explicitly mentioned features, e.g. vaccinated individuals have a lower risk of becoming infected or transmitting the virus, the mutant virus is more infectious, and cross-border infections are scaled by a factor to make them comparatively rare events. If $F_1 \neq F_2$, the stoichiometric coefficients are one. If $F_1 = F_2$, they are one for the reactants but two for the product, which is in this case only one compartment. We incorporate the additional features, represented by F_1 and F_2, within the reaction constants, which we label as *infection constants*

infection constant = infections per day × vaccine modifier × compartment adjustment

In the following, we elaborate on how to define the components of the *infections per day*, the *vaccine modifiers*, and the *compartment adjustments*.

To compute the infections per day we use the average number of contacts between infectious and susceptible individuals, and multiply it with the proportion of individuals that become infected while meeting an infectious individual.

Let $c \in R_+$ be the average number of contacts per individual and day and $\alpha \in [0, 1]$ be the proportion of susceptible individuals that become infected if they meet a wild type infected individual without any vaccination of both individuals. Let $\eta \in (1, 1/\alpha]$ be the factor with which the mutant is more infectious than the wild type. Then $\beta = \alpha c$ is the average number of individuals infected per day by i_1 if $i_1 \in \mathcal{C}_t(X_I, V_w, U_0)$. If $i_1 \in \mathcal{C}_t(X_I, V_M, U_0)$, the average infected number increases to $\eta\beta$. We label β as *baseline infection constant* since it covers the most basic case where the reaction happens between an unvaccinated susceptible individual and an unvaccinated wild type infected individual.

Vaccinations influence infections via two channels. First, vaccinated susceptible individuals are less likely to become infected, see Table 2 for a list of references. Second, vaccinated

infectious individuals are less likely to transmit the virus (Harris et al., 2021).

To account for the influence of the first channel, we introduce the parameters $\delta_{k,l} \in [0,1]$, where $k \in \{W, M\}$ indicates the virus type and $l \in \{1,2\}$ the vaccine type. $\delta_{k,l}$ is the reduction in the probability of becoming infected while meeting an infectious individual after being vaccinated. Thus, susceptible individuals are $1-\delta_{k,l}$ times less likely to become infected while meeting an infectious individual. This is incorporated within the infection constant by multiplying the baseline infection constant with $1 - \delta_{k,l}$ if $i_s \in \mathcal{C}_t(X_S, U_1) \cup \mathcal{C}_t(X_I, U_2)$.

We account for the second channel by introducing the parameter $\gamma \in [0,1]$. γ is the reduction in the probability of not transmitting the virus after being vaccinated, which we assume to be constant over time and across vaccines. Analogously to the first channel, we multiply the baseline infection constant with $(1-\gamma)$ if $i_1 \in \mathcal{C}_t(X_I, U_1) \cup \mathcal{C}_t(X_I, U_2)$ to reduce the number of infections caused by a vaccinated individual.

So far, we have only defined the average number of contacts per day c of an infectious individual $i_1 \in \mathcal{C}_t(X_I, F_1)$ but not specified how these contacts are distributed across compartments. We use $\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, C_j, F_2) | i_1 \in \mathcal{C}_t(X_I, F_1))$, the conditional probability that the second individual i_2 is susceptible and from compartment $\mathcal{C}_t(X_S, C_j, F_2)$, and multiply it by β to get the baseline infection constant adjusted by the average number of contacts between i_1 and individuals of the compartment $\mathcal{C}_t(X_S, F_2)$. To increase readability we omit conditioning on $Y(t)$ and directly define $\mathbb{P}_t$ to be conditioned on the state of the system $Y(t)$.

We assume that the vaccination status, the type of virus infection, and the exact general compartment (X_S, X_I, X_R) of i_1, are independent of $\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, C_j, F_2))$. Thus, the problem facilitates to finding $\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_{j'}))$. This is to say, the probability that the individual that can be infected (i_2) is susceptible, unvaccinated, and from area two given that individual i_1 is infected with the wild type, unvaccinated, and from area one. Assuming independence of the vaccination status implies that an unvaccinated individual i_1 does not change her contact habits, given a certain number of meetings, compared to her counterfactual vaccinated self. Note that this does not mean that we assume that vaccinated and unvaccinated individuals have the same average number of contacts, since the probabilities are defined on *conditioned a meeting occurs*, but rather implies that she does not meet more vaccinated individuals than her unvaccinated counterfactual. Differences in the aver-

age number of contacts between vaccinated and unvaccinated individuals can be incorporated implicitly via the vaccination parameter $\delta_{k,l}$. To facilitate notation, we subsequently take the perspective that the infectious individual lives in country A. However, the same math applies to country B. We provide a detailed derivation of the probabilities within Appendix A.2.1.

$$\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, C_j, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) = \begin{cases} 1 - \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A,B)), & j = A \\ \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A,B)), & j = B \end{cases} \tag{12}$$

The probability is in essence the relative population size adjusted for lower cross-border meeting frequencies by a penalty function $b : \mathbb{R}_+ \to [0,1]$ that depends on the distance between both countries $d(A,B)$. By mapping the distance into the unit interval, we allow the probability of a cross-border meeting to be maximal as high as the relative population size. The distance can be interpreted as geographical distance but it could also serve to incorporate other factors, like favored holiday destinations, that encourage or discourage cross-border meetings. We impose three conditions on the function b

$$\lim_{b \to \infty} = 0 \tag{B.1}$$

$$b(0) = 1 \tag{B.2}$$

$$b(d_1) < b(d_2) \quad \text{if } d_1 > d_2. \tag{B.3}$$

Condition $(B.1)$ ensures that countries that have a large distance only have small influences onto each other. $(B.2)$ defines a rather theoretical case where cross-border meetings are as likely as within-country meetings. $(B.3)$ ensures that countries that have a greater distance have a smaller influence onto each other.

With the derived specifications of the infections per day, the vaccine modifiers, and the compartment adjustments, we can specify the compartment-specific infection constants. We illustrate this with two examples.

Example 1. *Let the reactants be the compartments* $\mathcal{C}_t(X_I, C_A, V_W, U_0)$ *and* $\mathcal{C}_t(X_S, C_B, U_0)$.

The corresponding reaction is

$$y_t(X_I, C_A, V_W, U_0) + y_t(X_S, C_B, U_0) \xrightarrow{r_{j_1}} y_t(X_I, C_A, V_W, U_0) + y_t(X_I, C_B, V_W, U_0), \tag{13}$$

where r_{j_1} denotes the infection rate. To account for the infections per day, we use the baseline infection constant β, since the infectious compartment is infected with the wild type. The susceptible and the infectious compartments are unvaccinated. Therefore, we do not multiply by a vaccine modifier. However, the compartments are from different countries. We therefore adjust by multiplying with $\frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A, B))$

$$r_{j_1} = \beta \cdot \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A, B)) \tag{14}$$

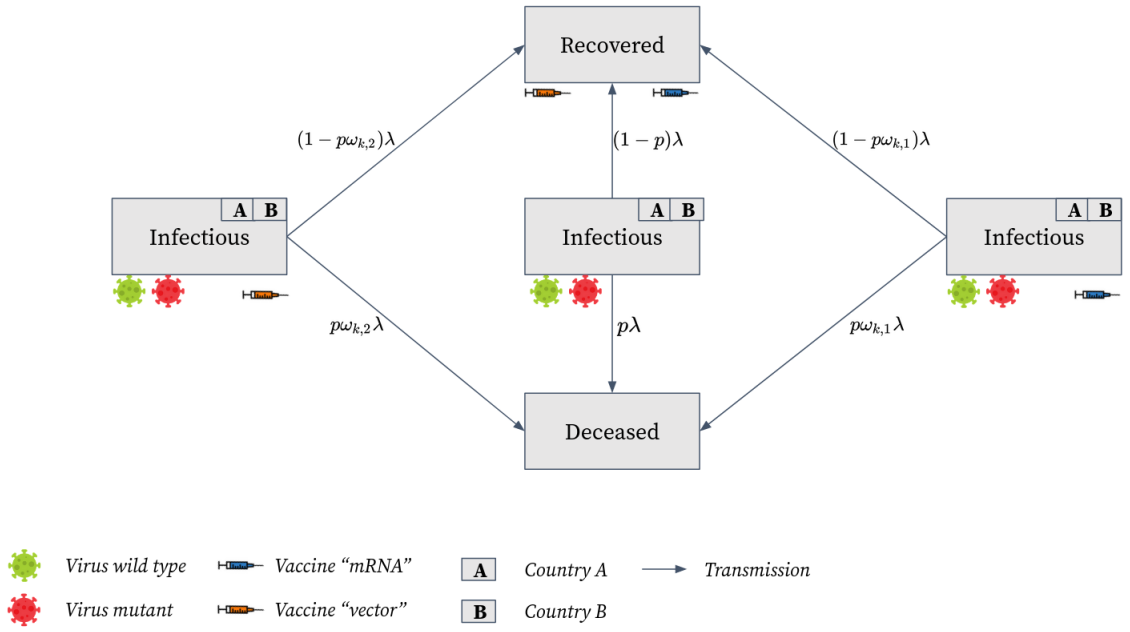
Example 2. *For the second example, we consider vaccinated and mutant infected compartments $\mathcal{C}_t(X_I, C_A, V_M, U_1)$ and $\mathcal{C}_t(X_S, C_B, U_2)$ as reactants to showcase the influence of the vaccine and the mutant modifier.*

$$y_t(X_I, C_A, V_M, U_1) + y_t(X_S, C_B, U_2) \xrightarrow{r_{j_2}} y_t(X_I, C_A, V_M, U_1) + y_t(X_I, C_B, V_M, U_2). \tag{15}$$

Since the infectious individual is infected with the mutant, we multiply the baseline infection constant with η. Since the infectious compartment is vaccinated, we multiply the constant with $(1 - \gamma)$. Since the susceptible compartment is vaccinated with vaccine U_2, we multiply the infection constant with $1 - \delta_{M,2}$. The compartments are from different countries. We therefore adjust by multiplying with $\frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A, B))$

$$r_{j_2} = (1 - \delta_{M,2})(1 - \gamma)\eta\beta \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A, B)). \tag{16}$$

To ensure readability we refrain from writing down all exact infections but they can be derived as shown in the two examples.



Note: Solid lines indicate transition paths. Shots below a compartment indicate that individuals from this compartment are vaccinated. Viruses below a compartment indicate that this compartment is infectious with the respective virus type. The letters in the top right corner of each compartment indicate the country of residence of individuals within the compartment. The formulas on top of the solid lines indicate the respective reaction constant.

Figure 3: Structure of recoveries and deaths

2.3.2 Recoveries and deaths

Figure 3 depicts the dynamics of the recoveries and deaths. The general reactions are defined by one infectious reactant and one product

$$\begin{aligned} \mathcal{C}_t(X_I, F_1) &\longrightarrow \mathcal{C}_t(X_D, F_1) \\ \mathcal{C}_t(X_I, F_1) &\longrightarrow \mathcal{C}_t(X_R, F_1). \end{aligned} \tag{17}$$

The reaction number is the product of the average number of individuals transmitting out of the infectious compartment $\mathcal{C}_t(X_I, F_1)$ and the fraction of individuals that transmit to the product compartment, either $\mathcal{C}_t(X_D, F_1)$ or $\mathcal{C}_t(X_R, F_1)$.

Let $\lambda \in \mathbb{R}_+$ be the average number of individuals that transmit out of $\mathcal{C}_t(X_I, F_1)$. We assume that a constant fraction $p \in [0, 1]$ of these individuals dies. Hence, $p\lambda$ individuals transmit to the deceased and $(1-p)\lambda$ individuals transmit to the recovered state. The explicit

reactions for unvaccinated individuals are for $i \in \{A, B\}$ and $k \in \{W, M\}$

$$\begin{aligned} \mathcal{C}_t(X_I, C_j, V_W, U_0) &\xrightarrow{p\lambda} \mathcal{C}_t(X_D, C_j, V_w, U_0) \\ \mathcal{C}_t(X_I, C_j, V_w, U_0) &\xrightarrow{(1-p)\lambda} \mathcal{C}_t(X_R, C_j, V_w, U_0) \end{aligned} \tag{18}$$

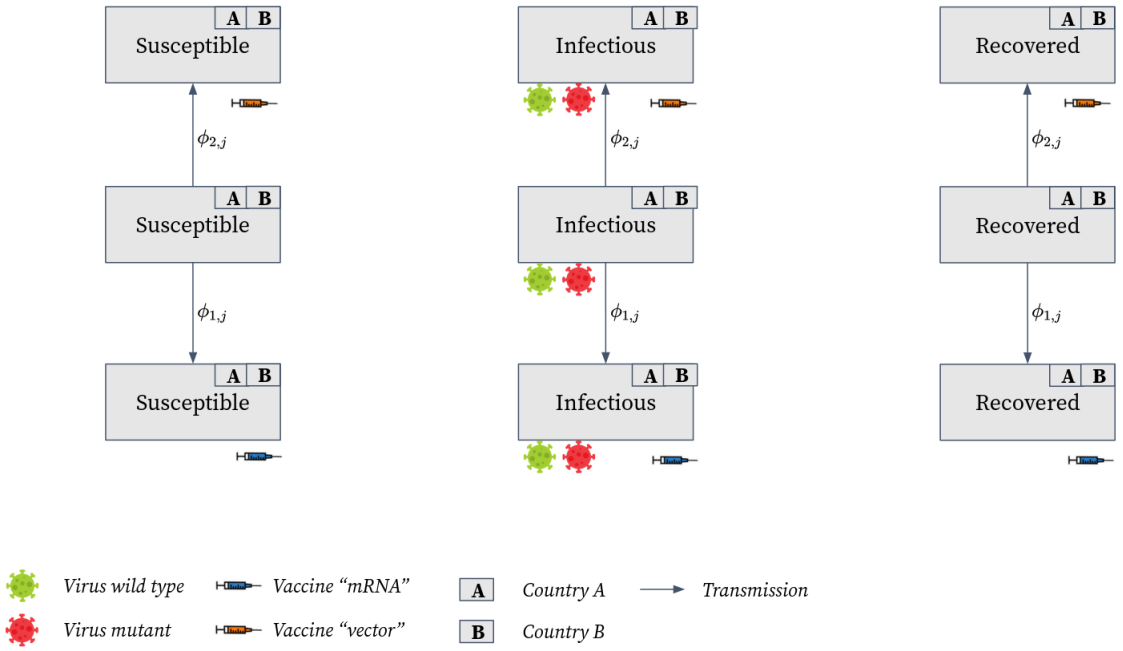
$1/\lambda$ is the average duration an individual spends within $\mathcal{C}_t(X_I, F_1)$. We have implicitly assumed that this time is the same for dying and recovering individuals, which might not be accurate in real-world examples since dying individuals have more severe cases and heavier viral loads, such that they stay longer infectious. However, incorporating separated average durations would raise the need for more compartments. Since we allow for vaccinations of recovered and infectious individuals, we assume that this simplification is negligible. Moreover, note that p does not depend on the virus type. The virus type therefore only influences the number of infections but not the probability of dying for infected individuals. According to Davies et al. (2021) this assumption might be violated due to higher mortality of mutants. However, we do so since we difference is rather low and we want to keep our model simple.

If the infectious individuals are vaccinated, they are less likely to decease (Tenforde, 2021; Voysey et al., 2021). To account for this reduction in the fraction that transmits to the deceased state, we introduce the parameters $\omega_{k,l} \in [0, 1]$, for $k \in \{W, M\}$ and $l \in \{1, 2\}$. We use $p\omega_{k,l}$ as a new probability of dying due to being infected with virus k after being vaccinated with vaccine l. $\omega_{k,l}$ is thus the reduction in the probability of dying. The corresponding reactions for vaccinated individuals are for $i \in \{A, B\}, k \in \{W, M\}$ and $l \in \{1, 2\}$

$$\begin{aligned} \mathcal{C}_t(X_I, C_j, V_k, U_l) &\xrightarrow{p\omega_{k,l}\lambda} \mathcal{C}_t(X_D, C_j, V_k, U_l) \\ \mathcal{C}_t(X_I, C_j, V_k, U_l) &\xrightarrow{(1-p\omega_{k,l})\lambda} \mathcal{C}_t(X_R, C_j, V_k, U_l) \end{aligned} \tag{19}$$

2.3.3 Vaccination

Figure 4 depicts the vaccination dynamics. We allow for vaccinations of susceptible, recovered and, deceased individuals. We vaccinate susceptible individuals to protect them from becoming infected. We vaccinate infectious individuals to account for asymptomatic cases (Byambasuren et al., 2020) and recovered individuals to account for the vaccine doses taken



Note: Solid lines indicate transition paths. Shots below a compartment indicate that individuals from this compartment are vaccinated with the respective vaccine. Viruses below a compartment indicate that this compartment is infectious. The letters in the top right corner of each compartment indicate the country of residence of individuals within the compartment. The formulas next to the solid lines indicate the respective reaction constant.

Figure 4: Structure of vaccinations

by them. The latter are vaccinated within the real world to increase their immunity (Skelly et al., 2021).

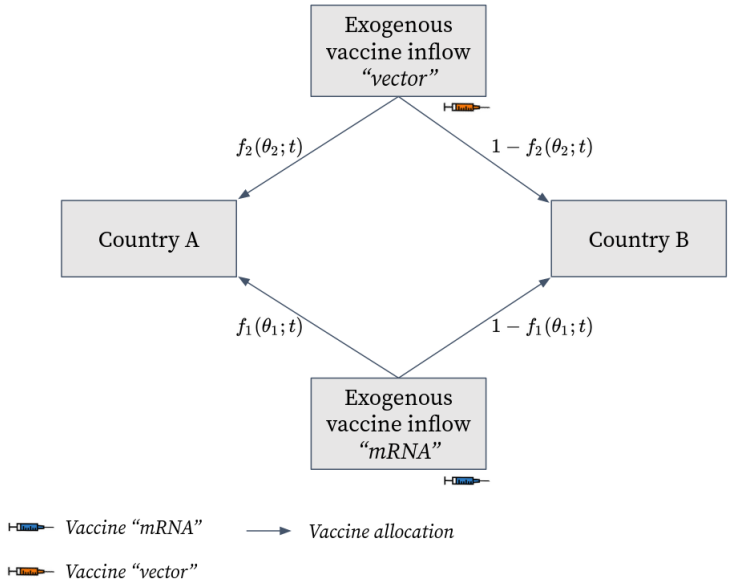
Let $\phi_{l,j} \in \mathbb{R}_+$ be the vaccination constant of vaccine l in country j at time t. The vaccination constant of one vaccine is assumed to be equal for all vaccination subcompartments of S, I, R within one country, which is to say, that the decision of vaccinating an individual is independent whether it is susceptible, infectious, or recovered. The corresponding reactions are for $j \in \{A, B\}$, $k \in \{W, M\}$ and $l \in \{1, 2\}$

$$\begin{aligned} \mathcal{C}_t(X_S, C_j, U_0) &\xrightarrow{\phi_{l,j}} \mathcal{C}_t(X_S, C_j, U_l) \\ \mathcal{C}_t(X_I, C_j, V_k, U_0) &\xrightarrow{\phi_{l,j}} \mathcal{C}_t(X_I, C_j, V_k, U_l) \\ \mathcal{C}_t(X_R, C_j, V_k, U_0) &\xrightarrow{\phi_{l,j}} \mathcal{C}_t(X_R, C_j, V_k, U_l). \end{aligned} \tag{20}$$

The vaccination constant is determined by the implemented vaccination policy. We explain how the vaccination constant is derived, given a vaccination policy, in Chapter 3.

3 Optimal vaccine allocation

The exercise to allocate vaccines across countries raises the need to specify the number of available vaccine shots. We define the number of available vaccines at any time t as exogenous and calibrate it based on the true number of COVID-19 vaccines that have been allocated to the EU within the start of 2021 and mid July 2021.



Note: Solid lines indicate vaccine allocations to a country. Shots below a box indicate the type of vaccines. The formulas next to the solid lines indicate the respective fractions of vaccines that are assigned to the country. The fractions depend on a parameter vector θ_l, over which we optimize to find the optimal solution.

Figure 5: Vaccine inflow and allocation across countries

Let $W_{l,j}(t)$ be the number of vaccination shots of vaccine l available at time t in country j and $W_l(t) = W_{l,A}(t) + W_{l,B}(t)$ be the total number of available vaccine shots of vaccine l at t. We assume that all vaccine shots are vaccinated immediately.

Assumption 2. *The total number of vaccine l available in country j equals the number of vaccinated individuals for all $t \in [0, T]$.*

$$W_{l,j}(t) = \phi_{l,j} \cdot y_t(\neg X_D, C_j, U_0). \tag{21}$$

Within the real world, vaccinations take around 2 weeks to yield full protection (CDC, 2021). With this regard, our model can be interpreted such that the number of lately vaccinated individuals is the number of individuals that lately received full protection by the vaccine. The

vaccination constant would then be the constant defining the reaction of becoming protected.

At each point in time t, country A receives a fraction $f_l(\theta_l; t)$, with $f_l : \mathbb{R}^z \times [0, \tau] \to [0, 1]$, of vaccine W_l. The fraction depends on the time t and a parameter vector $\theta_l \in \mathbb{R}^z$ that parameterizes $f_l(\theta_l; t)$.

We assume that all vaccines stay within the two countries and no vaccines are wasted

Assumption 3. *The total number of vaccine shots of country j is equal to the number of shots assigned to it*

$$\begin{aligned} W_{l,A}(t) &= f_l(\theta_l; t) W_l(t) \\ W_{l,B}(t) &= \left[1 - f_l(\theta_l; t)\right] W_l(t). \end{aligned} \tag{22}$$

We use Assumption 2, Assumption 3, and solve for the vaccination constants. They depend on the vaccine inflow, the fraction of vaccines assigned to the respective country, and the total numbers of individuals that potentially can be vaccinated within the country

$$\begin{aligned} \phi_{l,A} &= \frac{f_l(\theta_l; t) W_l(t)}{y_t(\neg X_D, C_A, U_0)} \\ \phi_{l,B} &= \frac{\left[1 - f_l(\theta_l; t)\right] W_l(t)}{y_t(\neg X_D, C_B, U_0)}. \end{aligned}$$

Note that the vaccination constant is actually not a constant since it depends on time dependent parameters. This is, however, just a naming convention that has no further implications for our model.

3.1 Objective function

Given a functional form of f_l, a specific $\bar{\theta}_l \in \mathbb{R}^z$ is called a *strategy* for vaccine l. A *vaccination strategy* $\bar{\Theta} = \begin{pmatrix} \bar{\theta}_1 \\ \bar{\theta}_2 \end{pmatrix}$ is a collection of strategies defined for both vaccines. We label the strategy Θ_{EU} that assigns the relative population size of country A to be the fraction of vaccines

assigned to country A,

$$f_l(\theta_{EU}, t) = \frac{y_0(\neg X_D, C_A)}{y_0(\neg X_D)}, \tag{23}$$

as *current EU strategy* or *current strategy* (European Commission, 2021a). Within the real world, member states of the EU can refrain from buying their whole quantity and therefore other member states can decide to buy it. We account for this implicitly within our optimization, since every allocation can be seen as a case where one country waives its right for a certain amount of vaccine doses.

We denote the number of deceased individuals in country A, conditioned on the current strategy, by $y_T(X_D, C_A; \Theta_{EU})$ and the corresponding number in country B by $y_T(X_D, C_B; \Theta_{EU})$. We use this strategy as a baseline case to examine how we can improve using an optimal strategy. An optimal strategy Θ^* is the solution to the minimization problem

$$\begin{aligned}
&\underset{\Theta \in \mathbb{R}^{2z}}{\arg\min} && y_T(X_D) \\
&\text{subject to} && \phi_{l,A} = \frac{f_l(\theta_l; t) W_l(t)}{y_t(\neg X_D, C_A, U_0)} && \text{for } l \in \{1, 2\}, && \text{(C.1)} \\
& && \phi_{l,B} = \frac{[1 - f_l(\theta_l; t)]\, W_l(t)}{y_t(\neg X_D, C_B, U_0)} && \text{for } l \in \{1, 2\}, && \text{(C.2)} \\
& && \Theta = \begin{pmatrix} \theta_1' & \theta_2' \end{pmatrix}', && && \text{(C.3)} \\
& && \beta, \eta, \gamma, \delta_{k,l}, \omega_{k,l}, Y(0), W_l(t) && && \text{(C.4)}
\end{aligned}$$

and we call it an *optimal vaccination strategy* for the given minimization problem. Conditions $C.1$, $C.2$, and $C.3$ indicate how the parameter vector Θ affects the model. $C.4$ specifies that all exogenous parameters are set to a constant value or exogenous function.

If additionally constraints $C.5$ and $C.6$ are satisfied,

$$y_T(X_D, C_A) < y_T(X_D, C_A; \Theta_{EU}) \tag{C.5}$$

$$y_T(X_D, C_B) < y_T(X_D, C_B; \Theta_{EU}) \tag{C.6}$$

the optimal strategy is Pareto optimal and we call it *Pareto optimal vaccination strategy.*

The Pareto optimality conditions ensure that both countries have fewer deceased individuals as within the current strategy. Taking the perspective that both countries can veto against strategies, non-Pareto optimal strategies might not be implementable since no country would agree to deviate from the current strategy if it experiences more deceased individuals with the new strategy.

We follow Bertsimas et al. (2020) and choose the total number of deceased individuals as objective. We decided to do so such that the death protection parameters $\omega_{k,l}$ influence the solution. Other objectives like the total number of infectious individuals, some combination of both, or ab objective that takes long-term measures into account could be considered as well.

3.2 Functional form of the vaccine allocation

We examine two functional forms of f_l. First, f_l is a stepwise function. Second, f_l is a logistically transformed third-order spline function. Both forms can be parameterized using the parameter vector θ_l. Both forms do not yield constructive vaccination strategies since we do not link the vaccine allocation directly to the state of the model but rather optimize over time-dependent parameters.

To define the functional forms, we subdivide the interval $[0, T]$ into a tagged partition $0 = t_0 < t_1 < \cdots < t_z = T$. Let $\mathcal{T}_i = [t_{i-1}, t_i)$, for $i = 1, \ldots, z$, be the corresponding intervals of the tagged partition. We label $\mathcal{T}$ as the *i-th decision period*. To be more precise on the functional form of f_l, we subdivide the parameter vector into its components $\theta_l = \begin{pmatrix} \theta_{l,1} & \theta_{l,2} & \ldots & \theta_{l,z} \end{pmatrix}'$.

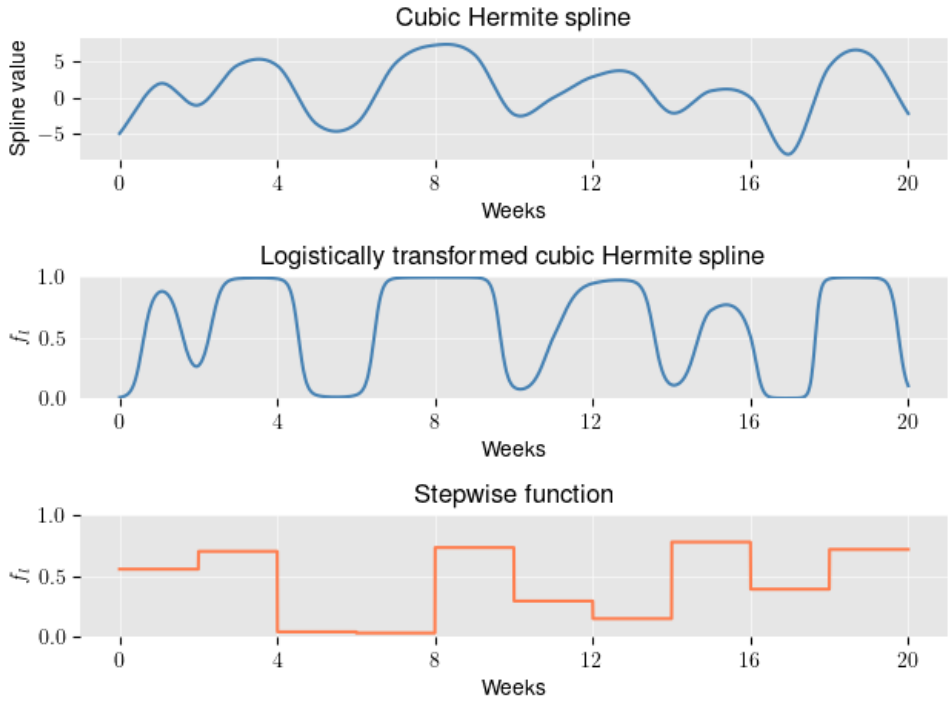
In a world with a piecewise constant vaccination channel, policymakers determine a fraction that is allocated to country A for a fixed decision period $\mathcal{T}_i$, evaluate, and then adjust before the next decision period T_{i+1} begins. In Figure 6 we show an exemplary vaccination strategy for vaccine l.

In mathematical terms, every $\theta_{l,i} \in [0, 1]$ is assigned to an interval $\mathcal{T}_i$. The parameters

$\theta_{l,i}$ are in this case the fractions of vaccines assigned to country A.

$$f_l(\theta_l; t) = \theta_{l,i} \quad \forall t \in \mathcal{T}_i. \tag{25}$$

Note that the current EU strategy is a special case of a step function that has $\theta_{l;1} = \theta_{l,2} = \ldots = \theta_{l,z} = y_0(\neg X_D, C_l)/y_0(\neg X_D)$, assuming that the allocations are not adjusted for changes in the population sizes over the course of the pandemic.



Note: Examples of a piecewise vaccine allocation in orange and a spline allocation in blue. The first graph depicts the values of the spline and the second graph shows the corresponding transformed function that maps the values into the unit interval. The third graph shows a different approach using a piecewise constant function. Decision intervals have a duration of 2 weeks.

Figure 6: Exemplary vaccination strategies for country A.

In a world with splines vaccination channel, policymakers decide on the start and end values of the vaccine allocations within each interval $\mathcal{T}_i$. Given the boundary values, one polynomial for each interval $\mathcal{T}_i$ is computed and logistically transformed to meet the unit interval domain of the fractions. By using polynomials, rather than constant functions, we allow for more complex policy decisions within one decision period $\mathcal{T}_i$ since fluctuations within one decision period can be taken into account. However, one should note that this exercise is rather theoretical and aims to show what strategies could be achieved theoretically.

We use splines instead of a global polynomial interpolation since they are practical with respect to construction and global interpolations might suffer from undesired properties, as in Runge's phenomenon (Runge, 1901).

Figure 6 shows an exemplary spline and how it is shrunk into the unit interval via the logistic function. Given a polynomial from the third-order polynomial ring over the real numbers $P_{l,i}(t) \in \mathbb{R}_3(t)$, the fraction is mathematically described by the composition of the polynomial and the logistic function

$$f_l(\theta; t) = \frac{1}{1 + \exp\left(-P_{l,i}(t)\right)} \quad \forall t \in \mathcal{T}_i. \tag{26}$$

We choose $P_{l,i}(t)$ to be in cubic Hermite form. The name cubic arises from the condition that every $P_{l,i}(t)$ is maximal a third-order polynomial. The name Hermite indicates that the derivatives at the boundaries $P'_{l,i}(t_{i-1})$ are approximated using finite differences. We use central finite differences for non-boundary values and forward as well as backward finite differences at the respective boundaries t_0 and t_z

$$\begin{aligned} P'_{l,1}(t_0) &\approx \frac{P_{l,1}(t_1) - P_{l,1}(t_0)}{t_1 - t_0} \\ P'_{l,i}(t_{i-1}) &\approx \frac{1}{2}\left[\frac{P_{l,i}(t_i) - P_{l,i}(t_{i-1})}{t_i - t_{i-1}} + \frac{P_{l,i-1}(t_{i-1}) - P_{l,i-1}(t_{i-2})}{t_{i-1} - t_{i-2}}\right] \\ P'_{l,z}(t_z) &\approx \frac{P_{l,z}(t_z) - P_{l,z}(t_{z-1})}{t_z - t_{z-1}}. \end{aligned} \tag{27}$$

Armed with the two functional values at the boundaries and approximations for their derivatives, we have four conditions to specify the polynomial of order three. Thus, we can parameterize the splines by specifying the polynomial values at the boundaries in terms of θ_l by setting the function values at the boundaries equal to the respective coefficient

$$\begin{aligned} P_{l,i}(t_{i-1}) &= \theta_{l,i-1} \\ P_{l,i}(t_i) &= \theta_{l,i}. \end{aligned} \tag{28}$$

The polynomial $P_{l,i}(t)$ is given as a linear combination of four basis polynomials $B_1(t)$, $B_2(t)$, $B_3(t)$ and $B_4(t) \in \mathbb{R}_3(t)$ with the boundary values of the polynomial and its derivative.

Let $t' = (t - t_{i-1})/(t_i - t_{i-1})$ for $t \in \mathcal{T}_i$ and

$$P_{l,i}(t) = B_1(t') \overbrace{P_{l,i}(t_{i-1})}^{\theta_{l,i-1}} + B_2(t')(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ + B_3(t') \underbrace{P_{l,i}(t_i)}_{\theta_{l,i}} + B_4(t')(t_i - t_{i-1})P'_{l,i}(t_i) \quad \forall t \in \mathcal{T}_i. \tag{29}$$

The scalars of the linear combination are dependent on the parameter vector θ_l through (27) and (28). The basis polynomials are defined by $B_1(t) = 2t^3 - 3t^2 + 1, B_2(t) = t^3 - 2t^2 + t, B_3(t) = -2t^3 + 3t^2$ and $B_4(t) = t^3 - t^2$. Note that the imposed structure of $P_{l,i}(t)$ is well-defined, which can be verified by evaluating the polynomial and its derivative at the boundaries t_{i-1} and t_i. We provide the calculations in Appendix A.2.2.

We show that the basis polynomials indeed form a basis of $\mathbb{R}_3(t)$. Showing the basis property proves that the four polynomials span $\mathbb{R}_3(t)$ and, therefore, we do not exclude any polynomials from the space of policies that could be implemented.

Theorem 2. *$B_1(t), B_2(t), B_3(t), B_4(t) \in \mathbb{R}_3(t)$ form a polynomial basis of $\mathbb{R}_3(t)$.*

Proof. The proof is moved to Appendix A.2.4. □

4 Simulation and optimization

We use values derived from the literature to calibrate our models fixed parameters. We simulate one model using a stepwise vaccination strategy and one model using s spline vaccination strategy.

4.1 Calibration

Within our model there exist two vaccines U_1 and U_2. Whereas in the EU, as of July 2021, 4 vaccines are approved and two are in the development phase (European Commission, 2021b). To establish the link from our theoretical model to the real-world COVID-19 vaccines, we use data based on the four approved vaccines to calibrate our model. Vaccine U_1 represents the messenger ribonucleic acid (mRNA) vaccines and vaccine U_2 represent the vector vaccines.

Currently EU-approved mRNA vaccines are Comirnaty, also known as BNT162b2, from Pfizer-BioNTech and Spikevax, also known as mRNA-1273, from Moderna. The approved vector vaccines are Vaxzevria from Oxford-Astra Zeneca and Janssen, also known as Johnson & Johnson COVID-19 vaccine, from Janssen Vaccines.

We use efficacy values reported within the literature to calibrate the vaccine-specific parameters $\delta_{k,l}$ and $\omega_{k,l}$. Efficacy describes the effect with respect to perfect conditions whereas effectiveness measures the effect under real-world clinical settings (Gartlehner et al., 2006). Therefore, real-world effectiveness could be lower than the numbers reported in Table 2. We use data from the early alpha virus type to calibrate the wild type parameters and data from the lately spreading delta variant to calibrate the mutant parameters. In contrast to conventional vaccines, mRNA vaccines do not contain viral proteins themselves. They only contain the information human cells need to produce a virus trait that triggers the desired immune response (Biontech, 2021). This new method has shown a significant improvement concerning immunity yielding higher efficiacy values in Table 2.

Vaccine	Efficacy		Sources
	alpha	delta	
Comirnaty	94%-95%	87%-95%	Callaway (2021), Nasreen et al. (2021), Polack et al. (2020), Prüβ (2021), Sheikh et al. (2021)
Spikevax	94%	-	Oliver (2021b), Prüβ (2021)
Vaxzevria	66%-73%	60%-71%	Callaway (2021), Emary et al. (2021), Prüβ (2021), Stowe et al. (2021)
Janssen	66%	-	Oliver (2021a), Sadoff et al. (2021)

Note: Efficacy is measured as protection against an infection after 14 days of the second vaccine shot.

Table 2: Vaccine efficacy

Due to the recent spread of the delta variant, data is still limited and we did not find reliable sources for the delta efficacy of Spikevax and Janssen. For the latter, a recent study by Jongeneelen et al. (2021) reports that, even though real-world effectiveness has been shown, they found no efficacy for the Janssen vaccine against the delta variant. Since their study only included 8 individuals and, therefore, we refrain from using the study to calibrate our model.

With respect to Table 2, we decided to set the protection of the mRNA vaccines against

infection with the wild type (alpha variant) to be $\delta_{1,W} = 0.94$ and against infection with the mutant (delta variant) to be $\delta_{1,M} = 0.9$. For the vector vaccines we chose for the wild type $\delta_{2,W} = 0.7$ and for the mutant $\delta_{2,M} = 0.65$.

Abu-Raddad et al. (2021) report Comirnaty to protect from hospitalization by 97.4%. Tenforde (2021) find that Comirnaty and Spikevax yield 94% protection against hospitalization within the age group of ≥ 65 aged individuals. Voysey et al. (2021) report a 100% efficacy against hospitalization regarding Vaxzevria and the alpha variant. We generalize the empirical results and set the value against death protection $\omega_{k,l} = 0.99$ for all $k \in \{W, M\}$ and $l \in \{1, 2\}$.

Harris et al. (2021) found that in a study of more than 365,000 British households, mixed with vaccinated and unvaccinated individuals, that full vaccination with Comirnaty or Vaxzevria reduces the transmission probability by 40%-60%. We therefore set $\delta = 0.5$.

The basic reproduction number R_l of virus type l is the average number of unvaccinated individuals infected by one unvaccinated infectious individual. Translated to our model, this yields the following equations

$$\begin{aligned} R_W &= \frac{\beta}{\lambda} \\ R_M &= \frac{\eta\beta}{\lambda}, \end{aligned} \tag{30}$$

Recall that $1/\lambda$ is the average time an individual is infected and β, or $\eta\beta$, is the average number of individuals infected by one infectious individual per day. The German Robert Koch Institut (2021) reports the basic reproduction number to be between 2.8 and 3.8. Moreover, they state that an individual is around 10 days infectious. We use $\lambda = 0.1, R_W = 3$ and $R_M = 3.6$, yielding $\beta = 0.3$ and $\eta = 1.2$. Note that these numbers do not take non-pharmaceutical measures, like testing and social distancing, into account, and therefore our simulated pandemic might have higher death numbers and be earlier terminated than the real-world COVID-19 pandemic.

Baud et al. (2020) find a death rate of 5.7% for symptomatic cases. However, this overestimates the true death rate due to undetected asymptomatic cases that did not result in death. Wu and McGoogan (2020) account for asymptomatic cases and find estimates to be between 2%-3%. We therefore use $p = 2.5\%$ for our simulations.

To define the initial value problem, we set the initial population size of susceptible individuals in both countries to $y_0(X_S, C_A) = y_0(X_S, C_B) = 80$ million, a country size similar to Germany. Country A starts with ten wild type infectious individuals $y_0(X_I, C_A, V_W) = 10$ and country B with ten mutant type infected individuals $y_0(X_I, C_B, V_M) = 10$. We initially separate the virus types by country to examine the influence of heterogeneous virus infectiousness of appearing mutants across countries. All other compartments are set to zero at the beginning.

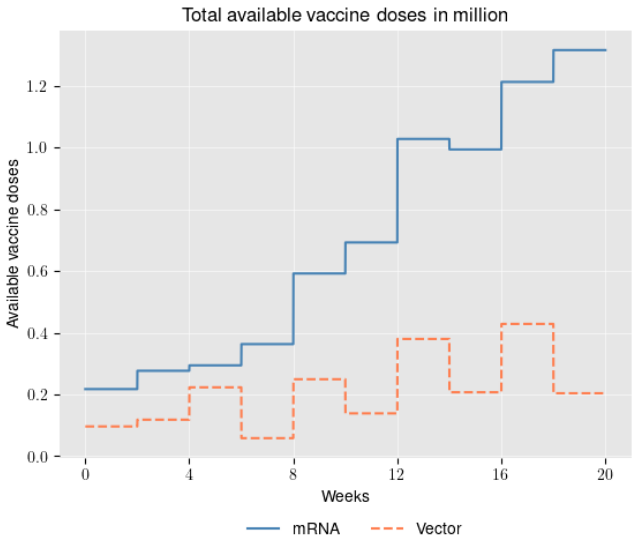
To specify the cross-border meeting modifier $b(d(A, B))$, we use tourism data from Germany and France. We use France since it is population-wise the largest country with a border to Germany. In 2016, $1,725,854$ individuals from France traveled to Germany and stayed on average for two days (Statistisches Bundesamt, 2017). We divide this number by 366 to get an estimate of the average number of French individuals in Germany at each day in 2016 and scale it by $\frac{80}{67}$ to adjust that our second country has a population size of 80 million but France has around 67 million inhabitants $\frac{2 \cdot 1,725,854}{366} \cdot \frac{80}{67} \approx 11,261$. Assuming that the same number of French individuals have been in Germany every day and using equation (34) with a constant proportion $y_t(\neg X_D, C_B)/y_t(\neg X_D)$ yields

$$b(d(A, B)) = \frac{11,261}{80,000,000} \approx 0.0002$$

Note that this estimate is rather conservative since we do not take commuters and unregistered visits, such as shopping trips, into account.

We set the length of the whole decision period to $T = 140$ and subdivide the length of each decision interval $\mathcal{T}_i$ to 14 days. Figure 7 depicts the inflow of both vaccines. The daily vaccine inflow $W_l(t)$ is computed using EU data of the vaccine inflow taken from the open-source data bank of the ECDC (2021b). The data reports the weekly inflow of vaccines

for all countries within the EU. We accumulate the numbers of Corminarty and Spikevax to compute the total numbers of mRNA vaccines and accumulate the total numbers of Vaxzevria and Janssen to compute the total numbers of vector vaccines per week. We scale this number down to our model's population size by dividing it through the total number of EU habitants and multiplicate it by the number of individuals in our model. We subsequently accumulate the vaccines within each 14-day interval $\mathcal{T}_i$ and divide this number by 14 to get the average number of vaccine doses inflow per vaccine and day. Thus, the inflow per day of each vaccine is constant within each interval $\mathcal{T}_i$ but varies across intervals and vaccines yielding the stepwise functions in Figure 7.



Note: The total inflow of mRNA and vector vaccines is accumulated for each 2-week decision period and equally distributed across days. Real-world numbers are scaled down by a population size adjustment to account for the population size of our model.

Figure 7: Time course of exogenous vaccine inflow.

Overall, the inflow increases over time. This is due to the improvement of manufacturer infrastructure over the time course of the pandemic in the real world and the constantly high demand for vaccines.

4.2 Deterministic simulations

We use Python and mainly its libraries libSBML (Bornstein et al., 2008) and AMICI (Fröhlich et al., 2021) to implement our models. pyPESTO (Schälte et al., 2021) is our main tool for optimization. To minimize the optimization problem, we use the L-BFGS-B algorithm

(Zhu et al., 1997) for which pyPESTO uses Scipy's (Virtanen et al., 2020) implementation. For each optimization we run a muli-start using 50 starts and choose the corresponding vaccination strategy that minimizes the objective. We provide waterfall plots for the piecewise constant and the spline optimization within Appendix A.1.3 in Figure 18 and Figure 19. For each start, we draw uncorrelated start parameters $\theta_{l,i} \sim \mathcal{U}(0,1)$. In the case of Pareto optimal constraints, we only accept a starting vector Θ if the Pareto constraints $C.5$ and $C.6$ are satisfied. Otherwise, we reject it and draw a new sample until 50 starts are reached.

The results using a piecewise constant form and a spline as functional forms of f_l yielded very similar results regarding the trajectories of the compartments, which we see as enhancement of the robustness of our findings. However, we refrain from showing the same results twice and move the results from the piecewise constant approach to Appendix A.1.1.

Figure 8 provides a visualization of the core results for the number of deceased individuals using splines as functional form of f_l. We show the results for the current strategy (first row), the Pareto optimal strategy (second row), and the unrestricted strategy (third row) and split up the numbers of deceased individuals with respect to their country of origin. Both optimized strategies outperform the current strategy. This is plausible, since within the optimized strategies, the model states are taken into account, whereas the current strategy is a pre-allocation that does not take model dynamics into account. The unrestricted strategy also outperforms the Pareto optimal strategy, which comes by nature of the optimization specification as they are in essence the same optimization problem but the Pareto parameter space is restricted by the two Pareto conditions $C.5$ and $C.6$.

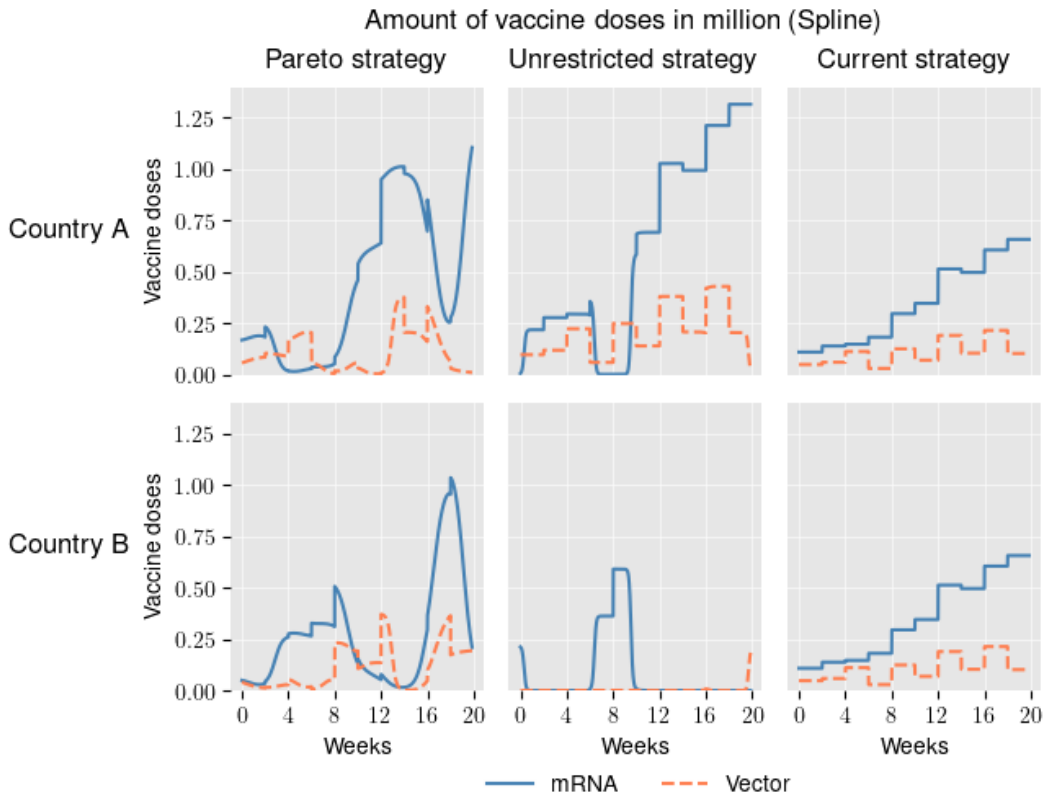
The unrestricted strategy yields a reduction in deaths by around 17%, relative to the current strategy. However, given full knowledge of the outcome, policymakers in country B would not agree to implement this strategy due to the increase of around 320,000 deaths in country B. The Pareto strategy yields the same death cases in country B as the current strategy. However, at the same time, death cases in country A can be reduced by around 130,000, yielding an overall improvement of around 5% relative to the current strategy. Thus, the Pareto optimal strategy might be approved by both countries as an overall improvement to society.

Note: The numbers within the boxes indicate the number of deceased individuals in million with respect to the respective country and strategy. Numbers at the x-axis represent the total number of deceased individuals within one country. The percentage numbers indicate the change relative to the optimal strategy, e.g. -5% indicates that by implementing the Pareto strategy 5% fewer individuals died in comparison to the current strategy.

Figure 8: Number of deceased individuals simulated

Figure 9 depicts the corresponding doses of vaccine inflow. We show the results for the three strategies (columns) and split up the results by countries (rows). The current strategy numbers are, due to the equi-allocation, 50% of the total inflow of each vaccine. Most strikingly, the unrestricted strategy only assigns vaccines to country B between the 5th and the 9th week, as well as at the start and the last periods. The period between the 5th and the 9th week is where the number of infectious cases increases exponentially within country B, see Figure 10. The vaccine shortage in country B partly explains the large number of death cases in country B which we find in Figure 8. On the contrary, the Pareto strategy assigns much more doses to country B, especially at the end of the decision horizon. As seen in Figure 8, this comes with the cost of more deaths in country A compared to the unrestricted strategy. With respect to the current strategy, we observe that the optimized strategies are very different from the current strategy. This is highlighted within plot 17 in Appendix A.1.2, where we plot the course of the functions f_l.

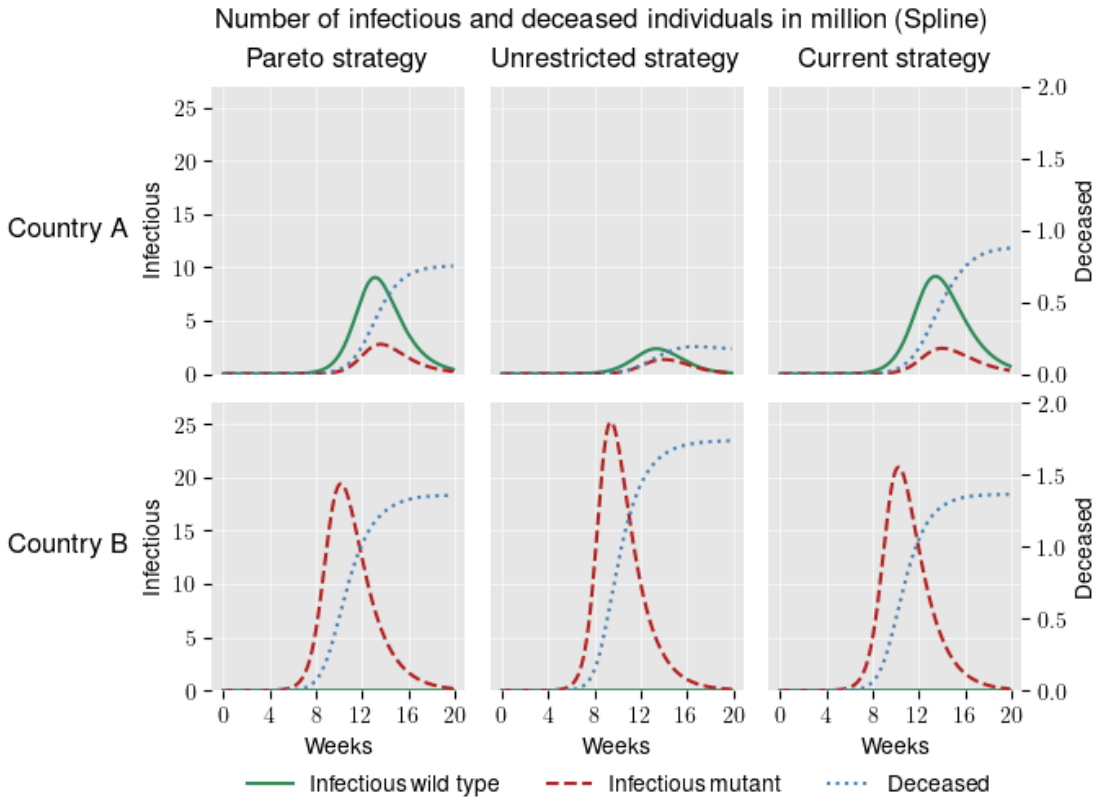
In Figure 10, we trace out the trajectories of the number of infectious and deceased individuals according to the respective strategies (columns) and countries (rows). Regardless of the strategy, only the mutant spreads in country B. This is due to the initial allocation of ten mutant infected individuals in country B and ten wild type infected individuals in country



Note: Every column represents one vaccination strategy and every row represents one country. Both vaccines are indicated by the colors that are used throughout the paper. Every curve is the product of a piecewise constant vaccine inflow and a spline. Thus, the lines appear to be discontinuous piecewise polynomials.

Figure 9: Number of allocated vaccine doses

A and the higher infectiousness of the mutant. The higher infectiousness of 20% prevents the wild type from spreading in country B via cross-border infections. On the contrary, country A has to deal with both variants due to the cross-border infections. The unrestricted strategy can keep infections in country A below 2 million, whereas the Pareto strategy and the current strategy experience more than 7 million cases.



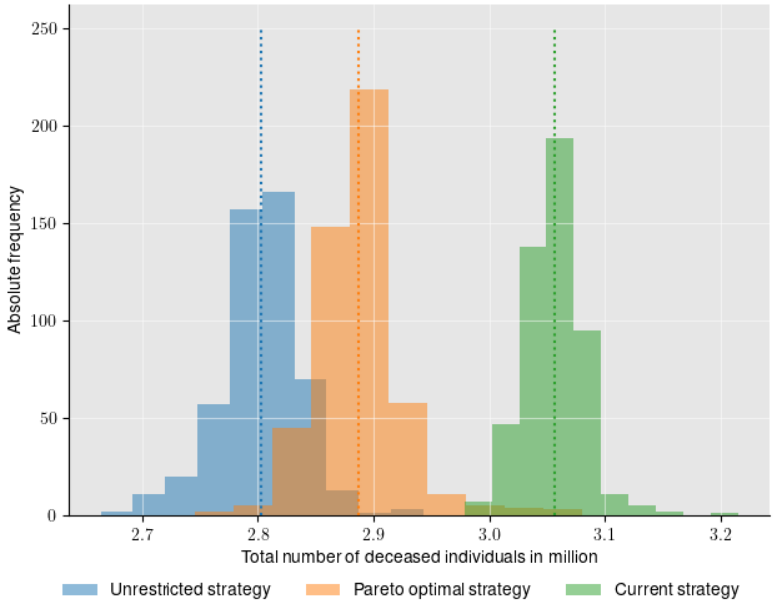
Note: Every column represents one vaccination strategy and every row represents one country. Every vaccine is indicated by its color that is used throughout the paper. The left y-axis is used for the number of infectious individuals (solid green and dashed red curves). The right y-axis corresponds to the number of deceased individuals (dotted blue line). Both viruses are associated with the color we have used throughout the paper.

Figure 10: Number of infectious individuals

4.3 Policy test with stochastic model

We test the deterministically derived strategies within the stochastic set-up from Section 2.2 to examine how they perform in an uncertain world where infections, recoveries, and deaths do not follow pre-determined patterns. We generate 500 samples per strategy by running Algorithm 1. Unfortunately, we cannot simualte the algorithm with a set of random variables and test every strategy for this set and compare the results with a counterfactual interpretation. This is due to the nature of the problem, the means of the Poisson random variables in Equation (7) are dependent on the system's state and therefore the magnitude of randomness changes with the strategies making counterfactual interpretations unfeasible.

Figure 11, depicts the histograms of the number of deaths clustered by the three strategies. The average number of deceased individuals is between 0.78 and 0.95 million higher as in the respective deterministically derived strategies. However, we observe on average the same order as for the deterministic case. The unrestricted strategy yields the fewest deaths whereas most deaths are observed for the current strategy. We plot the joint distribution of the deaths,

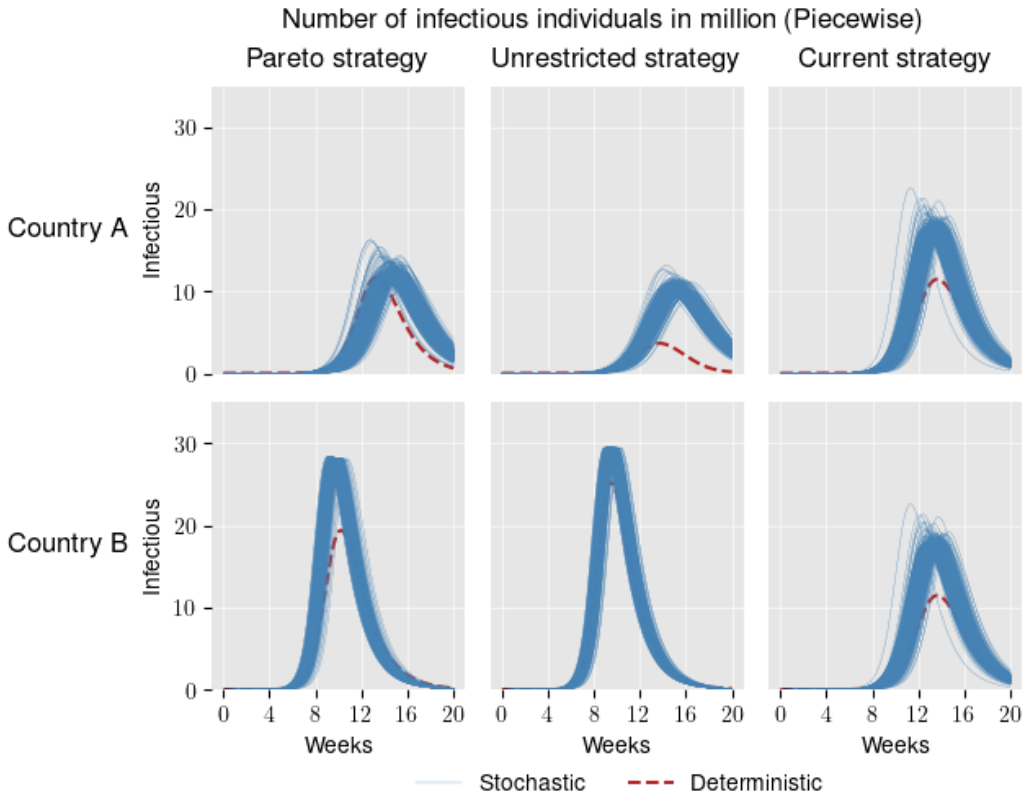


Note: Dotted lines are sample means. The total number of deceased individuals of a strategy is the sum of the respective number of deaths in in country A and country B. We draw 500 samples per strategy.

Figure 11: Stochastically observed frequencies (Splines)

split up by country, and the respective marginal histograms in Figure 22 in Appendix A.1.4.

In Figure 12, we explore how the number of infectious individuals varies within the samples. The course of infectious individuals of the unrestricted strategy in country B captures the deterministic numbers well. Within the other figures, the case numbers seem to be higher within the stochastic model, which is in line with the increased number of deaths observed in Figure 11.



Note: Every column represents one vaccination strategy and every row represents one country. The thin blue lines depict all 500 simulations of the stochastic algorithm using the respective strategy. The dashed red depicts the respective infections within the deterministic model.

Figure 12: Number of infectious individuals using Stochastic simulations

5 Conclusion

Our research aims to trace out if the population size based EU vaccination policy against the COVID-19 pandemic can be improved, such that it minimizes deaths across countries. We propose a deterministic SIRD compartment model, with two countries and two vaccines, to examine the effect of optimal strategies compared to the current EU strategy. We calibrate our model with parameters from the literature and the real-world vaccine inflow of the

COVID-19 vaccines. We construct the vaccination channels via piecewise constant functions and splines. We examine one case where we impose further restrictions on the optimal vaccine allocation and one case where we constrain the results to be an improvement for each country. We simulate the models numerically and validate the optimal strategies derived from the deterministic model in a stochastic extension to our model.

Our results show that the optimal derived vaccination strategies differ from the current EU strategy, which could indicate that more complex vaccination policies can lower the number of death cases caused by the pandemic. Enhancing the robustness of our results, we find qualitatively highly similar results using piecewise constant and spline vaccination channels. Leaving country-specific interests aside, we find it can be beneficial to assign most of the vaccine doses to one country, leading to a remarkable reduction of deaths within this country. The other country experiences a severe increase in death cases but the decrease of case numbers within the first country is substantially lower, leading to an overall decrease in the number of deaths. However, policymakers of the second country would not be willing to agree to this policy due to the higher case numbers. We find that imposing additional Pareto constraints yields an overall improvement in comparison to the current strategy but an overall deterioration in comparison to the unrestricted optimal strategy. The Pareto optimal strategy, we derive, assigns just enough vaccine doses to the second country such that it has the same case numbers as for the baseline EU strategy. However, the first country is better off, leading to an overall improvement of the Pareto strategy in comparison to the current strategy. Since both countries are not worse off, they have no incentive to vote against the Pareto optimal strategy, making it more likely to be implemented in practice. Stochastic simulations yielded higher death numbers but underlined the general findings with respect to the efficiency of the strategies.

In ongoing work, we pursue two avenues for further improvement. First, we implement neural networks as the third channel of vaccine allocation. The piecewise constant approach and the splines do not yield constructive vaccination strategies since we do not link the vaccine allocation directly to the states of the model. We use as inputs for the neural network model states and parameters that could be (at least approximately) observed in the real world, such as the current infected case numbers, the change in infected case numbers,

and the reproduction number. Due to the linkage of vaccine allocation output to the model states, an optimal allocation is in this scenario transferable to the real world in a sense that the real-world vaccination strategy can be adjusted according to the output of the neural network, given the real-world's state. Second, we plan to incorporate further compartments that account for different age structures of countries. Adding further age-dependent compartments helps us to understand how vaccination strategies must be adapted according to country-specific demographics. We especially aim to focus on the implications of child vaccinations.

In addition, it might be worth examining how the dynamics of the model change after including testing and quarantines. We are particularly interested in examining how testing and vaccinations can be optimally exploited together, or if tests can even substitute vaccinations up to a certain degree. Moreover, our analysis does not take non-death related disutilities, like physical long-term damage caused by infection into account. A modified objective that takes long-term measures into account could help to address this issue.

Our findings about the unrestricted optimization trace out an important dilemma for policy makers of supranational institutions, such as the European Union, when it comes to choosing a vaccination strategy for the current COVID-19 pandemic. On the one hand, choosing the overall number of death cases seems to be a plausible objective. On the other hand, the supranational policymakers cannot outweigh the disutility of one country with the benefits of another country. However, our findings concerning the Pareto optimality enhance that given the current strategy, a Pareto improvement might be possible, which could be adapted by policymakers if further research is processed.

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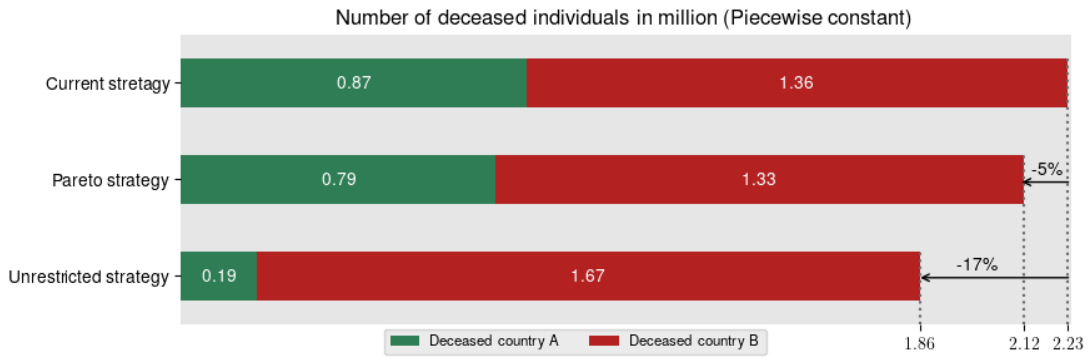
A Appendix

A.1 Additional Figures

We plot Figures that enhance our line of argumentation but would disturb the train of reading within the main section.

A.1.1 Piecewise constant results

Figure 13 provides a visualization of our core results for the number of deceased individuals using piecewise constant vaccination channels as functional form f_l. The values do qualitatively not differ form the corresponding spline values depicted in the main text in Figure 8.

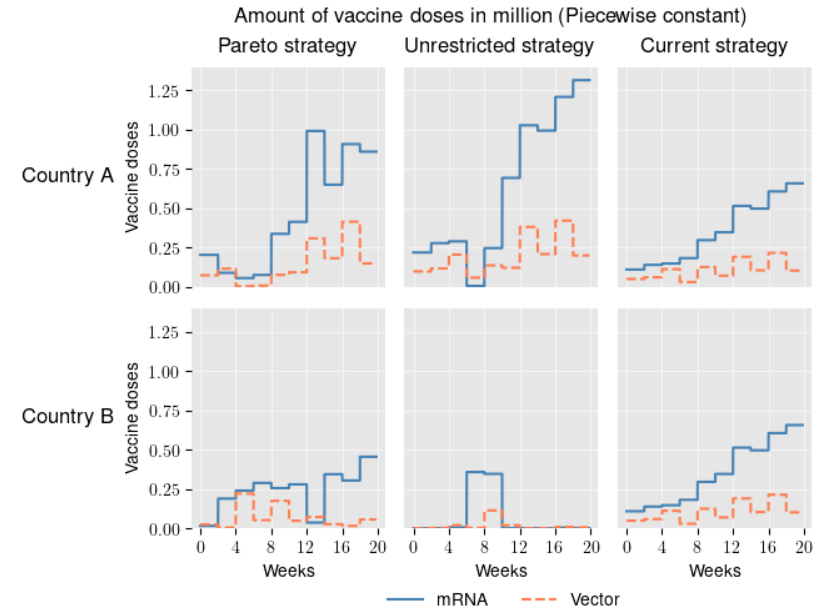


Note: The numbers within the boxes indicate the number of deceased individuals in million with respect to the respective country and strategy. Numbers at the x-axis represent the total number of deceased individuals within one country. The percentage numbers indicate the change relative to the optimal strategy, e.g. -5% indicates that by implementing the Pareto strategy 5% less individuals died in comparison to the current strategy.

Figure 13: Simulation results for piecewise constant vaccination strategies.

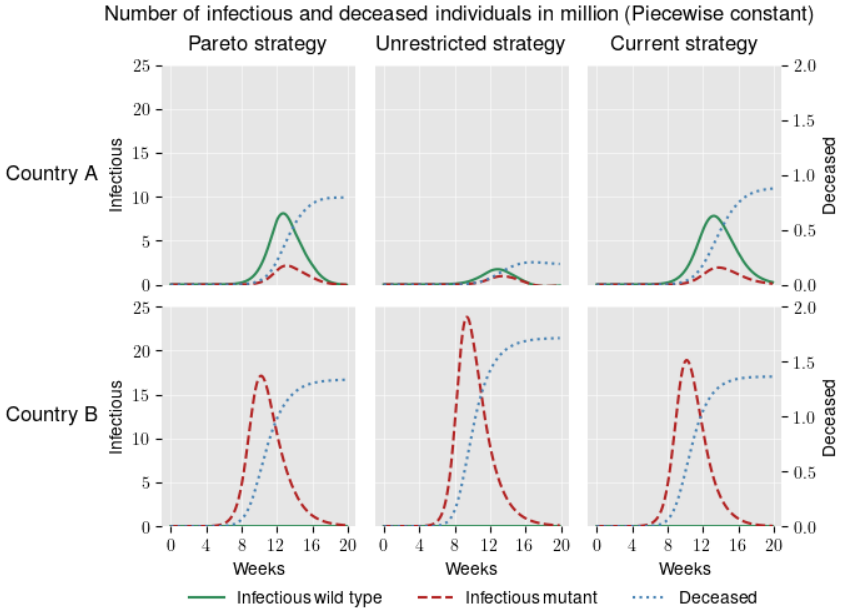
Figure 14 depicts the optimal doses of vaccine inflow using piecewise constant vaccination channels as functional form f_l. As for the number of deceased individuals, the values do qualitatively not differ form the corresponding spline values depicted in the main text in Figure 9.

In Figure 15, we trace out the trajectories of the number of infectious and deceased individuals according to the respective strategies (columns) and countries (rows). The values do qualitatively not differ form the corresponding spline values depicted in the main text in Figure 10.



Note: Every column represents one vaccination strategy and every row represents one country. Both vaccines are indicated by their colors that are used throughout the paper. Every curve is the product of a piecewise constant vaccine inflow and a spline. Thus, the lines appear to be discontinuous piecewise polynomials.

Figure 14: Number of allocated vaccine doses.

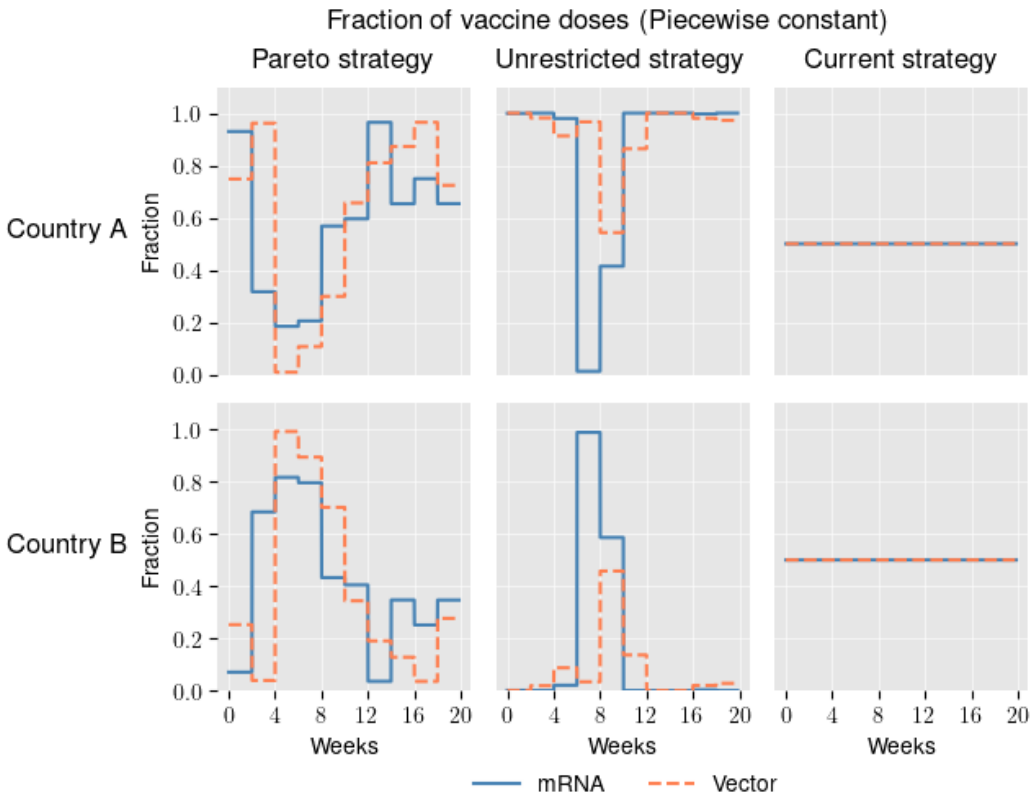


Note: Every column represents one vaccination strategy and every row represents one country. Every vaccine is indicated by its color that is used throughout the paper. The left y-axis is used for the number of infectious individuals (solid green and dashed red curves). The right y-axis corresponds to the number of deceased individuals (dotted blue line). Both viruses are associated with the color we have used throughout the paper.

Figure 15: Number of infectious individuals

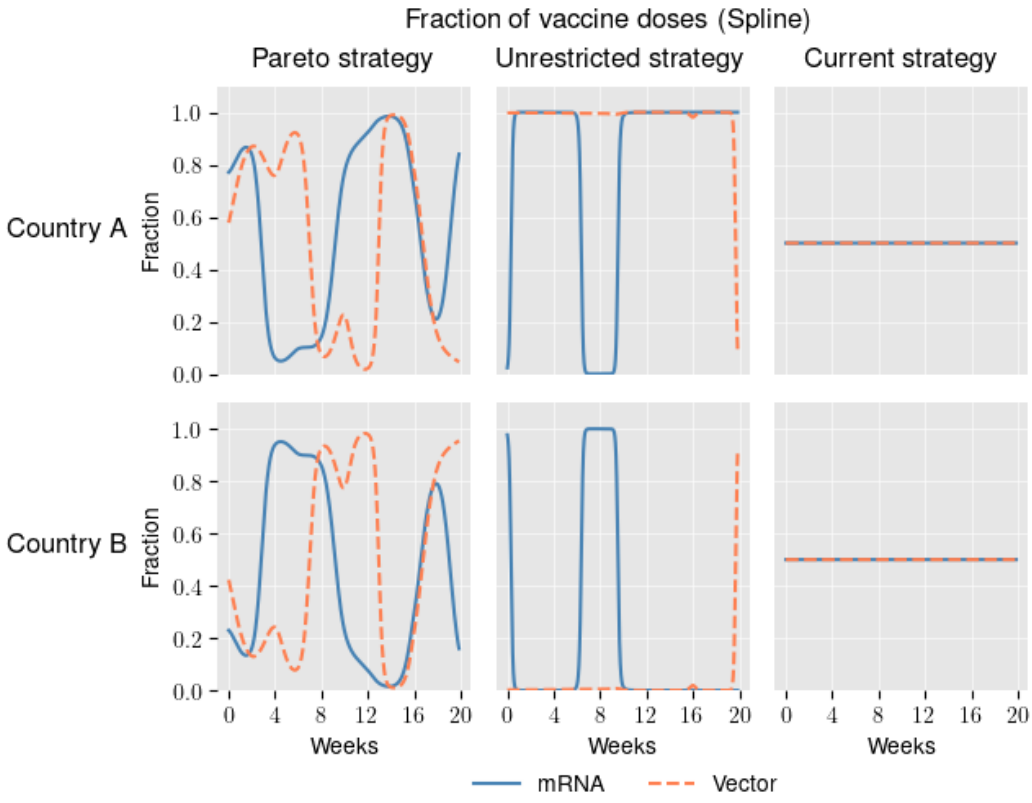
A.1.2 Vaccination allocation fractions

Figure 16 depicts the course of f_l over the whole decison period using a piecewise vaccination channel. Figure 17 depicts the respective values for the spline vaccination channels. The values are the quotient of the curve of the vacicne inflow in 7 and the optimal total number of vaccine doses inflow in Figure 14 and Figure 9.



Note: Every column represents one vaccination strategy and every row represents one country. Both vaccines are indicated by their colors that are used throughout the paper.

Figure 16: Fractions of vaccines

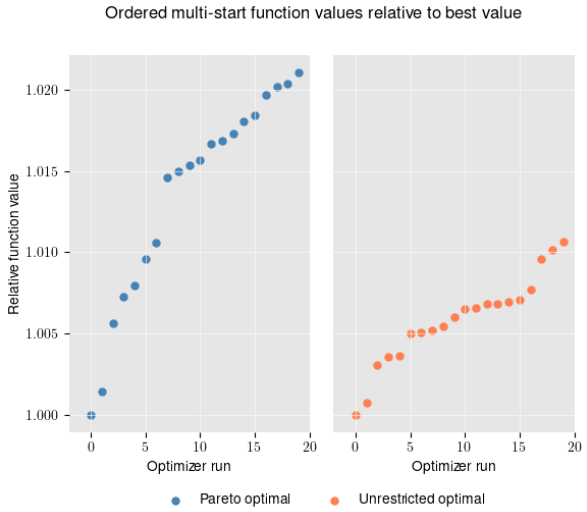


Note: Every column represents one vaccination strategy and every row represents one country. Both vaccines are indicated by their colors that are used throughout the paper.

Figure 17: Fractions of vaccines

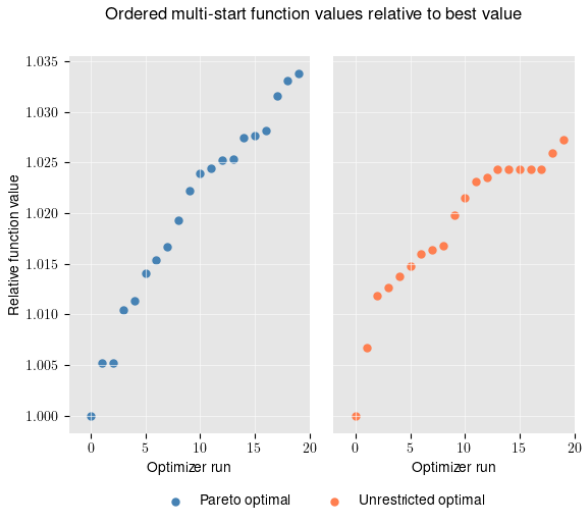
A.1.3 Waterfall plots of optimization

Figure 18 and Figure 19 show the 20 best optima of the multi-start optimization runs. We find that the descend is rather continuous and the optimal values are obtained only once. Hence, it might be possible to find even lower values using more multi-start runs.



Note: Values are relative to the start yielding the lowest optimal minimum value. Only the best 20 starts are used to increase readability.

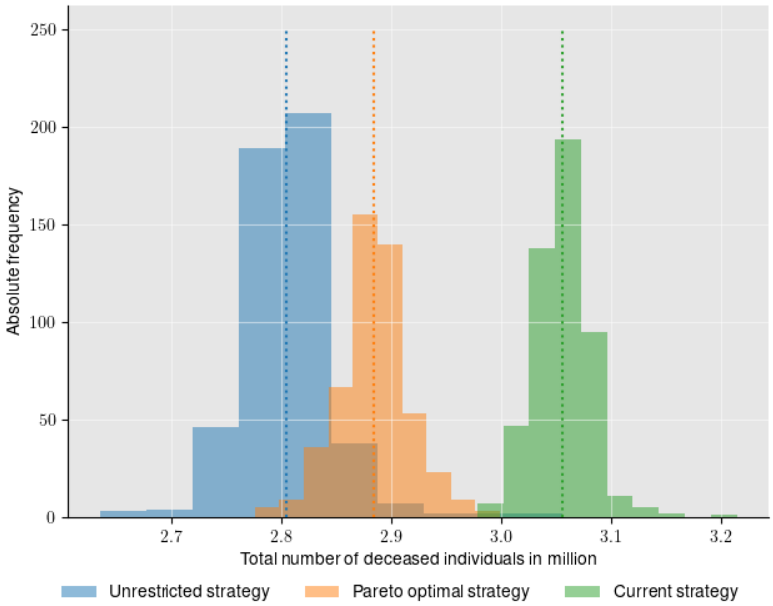
Figure 18: Waterfall plot of the 20 best multi-start runs using piecewise constant functions.



Note: Values are relative to the start yielding the lowest optimal minimum value. Only the best 20 starts are used to increase readability.

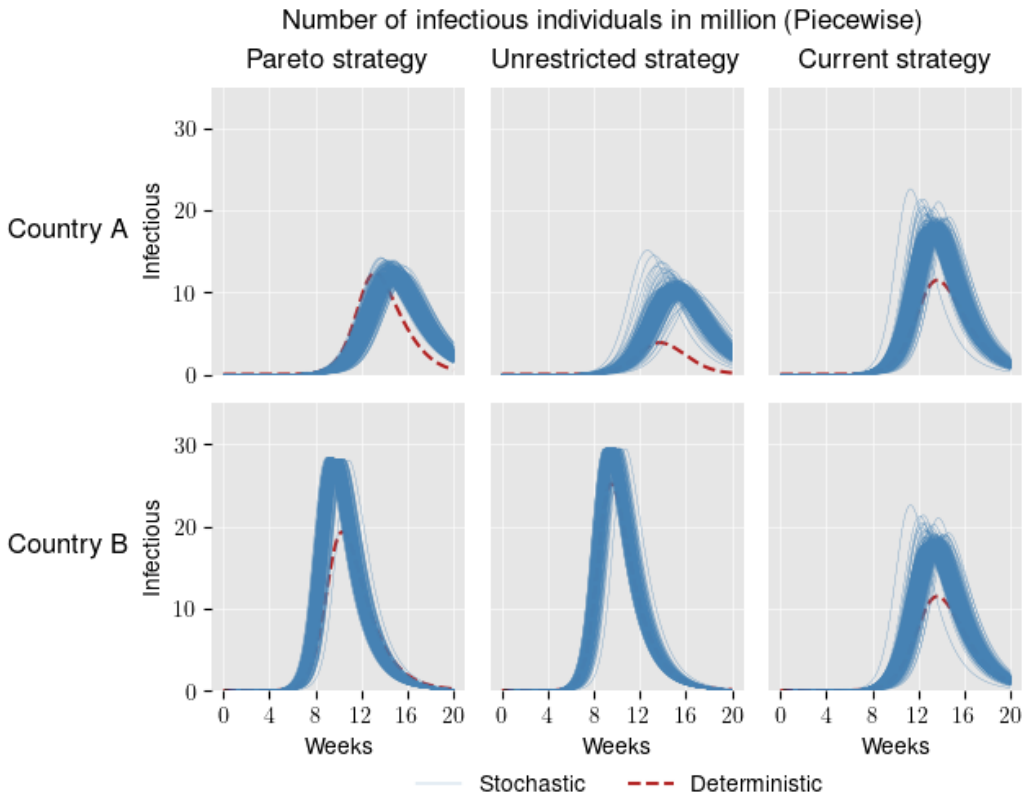
Figure 19: Waterfall plot of the 20 best multi-start runs using splines.

A.1.4 Simulated distribution of number of deceased individuals



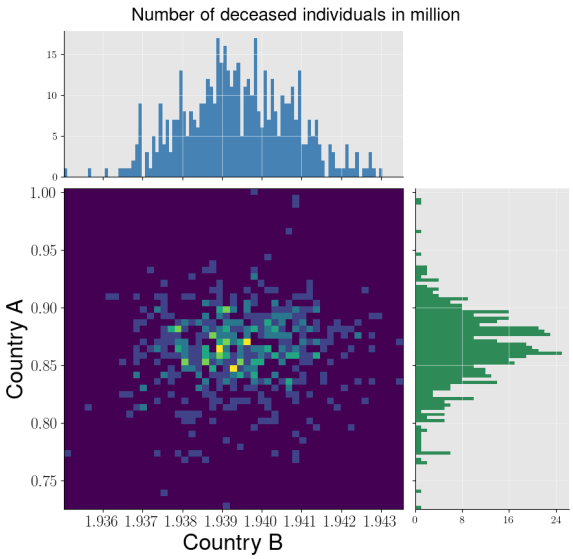
Note: Dotted lines are sample means. The total number of deceased individuals of a strategy is the sum of the respective number of deaths in in country A and country B. We draw 500 samples per strategy.

Figure 20: Stochastically observed frequencies (Piecewise)

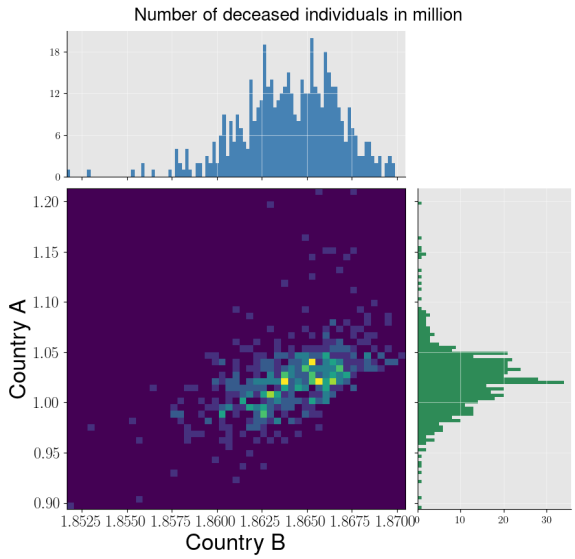


Note: Every column represents one vaccination strategy and every row represents one country. The thin blue lines depict all 500 simulations of the stochastic algorithm using the respective strategy. The dashed red depicts the respective infections within the deterministic model.

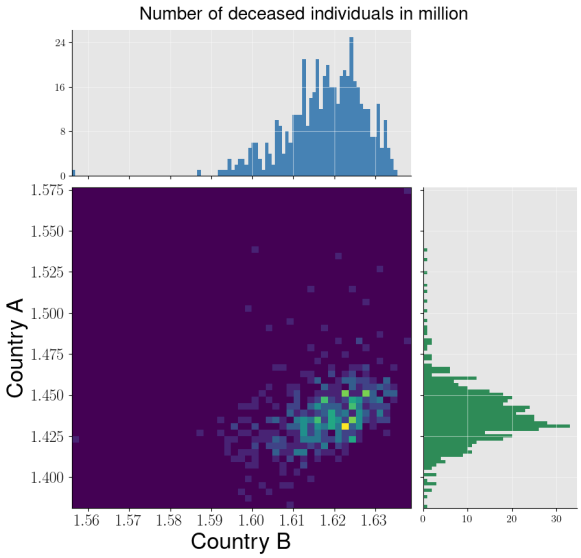
Figure 21: Number of infectious individuals using Stochastic simulations



(a) Unrestricted strategy



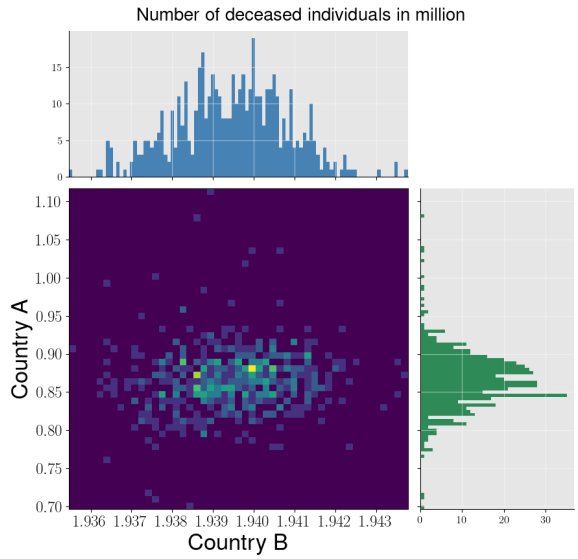
(b) Pareto optimal strategy



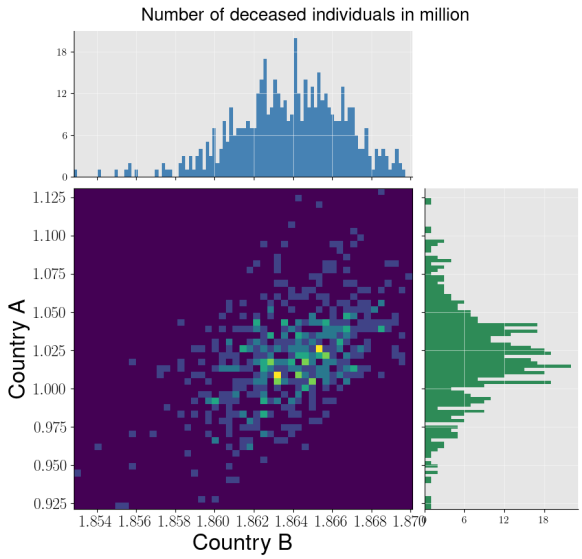
(c) Current strategy

Note: Purple temperature boxes indicate the joint frequencies. Histograms on top are the histograms corresponding to country B and histograms at the right-hand side are the histograms corresponding to country A. Histograms are computed using 500 simulations of the stochastic model using the Policies derived from splines.

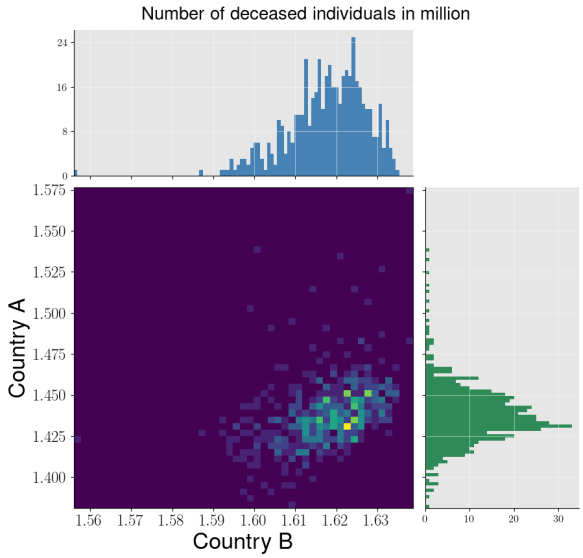
Figure 22: Frequencies of number of deceased individuals using strategies derived from splines



(a) Unrestricted strategy



(b) Pareto optimal strategy



(c) Current strategy

Note: Purple temperature boxes indicate the joint frequencies. Histograms on top are the histograms corresponding to country B and histograms at the right-hand side are the histograms corresponding to country A. Histograms are computed using 500 simulations of the stochastic model using the Policies derived from splines.

Figure 23: Frequencies of number of deceased individuals using strategies derived from piecewise vaccination channels

A.2 Calculations and proofs

We provide calculations and proofs that enhance our line of argumentation but would disturb the train of reading within the main section.

A.2.1 Meeting probabilities

Using Bayes formula, we can rewrite the conditional probability as follows

$$\begin{aligned}
&\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, C_j, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) \\
&= \mathbb{P}_t(i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) \\
&\quad \cdot \mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S) | i_1 \in \mathcal{C}_t(\neg X_D, C_A), i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2)) \\
&= \mathbb{P}_t(i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) \\
&\quad \cdot \mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S) | i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2)
\end{aligned} \tag{31}$$

We use the relative number of susceptible individuals $\mathcal{C}_t(X_S, C_j, F_2)$ across all individuals of $\mathcal{C}_t(\neg X_D, C_j, F_2)$ as approximation of the probability at the second line of the right-hand side

$$\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, F_2) | i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2)) = \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D, C_j, F_2)}. \tag{32}$$

To account for the origin of i_1 within the first line of the right hand-side, we distinguish between the cases where $i_2 \in \mathcal{C}_t(C_A)$ and $i_2 \in \mathcal{C}_t(C_B)$. Assume that $i_2 \in \mathcal{C}_t(X_S, C_B, F_2)$. If there were no spatial effects to influence the cross-border meeting frequency we would use the unconditional probability

$$\mathbb{P}_t(i_2 \in \mathcal{C}_t(\neg X_D, C_j, F_2)) = \frac{y_t(\neg X_D, C_j, F_2)}{y_t(\neg X_D)}. \tag{33}$$

To account for the spatial effects, we introduce a penalty function $b : \mathbb{R}_+ \to [0, 1]$ that depends on the distances between both countries $d(A, B)$

$$\mathbb{P}_t(i_2 \in \mathcal{C}_t(\neg X_D, C_B, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) = \mathbb{P}_t\left(i_2 \in \mathcal{C}_t(\neg X_D, C_B, F_2)\right) \cdot b(d(A, B)), \tag{34}$$

Yielding

$$\mathbb{P}_t(i_2 \in \mathcal{C}_t(X_S, C_B, F_2) | i_1 \in \mathcal{C}_t(\neg X_D, C_A)) = \frac{y_t(X_S, C_j, F_2)}{y_t(\neg X_D)} \cdot b(d(A, B)) \tag{35}$$

A.2.2 Well-conditioning of the polynomial basis

First note that $B_1(0) = 1$ and $B_2(0), B_3(0), B_4(0) = 0$. Furthermore, $B_1(1), B_2(1), B_4(1) = 0$ and $B_3(1) = 1$. We first compute the function values at the boundaries t_{i-1} and t_i.

$$\begin{aligned}
P_{l,i}(t_{i-1}) &= B_1(0)P_{l,i}(t_{i-1}) + B_2(0)(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\
&\quad + B_3(0)P_{l,i}(t_i) + B_4(0)(t_i - t_{i-1})P'_{l,i}(t_i) \\
&= 1 \cdot P_{l,i}(t_{i-1}) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\
&\quad + 0 \cdot P_{l,i}(t_i) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_i) \\
&= P_{l,i}(t_{i-1})
\end{aligned}$$

$$\begin{aligned}
P_{l,i}(t_i) &= B_1(1)P_{l,i}(t_{i-1}) + B_2(1)(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\
&\quad + B_3(1)P_{l,i}(t_i) + B_4(1)(t_i - t_{i-1})P'_{l,i}(t_i) \\
&= 0 \cdot P_{l,i}(t_{i-1}) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\
&\quad + 1 \cdot P_{l,i}(t_i) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_i) \\
&= P_{l,i}(t_i)
\end{aligned}$$

The derivatives of the basis polynomials are

$$\begin{aligned}
B'_1(t) &= 6t^2 - 6t \\
B'_2(t) &= 3t^2 - 4t + 1 \\
B'_3(t) &= -6t^2 + 6t \\
B'_4(t) &= 3t^2 - 2t
\end{aligned}$$

with $B_1(0)' = B_3(0)' = B_4(0)' = 0$ and $B_2(t)' = \frac{1}{t_i - t_{i-1}}$. Moreover, $B'_1(1)' = B_2(1)' =$

$B_3(1)' = 0$ and $B_4(1)' = \frac{1}{t_i - t_{i-1}}$. The derivative of the polynomial is simply

$$\begin{aligned} P'_{l,i}(t) = B'_1(t')P_{l,i}(t_{i-1}) + B'_2(t')(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ + B'_3(t')P_{l,i}(t_i) + B'_4(t')(t_i - t_{i-1})P'_{l,i}(t_i) \end{aligned}$$

and therefore

$$\begin{aligned} P'_{l,i}(t_{i-1}) &= B'_1(0)P_{l,i}(t_{i-1}) + B'_2(0)(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ &\quad + B'_3(0)P_{l,i}(t_i) + B'_4(0)(t_i - t_{i-1})P'_{l,i}(t_i) \\ &= 0 \cdot P_{l,i}(t_{i-1}) + \frac{1}{t_i - t_{i-1}} \cdot (t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ &\quad + 0 \cdot P_{l,i}(t_i) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_i) \\ &= P'_{l,i}(t_{i-1}) \end{aligned}$$

and

$$\begin{aligned} P'_{l,i}(t_{i-1}) &= B'_1(1)P_{l,i}(t_{i-1}) + B'_2(1)(t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ &\quad + B'_3(1)P_{l,i}(t_i) + B'_4(1)(t_i - t_{i-1})P'_{l,i}(t_i) \\ &= 0 \cdot P_{l,i}(t_{i-1}) + 0 \cdot (t_i - t_{i-1})P'_{l,i}(t_{i-1}) \\ &\quad + 0 \cdot P_{l,i}(t_i) + \frac{1}{t_i - t_{i-1}} \cdot (t_i - t_{i-1})P'_{l,i}(t_i) \\ &= P'_{l,i}(t_i). \end{aligned}$$

A.2.3 Convergence in distribution

Theorem 1. *$B\left(\frac{\tau}{dt}, a_j(y) \cdot dt\right) \xrightarrow{d} Po(a_j(y) \cdot \tau)$ if $dt \to 0$.*

Proof. Let p_n be a sequence with $\lim_{n\to\infty} p_n = 0$. We first show that if $\lambda' = n \cdot p_n$ is constant, $n \to \infty$ and $p_n \to 0$, a general Binomial random variable $\mathrm{B}(n, p_n)$ converges in distribution to a Poisson random variable $\mathrm{Po}(\lambda')$. Note that this proof is in essence just a restatement of

the Poisson limit theorem of Poisson (1835).

$$\begin{aligned}\lim_{n\to\infty}\binom{n}{k}p_n^k(1-p_n)^{n-k} &= \lim_{n\to\infty}\frac{n\cdot(n-1)\cdot\ldots\cdot(n-k+1)}{k!}\left(\frac{\lambda'}{n}\right)^k\left(1-\frac{\lambda'}{n}\right)^{n-k}\\ &= \lim_{n\to\infty}\frac{n^k+O(n^{k-1})}{k!}\left(\frac{\lambda'}{n}\right)^k\left(1-\frac{\lambda'}{n}\right)^{n-k}\\ &= \frac{(\lambda')^k}{k!}\exp\left(-\lambda'\right)\end{aligned}$$

Note that by definition τ is fixed and by assumption $a_i(y)$ is constant within $[t, t+\tau)$. Thus, $\lim_{dt\to 0}\frac{\tau}{dt}=\infty$, $\lim_{dt\to 0} a_i(y)\cdot dt = 0$ and $\frac{\tau}{dt}\cdot a_i(y)\cdot dt = \tau\cdot a_i(y)$. Using the convergence property mentioned above yields the result. □

A.2.4 Polynomial basis

Theorem 2. *$B_1(t), B_2(t), B_3(t), B_4(t) \in \mathbb{R}_3(t)$ form a polynomial basis of $\mathbb{R}_3(t)$.*

Proof. We need to show that the four polynomials are linearly independent. We do so by writing the polynomials in vector form, collect them in a matrix and show that this matrix has full rank.

$$\begin{pmatrix}2&1&-2&1\\-3&-2&3&-1\\0&1&0&0\\1&0&0&0\end{pmatrix}\Leftrightarrow\begin{pmatrix}0&0&-2&1\\0&0&1&-1\\0&1&0&0\\1&0&0&0\end{pmatrix}\Leftrightarrow\begin{pmatrix}0&0&0&-1\\0&0&1&-1\\0&1&0&0\\1&0&0&0\end{pmatrix}\Leftrightarrow\begin{pmatrix}0&0&0&1\\0&0&1&0\\0&1&0&0\\1&0&0&0\end{pmatrix}$$

Since $B_1(t), B_2(t), B_3(t), B_4(t)$ are four linearly independent polynomials of degree 3, they form a basis of $\mathbb{R}_3(t)$. □

Schriftliche Versicherung

Ich versichere hiermit, dass ich die vorstehende Masterarbeit selbstständig verfasst und keine anderen als die angegebenen Quellen und Hilfsmittel benutzt habe, dass die vorgelegte Arbeit noch an keiner anderen Hochschule zur Prüfung vorgelegt wurde und dass sie weder ganz noch in Teilen bereits veröffentlicht wurde. Wörtliche Zitate und Stellen, die anderen Werken dem Sinn nach entnommen sind, habe ich in jedem einzelnen Fall kenntlich gemacht.

Ort, Datum Unterschrift