1 The model

A pandemic is in our case modeled as a dynamic system which likewise in a very general for is described by:

$$\frac{d}{dt}X = f(X(t), t, u; \psi), \tag{1}$$

where $X(t)$ describes the state of our dynamic system at time t. u in general describes the actuation or control that allows us to manipulate the syste, and ψ the parameters, that allow one either to generalize the system, or fit a generalized system to a specific case. The function f as such describes the complete dynamics of the system and allows us to understand the evolution of the system. In our case the vector X is described by compartments of susceptible, infected but non contaigious, infected and contaigious and vaccinated population, and the flow between these compartments is governed by f. u in our case are vaccination and non pharmaceutical interventions that are modelled in our system. ψ in general are the rate constants that link the different compartments that we either guess, measure or fit. Modelling the system is challenging as we first of all do not know what f might be in reality and can only make guesses using classical, compartment models. Second, the system further is probably chaotic in the sense that small differences in inital conditions yield huge differences as the system evolves in time. Further the system contains latent states, that are hard to be measured i.e. an infected, non contaigous population that can not be measured by SARS-CoV-2 testing.

The current model implemented is goverend by a system of differential equations (2-8).

$$dS_{ij} = \left[\zeta_i V_{ij} + \eta_i R_{ij} - S_{ij}\left(\sum_{k=1}^{n}\sum_{l=1}^{m}\epsilon_{ik}\beta_{jlk}I_{kl} + \frac{v_{ij}(t)S_{ij}p_{ij}}{D_{ij}}S_{ij}\right)\right]dt, \tag{2}$$

$$dE_{ij} = \left(S_{ij}\sum_{l=1}^{m}\beta_{jli}I_{il} - \delta_i E_{ij}\right)dt, \tag{3}$$

$$dI_{ij} = (\delta_i E_{ij} - \gamma_i I_{ij})dt, \tag{4}$$

$$dV_{ij} = (v_{ij}(t)\frac{S_{ij}^2}{D_{ij}}p_{ij}) - \zeta_{ij}V_{ij})dt, \tag{5}$$

$$R_{ij} = \frac{N_j}{N} - S_{ij} - E_{ij} - I_{ij} - V_{ij}, \tag{6}$$

$$D_{ij} = S_{ij} + E_{ij} + a_{ij}I_{ij} + (1-r)\,R_{ij}, \tag{7}$$

$$v_{ij}(t) = \frac{d}{dt}\frac{L_{ij}}{1+e^{-k_{ij}+(t-t'_{ij})}}, \tag{8}$$

with

$$\beta_{jlk} = \hat{R}_k(t)\frac{\gamma_k \sigma_{jk} N C_{jl}}{\rho_k N_l}, \tag{9}$$

where, ρ_k is the largest eigenvalue of the matrix:

$$M_{jl}^k = f_j \sigma_{jk} C_{jl} \frac{N_j}{N_l}, \tag{10}$$

specific for each variant k. The system is a multicompartment model, simulating n variants and m age classes. S is representing a susceptible population, E an intermediate comporatment that considers a latent population of infected, that is *non contaigious* so far. I shall consider the population that is infectious and contaigious. Furhter a compartment V the currently vaccinated and immune population, that can source from compartment S at rate $\frac{v(t)Sp}{D}$, considering a population that can be still be immunized by vaccination. D in this rate can be evaluated on the straightforward using equation 7, where a is proportion of asymptomatic cases, and r the dedection (reporting) rate of infected individuals. Compartment R considers a population that is effectivly immunized by the fact that it underwent infection and has recovered from the desease. ζ and η are as such the immune waning constants for in the case of ζ the immune waning after vaccination and η the immune waning after being immunized by infection. Index i descerns different variants while index j descerns different age classes. The system total population is N individuals, devided into N_j age groupes, where N_j holds the population of age classe j. As such all compartments can in the equations only vary on between 0, no individuals are found in such a state, to 1, all individuals are found in this state. Maybe counterintuitive at first glance, summing specific compartment states over the variant index i may yield a number > 1 , which can be attributed to the fact that a person is indeed, for instance, susceptible to be infected by different variants. β describes the current infection rate which is modelled in equation (9). In this equation (9) $\hat{R}_k(t)$, represents the current infection rate at moment time t, which can vary due to non pharmaceutical measures taken by the government, i.e. imposing social distancing measures or wearing masks. The current model however considers $\hat{R}_k(t)$, at least over a simulated time interval, to be constant. γ_i found in equations (4) and (9) represents the conversion rate, the rate at which individuals in the latent compartment E are transfered to compartment I. Vaccination is currently modelled by a logistic curve as outlined in equation (8). L in this equation represents the maximum number of vaccines given, k the steepness of the logistic curve and hance, how fast the population is vaccinated and t' is the midpoint of the logistic curve and hence the time given that half of L vaccines are injected. This curve can either be estimated or fitted to specific

k	A(k)	B(k,1)	B(k,2)	B(k,3)	B(k,4)	B(k,5)
1	0					
2	1/4	1/4				
3	3/8	3/32	9/32			
4	12/13	1932/2197	-7200/2197	7296/2197		
5	1	439/216	-8	3680/513	-845/4104	
6	1/2	-8/27	2	-3544/2565	1859/4104	-11/40
	1	2	3	4	5	6
C(k)	25/216	0	1408/2565	2197/4104	-1/5	2/55
CH(k)	16/135	0	6656/12825	28561/56430	-9/50	2/55

Table 1: Coefficients for the Runge Kutta Fehlberg method with adaptive step size.

age groups or variants. Equation (8) describes the derivative of the number of vaccines given at a certain moment t.

The variants interact with each other with a modelled cross immunity defined by the matrix ϵ_{ik}. The different age groups using a matrix C that models the probablities that persons from different age classes might encounter each other. Finally σ_{ji}, part of β as outlined in equation 9 represents the susceptibility for a specific age group j to a variant i.

Vaccination is still of concern in this system and a further discussion has to be made to clarify if equation (7) can be modelled as such. Further it is unclear if the cross imunity and ϵ can be written down as such taking vaccination into account. Recently introduced immune waning ζ, η and as such the importance given to compartments V and R further reopen the question if vaccination is modelled correct. Further the very vaguely formulated proportion of asymtotics a and reporting rate r in equation (7). As such we currently do not recommend to make use of the vaccination code without further modifications. Vaccination can simply be disabled by setting L_{ij} in equation 8 to 0.

1.1 Integration

In our current system we have n variants and m age classes. As such in the current numerical implementation of our system described in section 1

We have implemented a multiequation Runge-Kutta-Fehlberg solver with adaptive step size and error control. The method that we have implemented uses the coefficents introduced by Fehlberg outlined in table 1. With these

coefficients at hand we integrate a system described by equation (1) like:

$$\begin{aligned} k_{1,i} &= f(t + A(1)\Delta t, X_i)_i \Delta t, && (11)\\ k_{2,i} &= f(t + A(2)\Delta t, X_i + B(2,1)k_{1,i})_i \Delta t, && (12)\\ k_{3,i} &= f(t + A(3)\Delta t, X_i + B(3,1)k_{1,i} + B(3,2)k_{2,i})_i \Delta t, && (13)\\ \vdots &= \vdots, && (14)\\ k_{6,i} &= f(t + A(6)\Delta t, X_i + B(6,1)k_{1,i} + B(6,2)k_{2,i} + B(6,3)k_{3,i}, \\ &+ B(6,4)k_{4,i} + B(6,5)k_{5,i})_i \Delta t, && (15) \end{aligned}$$

where X_i describe the states of our system. f_i the state equations that govern our system. The reader may note that f yields a i results and hance i coefficents $k_{1,i}$ that all have to be available in order to evaluate $k_{2,1}$ and so on. We further define:

$$E_{c,i} = X_i + \sum_{l=1}^{6} k_{l,i}(\mathrm{CH}(l)), \tag{16}$$

and

$$X(t + \Delta t)_i = \sum_{l=1}^{5} k_{l,i}(\mathrm{C}(l)), \tag{17}$$

where $X(t + \Delta t)_i$ are the new states at $t + \Delta t$ if the largest of the estimated errors, between a 4th (16) and 5th (17) order integration:

$$E_{e,i} = \left| E_{c,i} - X(t + \Delta t)_i \right|, \tag{18}$$

is smaller than a defined error E_d and hence,

$$\max(E_{e,i}) < E_d. \tag{19}$$

If the condition is not met, this step is discarted. Further after each step a new step size is estimated:

$$\Delta t_{\mathrm{new}} = \Delta t \left[\frac{E_d}{2 \max(E_{e,i})} \right]^{1/4}. \tag{20}$$

Implementation wise the components of f_i are implemented using the *state_eqn* structure as defined in *runge-kutta-fehlberg.h*. For each state X_i one is therefore required to define a state equation. The *state_eqn* structure takes a function pointer, and a pointer with parameters to that function. As such an arbitrary array of C functions toghether with their parameters can constituate the evolution f as in equation (1).

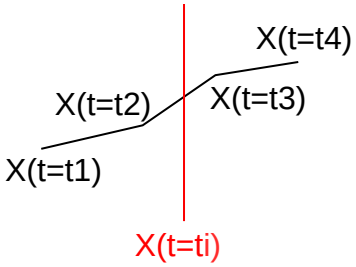

Figure 1: Interpolation between 4 points on a trajectory

1.2 Trajectory

The resulting trajectory can currently be displayed for all states, and hence compartments that are solved by the methods outlined above. As the states are not stored equidistant the value at a certain point in time t can be obtained by interpolation. In order to obtain a value at any point t first the interval between two evaluated points is searched. This is done with an efficent implementation of a bisection search algorithm. In the next step, four calculated points are considered. The situation is summerized in figure 1, where we search for a value at location t_i shown with the red line.

As a quick solution to this problem we have interpolate a polynom of third order using the four points. Straightforward we solve the system of equations:

$$\begin{bmatrix} 1 & t_1 & t_1^2 & t_1^3 \\ 1 & t_2 & t_2^2 & t_2^3 \\ 1 & t_3 & t_3^2 & t_3^3 \\ 1 & t_4 & t_4^2 & t_4^3 \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \\ c_3 \\ c_4 \end{bmatrix} = \begin{bmatrix} X(t_1) \\ X(t_2) \\ X(t_3) \\ X(t_4) \end{bmatrix}, \tag{21}$$

using the Gauss-Seidel method with the interpolated point being:

$$X(t_i) = c_1 + c_2 t_i + c_3 t_i^2 + c_4 t_i^3. \tag{22}$$

2 Input format

2.1 Input files

In order to perfom a fit the system needs a

Keyword	Format	Description
runtime	int	Number of days to simulate
error_tolerance	float	The error tolerance E_d as in equations (19) and (20).
n_variants	int	The number of variants to consider.
n_classes	int	The number of age classes to consider.
Rzero	n_variants*float	The constant $\hat{R}$ value as in equation (9).
variant_introduction_date	n_variants*int	Relative day offset of variant introduction.
total_population	float	The total population to consider
population_class_distribution	n_classes*float	The distribution into age classes.
contacts_between_classes	n_classes^2*float	The values of C as in equations (9) and (10).
reporting_rate	float	Fraction of cases reported.
asymptomatics_fraction	n_classes*n_variants*float	fraction of undetected per age and variant.
initial_intermediate_fraction	n_classes*n_variants*float	Fraction of the total population in E.
initial_infected_fraction	n_classes*n_variants*float	Fraction of the total population in I.
epsilon	n_variants^2*float	Cross immunity as in equation (2).
recovery_rate	n_variants*float	Recovery rate as of γ in equation (4)
conversion_rate	n_variants*float	Conversion rate as of δ in equations (3) and (4).
pre_immune_fraction	n_classes*float	Proportions of primmunized before the start of the simulation.
sigma	n_classes*n_variants*float	The susceptibility of a certain age group to a certain variant, as of σ in (10).
immune_drain	n_variants*float	Rate constant describing the loss of immunity from previous infections. As of η in equation (2).
vaccine_drain	n_variants*float	Rate constant describing the loss of immunity from vaccination. As of ζ in equation (2).
vaccine_logistic_maximum	n_variants*n_classes*float	The maximum of the logistic. function describing vaccination.
vaccine_logistic_growth	n_variants*n_classes*float	The speed of vaccination.
vaccine_logistic_midpoint	n_variants*n_classes*float	The midpoint of the logistic function describing vaccination
vaccine_efficiency	n_variants*n_classes*float	The efficiency of a vaccine towards a variant.

Table 2: The parameters passed to the model found in its input file. These are all the parameters needed if a simple model simulation is performed, run with *execute_model*. If a fit using *covid_fit* is performed serveral of the parameters are overwritten by either the regional data: i.e. total_population or age distribution, or the fit itself: i.e. Rzero.

Model input parameter file:
A general file that normaly can be passed to the covid model solver without a fit. All values in this file serves as inital conditions. The file adheres to a keyword - parameters structure where a line has to begin with the keyword in question and all parameters have to follow space separated on the same line. The *n_variants* and the *n_classes* keywords shall be on top of the file as these are needed by the file parsing mechanism in order to determine the number of arguments to the following keywords. Table 2 oulines each keyword with the parameter format and a description.