Project report

of

The effect of time dependent vaccination protection (SIR-model)

for

250070 SE Seminar Applied PDE (2022S)

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Introduction

On August 31st, 2021 the Austrian *COVID Prognose Konsortium* published an updated policy brief to evaluate the country's pandemic situation. This policy brief played an important role in the Austrian Covid-19 management. It was used to predict the upcoming pandemic development until December 2021. However, the simulations were based on naïve model assumptions and a rather simple model prone to input errors. One assumption, which led to a severe misprediction, was that Covid-19 vaccinations would maintain their full protection during the specified protection period. Thus, the effect would not decrease, and consumers would become de facto immune over the considered time period. The question arises in how far this simple assumption changes the model's prediction.

Method

The epidemic model used by the *COVID Prognose Konsortium* is the SIR model which is a continuous compartment model that uses fluxes to simulate transmission rates, recovering rates, etc. In its most trivial form, the model consists of the following three compartments: Susceptible, Infected, Recovered. The first group can be infected, the second group is infected and spreads the disease and the third group is (temporarily) immune.

The central question of this report is, how the results of two SIR models for Covid-19 infection dynamics differ if one considers time dependence of vaccination protection?

Therefore, the two models (A and B) are defined by a system of three coupled ordinary differential equations (ODEs). Each equation describes the growth rate of its corresponding compartment.

$$\frac{dS}{dt} = -\beta SI + f\epsilon_{A,B}R + (1-e)\gamma I \quad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (2)$$

$$\frac{dR}{dt} = e\gamma I - f\epsilon_{A,B}R \quad (3)$$

The coefficient β describes the transmission rate that determines how many susceptible people will be infected over time. The value of β was defined to be the infection rate at the beginning of the modelled period and thus $\beta = 1.07$. This value was the reported effective reproduction rate on September 1st, 2021 (ORF.at, 2022).

The factor γ is the recovery rate, which defines how many people pass from the compartment of infected to the compartment of recovered over time. In Austria it is assumed that a Covid-19 infection is healed after ten days on average. As time steps dt are set to one day, $\gamma = 0.1$ to model the recovery after ten days.

The coefficient $\epsilon_{A,B}$ defines the rate of decay in vaccination protection over time. Model A assumes that over the regarded period (September 1st, 2021, until January 31st, 2021) the compartment of recovered will not decrease. This is implemented by setting $\epsilon_A = 0$.

For model B two functions are considered to describe the decay in protection. The first one assumes a constant decay rate over time. The second function describes the first half of a normalized Gaussian function. Thus, designing a rather natural development typical for biological systems (see figure 1).

Additionally, the value e is introduced to model the level of immunity which is gained through either vaccination or convalescence. The parameter e is assumed to be 80% in fully immune individuals like in the policy brief (COVID_Prognose_Konsortium, 2021). In this model this value can be interpreted as the ratio of infected that gain immunity and then belong to the recovered compartment. On the other side this parameter is also used in the last term of formula (1), where the population ratio is defined that did not gain immunity.

The ϵ parameter has a damping coefficient f, to reduce its effect on the epidemic dynamics and to further calibrate the model to the recorded data. This damper is supposed to compensate for various rough assumptions.

For reasons of simplicity this model assumes that no new vaccinations are administered during the regarded period. So, immunity in the whole population stems from the from infections or from the initial state (vaccinations and former infections).

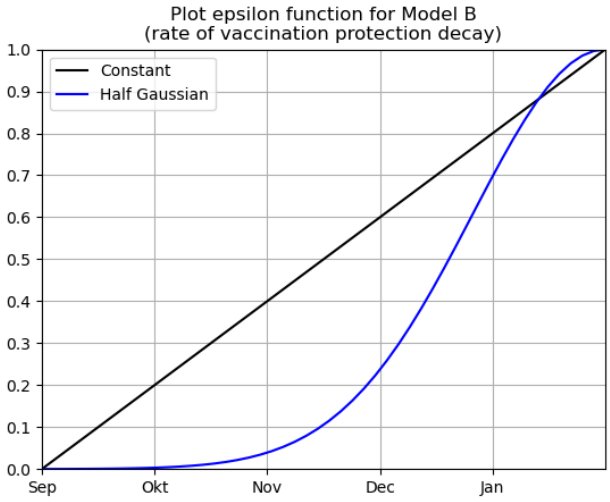

Figure 1: Rate of decay in vaccination protection ϵ_B over time. The black line is the constant decay rate, and the blue line is the first half of a normalized Gaussian function. Their value is scaled by f.

The official Covid-19 infection numbers of Austria were extracted from the ORF "Infopoint" website (ORF.at, 2022) and the BMSGPK open data website (BMSGPK, 2021). With these sources the initial values for the problem were determined. For more information see Appendix.

The data for recorded numbers of infected per day are extracted from (BMSGPK, 2021). As the model assumption of recovery rate $\gamma = 0.1$ is made for the two models A and B, the same assumption was applied to the official data that is plotted as reference. Thus, the recorded total number of infected over the modelled timespan, is reduced by a factor γ each day in order to model the flux of recovery.

Implementation

In order to simulate the epidemic dynamics, the model was implemented in a Python 3.9 script. This script numerically solves the system of equations and approximates a solution that can be plotted. The ODEs were solved with `scipy.integrate.solve_ivp` using the "RK45" method (The_SciPy_community, 2022).

Results

The model was simulated with the initial values and parameter values as given in the appendix table 2. Then the resulting population ratios in each compartment were plotted over time. Additionally, the official infection numbers were plotted on the same illustration to compare each model's accuracy.

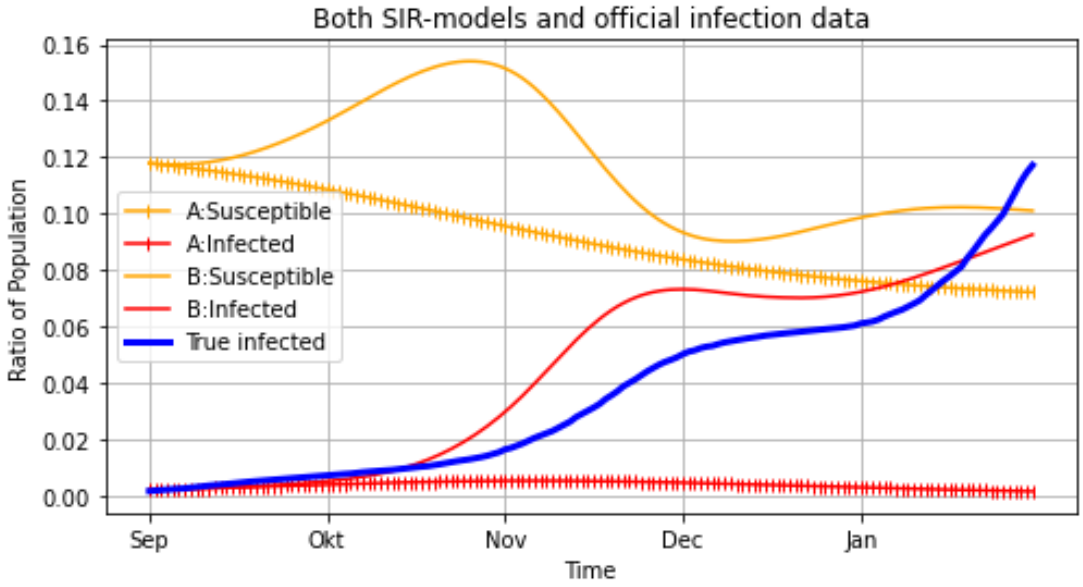

Figure 2 shows the phase lines for susceptible and infected compartments of model A and model B with constant vaccination protection decay in Model B. The blue line describes the development of the real-world data on infections (BMSGPK, 2021). The thin lines are the model B, and the dashed line is model A.

When looking at figure 2 we can compare the two models A and B and how well they approach the blue line of reported infections. Model A does not predict any significant "infection wave", while the blue line describes how the number of infections started to rise in Autumn of 2021. The global infection maximum of model A is 0.5% of the population in contrast to 11.7% that were actually infected by the end of the simulated timespan (see table 1). In this model the numbers of infected and susceptible population decrease almost steadily over time and the ratio of recovered population increases steadily (see figure 4 in appendix for full plot).

Model B correctly predicts a rise in infections. Additionally, its infected graph exhibits similar shape and rate of increase as the blue line. However the simulated curve is shifted in time and predicts high infection number partially earlier than actually recorded, while the global maximum is too low.

Table 1: Maximum number of infections				
	Model A	Model $B_{constant}$	Model B_{nGauss}	Official data
Percent of population	0.5	9.3	11.6	11.7
Total	45 000	837 000	1 044 000	1 056 167
Percent error	95.7	20.8	1.2	0

Table 1 contains the results and error values for three predictions of maximum infections. Most notably in table 1 is that the percent errors of both model B simulations are much smaller than the error in model A.

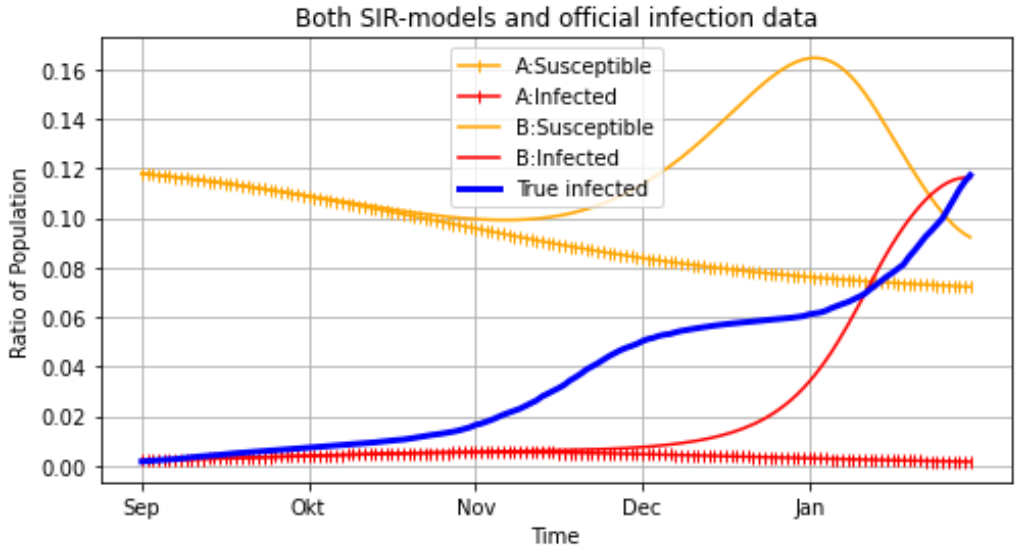

Figure 3 shows just the susceptible and infected phase lines of both models with vaccination protection decay in Model B following the normalized Gaussian function. The blue line describes the development of the real-world data of infections from (BMSGPK, 2021).
The decay function of Model B failed to capture the build-up of the "infection wave".

In figure 3 we can observe model A and model B with the more natural function of vaccination protection decay rate (normalized Gaussian). While the global maximum of this variant of model B was very close to the recorded data, the shape of the infections curve is very different from the recorded data. Furthermore, the model curve seems to reach a local maximum unlike the blue line.

Discussion

In epidemic modelling and especially in Covid-19 models some of the most important questions a model needs to answer are: "When is the next 'wave' of infections coming?" and "How many infections will there be?". The maximum number of infected people at one point in time is a crucial measure for public health and essentially determines the severity of an infection "wave". This is why the local maxima of infection graphs are compared in this project.

The central model assumption studied in this project is a time dependent vaccination protection. Both model B variants that have this assumption outperform model A by far. The model B with constant decay rate made good predictions considering the simplicity of the three-compartment SIR model. In this model not only the development of the infected population ratio over time is close to the real-world records. Also the result only had a percent error of 20.8% in contrast to the model A error of 95.7%.

Interestingly, the second model B with the more natural function of vaccination protection decay rate performed worse than expected, when considering the shape of the graph. While the maximum is very close to official data (only 1.2% error), this model will probably not perform well under different initial conditions.

Overall, both decay functions assumed can be considered robust, because the final result are rather close to each other and the observed number of infections (see figure 2 and 3).

It is worth noting that the damper ($f = 0.01$) plays an important role in calibrating the model to the observed data. The effect of the damper can be interpreted such that even 1% of the effect of the central model assumption leads to drastically different predictions. Also the immunity level e which was assumed to be 80% has only very little effect on the system.

In conclusion, the simple model assumption of decaying vaccination protection has a severe impact on the predictions – more than any other factor in this kind of SIR model.

Outlook

Model B with constant decay rate and corresponding damper is recommended to use for future simulations of this kind. Furthermore, the SIR model B can be further expanded to comprise more compartments such as "exposed but not infectious" or "quarantined" populations. Moreover, the vaccination rate should be considered in models of this kind.

It is worth noting that this model always considers the compartment of infected to be the number of recorded infections, because this measure is used in Austria's public communication. However, these numbers do not reflect the virulence of the virus, but only the transmission rate. The harmfulness of a virus should be measured in numbers of severe infection cases (e.g. number of hospitalized patients). Thus, a better solution which was already proposed in the past would be to scale the current number of infections by the number of hospitalized infected patients.

$$number\ of\ infections_{scaled} = \frac{number\ of\ hospitalized\ infected\ patients}{number\ of\ of\ recorded\ infections} \qquad (4)$$

References

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Notes on Covid-19 data:

- The official time series data (BMSGPK, 2021) had a missing row on November 14th, 2021, so this datapoint was interpolated.
- The data used was recorded each day at midnight.

Appendix

Table 2: Parameter values	
$t_0 = 0$	starting time day 0 (September 1st, 2021)
timespan = 150 days	simulated period in time
dt = 1 day	timestep for numerical approximation
N = 9 000 000	Austrian population rounded
$S_0 = 11.79\%$	initial value for susceptible population ratio
$I_0 = 0.21\%$	initial value for infected population ratio
$R_0 = 88.0\%$	initial value for recovered population ratio: 58% fully vaccinated plus roughly estimated 30% that avoid infections
$\beta = 1.07$	transmission rate
$\gamma = 0.1$	recovery rate
$\epsilon_A = 0.0$	vaccination decay rate of Model A
$\epsilon_B = f(t)$	vaccination decay rate of Model B: either constant or first half of a normalized Gaussian function
$f = 0.01$	(damper) damps the effect of epsilon
$e = 80\%$	immunity level is the protection against infection

Table 2 holds the exact parameter values extracted from (ORF.at, 2022) and parameters of model assumptions.

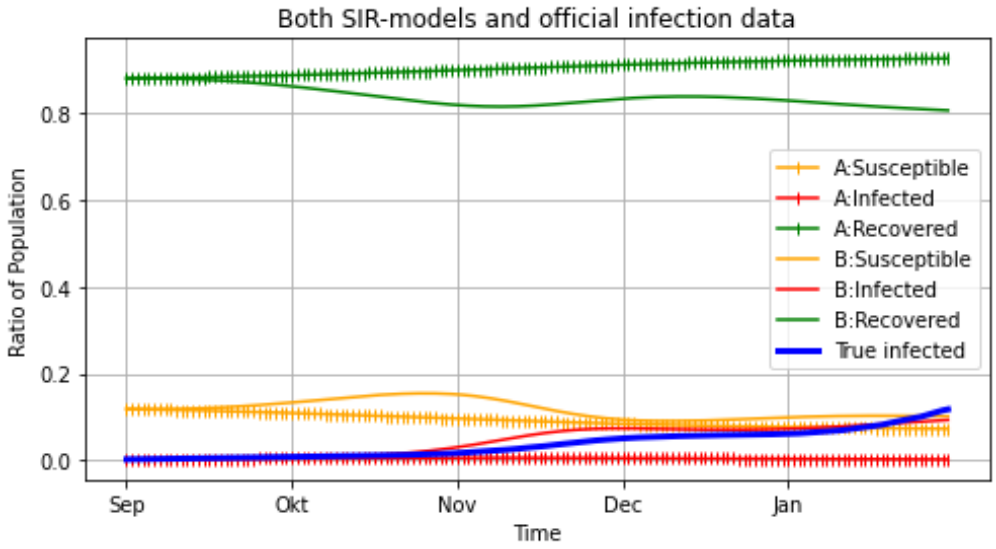

Figure 4 shows all phase lines of both models with constant vaccination protection decay in Model B. The blue line describes the development of the official data on infections from (BMSGPK, 2021).