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Adjoint-based Data Assimilation of an Epidemiology Model for the COVID-19 Pandemic in 2020

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Abstract Data assimilation is used to optimally fit a classical epidemiology model to the Johns Hopkins data of the COVID-19 pandemic. The optimisation is based on the confirmed cases and confirmed deaths. This is the only data available with reasonable accuracy. Infection and recovery rates can be inferred from the model as well as the model parameters. The parameters can be linked with government actions or events like the end of the holiday season. Based on this numbers predictions for the future can be made and control targets specified.

With other words:

We look for a solution to a given model which fits the given data in an optimal sense. Having that solution, we have all parameters.

Keywords: Adjoint-based Data Assimilation, Epidemology Model, Corona Virus, COVID-19

1 Introduction

The COVID-19 outbreak is threatening our health and lives. Without intervention, the numbers of infected people worldwide will rise to millions and leave hundreds of thousands of casualties behind, prior to settling down because the spread is stopped due to the fact that the virus sees no susceptible victims in a large enough number to further spread. This moment is reached, when the spreading rate β and recovery rate γ have a specific ratio or the number of susceptible people has become low enough. Waiting for the latter

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means a long time and a high death toll. There is no way of controling γ, only β depends on the behaviour of the people and is thus amendable to our intervention. In lack of either a vaccine or a cure this is the only amendable parameter. [1] have studied how this can be done. This currently goes by the term *flattening the curve*. In order to make a valid assessment of actions taken in the past or to make reliable predictions for the future, reliable numbers are needed, but hard to get. Even if specific numbers were available, the presently infected or recovered people can only be infered by means of a model.

A good data source for global data is the github repository of the Johns Hopkins project Systems Science and Engineering [2]. Initially they distributed confirmed cases (C), recovered cases (R) and deaths (D). Due to the notorious unreliability of (R) this datum was discontinued. The task now is to get from this data good estimates of the real numbers as well as the hidden states. Data assimilation is capable of recovering the full state of a model from partial information.

In the sequel data assimilation will be applied to the COVID-19 data. The method can be summarised as a mathematical method to get out of a set of empirical data C_e, D_e plus a model $\mathcal{M}$ the full state S, I, R, D and model parameters β, γ, δ such that the data is optimally described:

$$C_e, D_e, \mathcal{M} \longrightarrow S, I, R, D, \beta, \gamma, \delta.$$

In addition to the variables introduced above, S is the number of susceptible individuals in the population. It is effectively this number of not immune people, which stops the outbreak when it falls low enough in the natural case.

The result will obviously not be better than the model, but even with a classical epidemiology model they are much better than using statistical means of getting the information. At this point, there is ample room for improvement and the author, being a physisist, solicitates colleagues with better knowledge about epidemology models to contact him.

2 Method

2.1 Adjoint Method

Lemke et al. [5] presented a method for a sensitivity analysis of complex reaction mechanisms based on an adjoint approach. The basic structure of the equations is similar and the method is applicable to epidemics.

Here a very brief sketch is given to ease understanding of the procedure without all the details from the previous publication. The governing equations have the form

$$\mathcal{M} = \partial_t q - f(q, \alpha) = 0.$$

While in the cited paper different chemical species are considered, we use the identical governing form for a model adopted from the classical SIR model [3] modified for a mortal class. Imagine the number of susceptible, infected, recovered and dead people $q = (S, I, R, D)^T$ as being the chemical species in a reaction, α are the parameters of the model and in our case they are taken to be $\alpha = (\beta, \gamma, \delta)^T$ for the contact, recovery and mortality rate of the epidemic. The model was augmented by the number of confirmed deaths D, because that is known from the data, whereas the recovered class R is uncertain and no longer provided by the source since 2020-03-23.

2.2 Epidemology Model

The model then reads

$$\partial_t S = -\beta IS/N \tag{1}$$

$$\partial_t I = \beta IS/N - (\gamma + \delta)I \tag{2}$$

$$\partial_t R = \gamma I \tag{3}$$

$$\partial_t D = \delta I \tag{4}$$

with $N = S + I + R + D$ being the total population, including, suscepible, infected, recovered, and the dead. The model can easily be augmented to accommodate several other classes like age classes or local distributions representing several countries. This set of equations has to be solved with an initial state $q_0 = (S_0, I_0, R_0, D_0)^T$ subject minimising a constraint

$$\mathcal{J} = \int (C^T q - (C^T q)_e)^2 dt. \tag{5}$$

$(C^T q)_e$ is the empirical data towards which the assimilation is performed. It is known only as a compound and can not be disentangled into its components. This is indicated by the brackets $(\cdot)_e$. C describes that compound in form of an observation matrix.

With other words:

we look for a solution to a given model which fits the given data in an optimal sense. Having that solution, we have all parameters.

The data was taken from the Johns Hopkins github repository Systems Science and Engineering (2020). We observe the total confirmed cases $I+R+D$ and the confirmed deaths D. Thus we have

$$C = \begin{pmatrix} 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 1 \end{pmatrix}.$$

Note, that it is possible to weight each row differently, in case we rely better on one source or the other. This is not done in this article.

The augmented Lagrangian to be minimised reads

$$\mathcal{L} = \mathcal{J} + q^* \mathcal{M}.$$

q^* is a Lagrangian multiplier which will be the adjoint state vector. The trick is, that we added zero for any value of q^* since $\mathcal{M} = 0$.

Linearisation of $\mathcal{M}$ and $\mathcal{J}$ yields after some steps, ([5]), an adjoint equation to be solved:

$$\partial_t q^* = -\underbrace{\left(\frac{\partial f}{\partial q}\right)^T}_{A^T} q^* - \underbrace{((C^T q - (C^T q)_e)^T C^T)^T}_{g}$$

or in short

$$\partial_t q^* = -A^T q^* - g. \tag{6}$$

This is an equation for a particular q^*. Rearranging the terms, it turns out that our choice q^* is the key to assess changes in model parameters:

$$\int q^{*T} \frac{\partial f}{\partial \alpha} dt \approx \frac{\partial \mathcal{J}}{\partial \alpha}.$$

This expression is called the **sensitivity** with respect to changes in the control parameters $\alpha = (\beta, \gamma, \delta)^T$. This tells us which change to the governing parameters are important and which not. They can be interpreted as the direction in which the cost functional gets worse if the governing parameters α are changed. In order to get closer to the data, we need to follow its negative direction. In figurative terms, it directs us to where it goes up or down on a mountain, and we need to follow the route down into the valley in our case.

3 Results and Discussion

In the sequel several data-sets are studied individually. China was the origin of the pandemic and has been able to bring the outbreak under control. We first study shortly the convergence towards the assimilated state and then discuss the full states and the underlying epidemic parameters.

3.1 Convergence

Convergence is measured as the norm of the discrepancy between data and simulation, normalised by the norm of the data:

$$\frac{\|C^T q - (C^T q)_e\|_2}{\|(C^T q)_e\|_2}.$$

The calculation was started with an arbitrary value of $(\beta, \gamma, \delta) = (1/4, 1/7, 0)$. This leads to an exorbitant growth in the shown case of China and correspondingly the norm is initially very high as compared to the provided data. Within a few iterations it comes down to approximately 7% and then slowly converges until the computation is stopped at an agreement of 2%.

This value is sufficient to match the development of the pandemic well. The start, when numbers are exceedingly small with one or two infected is not covered.

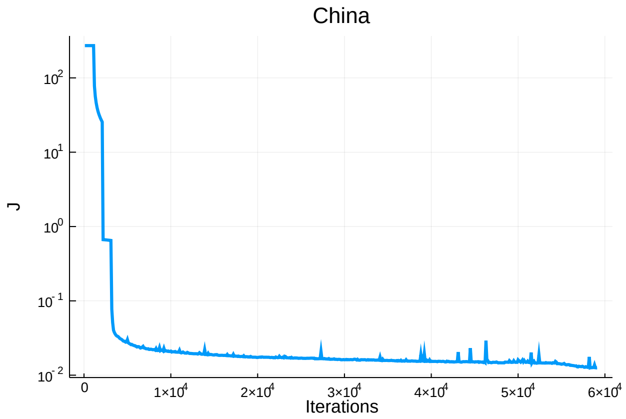


Fig. 1: Exemplary Convergence history for the case of China.

The present speed of convergence is not satisfactory when considering large scale fluid-dynamical problems, which is, what the author usually deals with, but since the present calculations run within less an hour on a standard laptop, no attempt was made to improve convergence in addition to what a brute force linesearch provides.

This needs to be improved upon, especially, when the onset of the outbreak is to be studied.

3.2 Case Studies

Several case studies will be presented: China, Italy, Germany, Bavaria, the United States and the United Kingdom. China has been the first country, where we can observe the full outbreak and decay. Italy was the first European country affected and the first to take action. Germany including Bavaria reacted next, and US and UK are very early in the development.

3.2.1 China

The data for China in the Johns Hopkins data starts on January 22 and is assimilated until present. Reported are the confirmed cases, which represent the sum of infected, recovered and dead people, $C = I + R + D$ and deaths D. After the first three weeks, there is an enormous jump in the data which is likely due to a change in information policy of the Chinese government or a change in how cases are reported. This corresponds to a rise in presumably infected people. Unfortunately this happened right before government action on February 26th.

Better than the full recovered state, the parameters $\beta(t), \gamma(t), \delta(t)$ show the development of the crisis, and how effective were government activities.

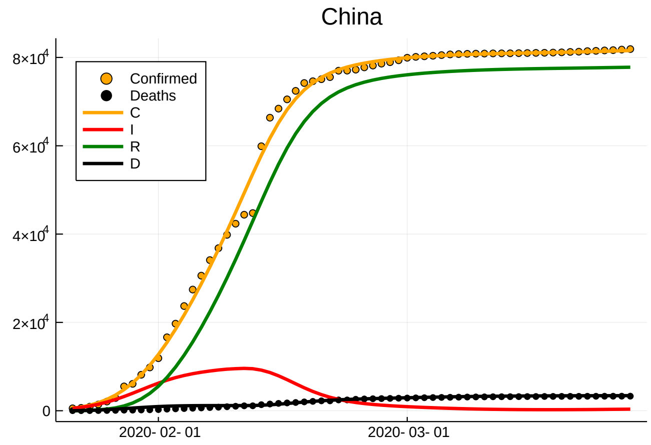


Fig. 2: Data from China (dots) and assimilation (lines)

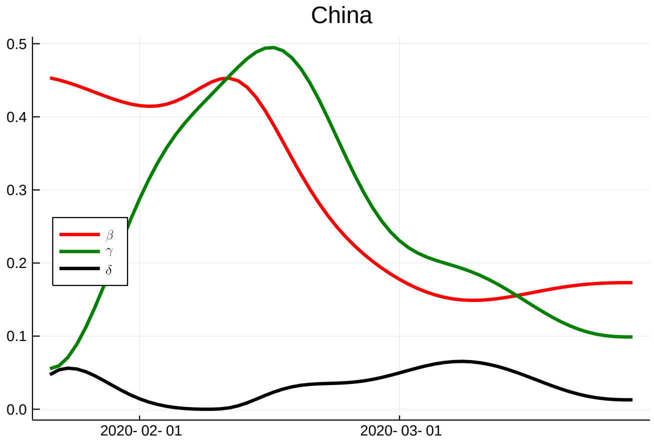


Fig. 3: Model parameters β, γ, δ for China

The dependence on time was explicitly noted in the expression, to indicate that these parameters are not constants, but are fitted to match the data.

On January 26, China closed universities, prescribed remote working measures and installed several other measures to contain the spreading of the virus. These measures seem not to be effective until a week later or obscured by the jump in reported confirmed numbers right at the same time.

The transmission rate β then shows a drop from $\beta = 0.45$ to $\beta = 0.16$ only from February 10 until March 1. This stopped the outbreak. Also seen in the figure is the spurious trough in death rate δ at the end of January. This is likey due to the spurious large number of new infects the algorithm tries to compensate.

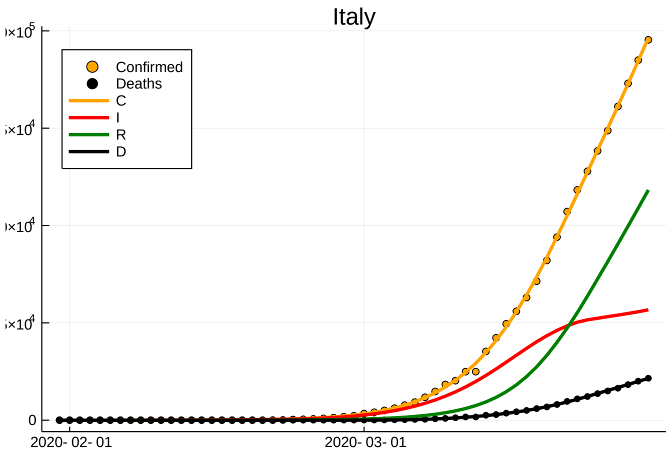
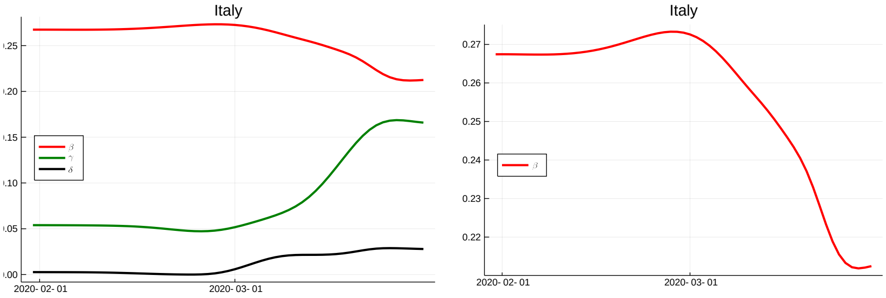


Fig. 4: Data from Italy (dots) and assimilation (lines)



(a) β, γ, δ for Italy

(b) β for Italy

Fig. 5: Model parameters β, γ, δ for Italy

It is also visible that the infection rate β rises slightly again since the second week of March.

3.2.2 Italy

Italy was the first European country hit by the outbreak. The assimilated data start at January 30 with the first infected being reported but the fact that β is already at $\beta = 0.27$ indicate that the rise, as obvious from the Chinese data and even more visible in the cases of below, occurred previously. Italy started its response in the first days of March and the β-value starts to fall significantly to about $\beta = 0.22$ as of today and seems to have levelled off there. As already seen in China, the response time of the β to government action is one month. It is also an important indicator that the number of infected people is below the ones already recovered. So far this is only visible in China and Italy, whereas the cases below are far from there.

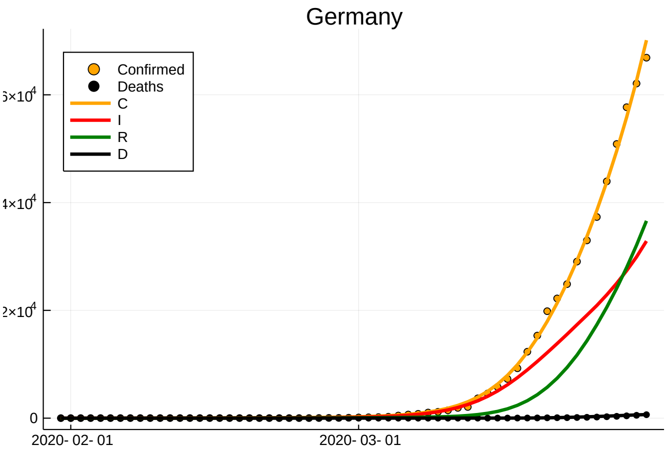
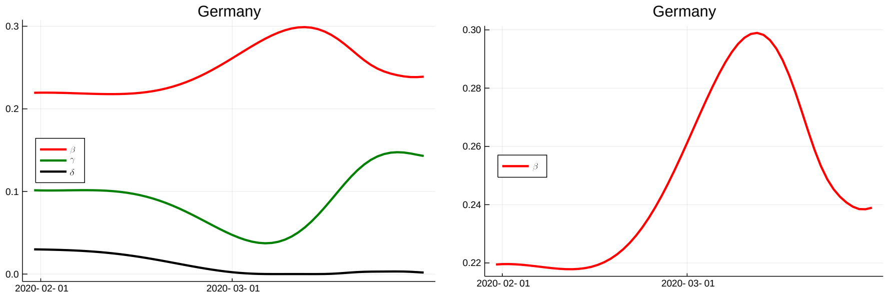


Fig. 6: Data from Germany (dots) and assimilation (lines)



(a) β, γ, δ for Germany

(b) β for Germany

Fig. 7: Model parameters β, γ, δ for Germany

3.2.3 Germany

The German data is relatively plain and shows nicely the onset of the development and the effectiveness of the actions taken. There is an almost exponential growth and with the naked eye it is hard to tell when the parameters vary significantly.

A look at the assimilated model parameters show, that there is a significant increase with a peak around March 15th, starting three weeks earlier. After March 15th, there is a drop below the originally constant value within one week. This shows the effectiveness of the government actions taken mid March. The response time seems to be substantially faster than in China. The author expects the numbers to decrease further to about $\beta = 0.2$ within the next two weeks as seen in the case of China and Italy. As shown in the prognosis for Germany below, the present state is not sufficient to terminate the outbreak

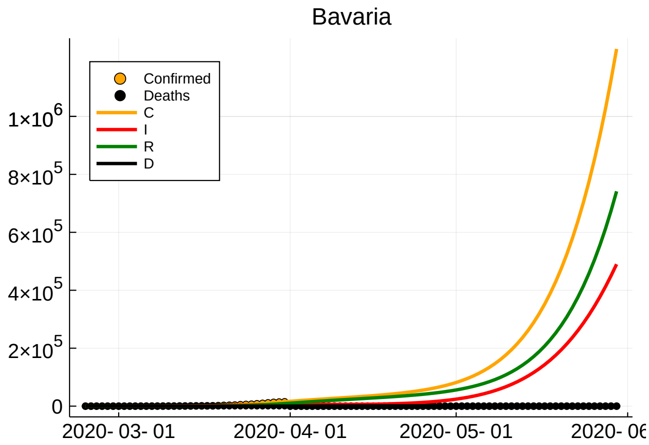
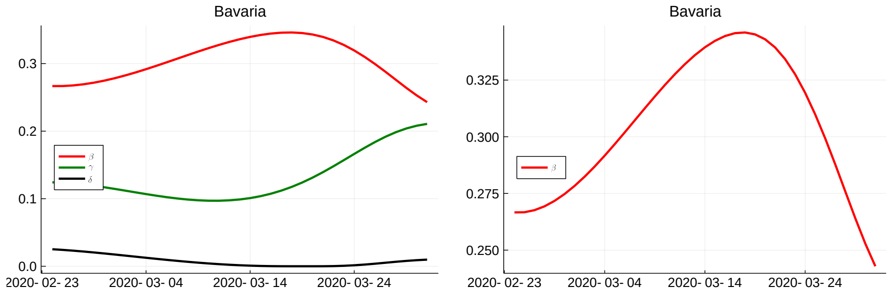


Fig. 8: Data from Bavaria (dots) and assimilation (lines)



(a) β, γ, δ for Bavaria

(b) β for Bavaria

Fig. 9: Model parameters β, γ, δ for Bavaria

but delays its peak. Terminating the countermeasures will likely not *flatten the curve* but only delay its peak.

3.2.4 Bavaria

In Bavaria a rise in β occurs March 1st.[1] Note that at this time the outbreak is already ongoing with 14 cases reported. Therefore this rise in β significates a substantial acceleration, not the onset. Note also that the values are subtantially higher than the German-wide average, where this numbers are included. The situation is therefore more severe in Bavaria than on German average. Additional action surpassing the German-wide restiction was taken 21st of March, which is clearly visible in a drop of β in the assimilation.

[1] Data scraped from [4]

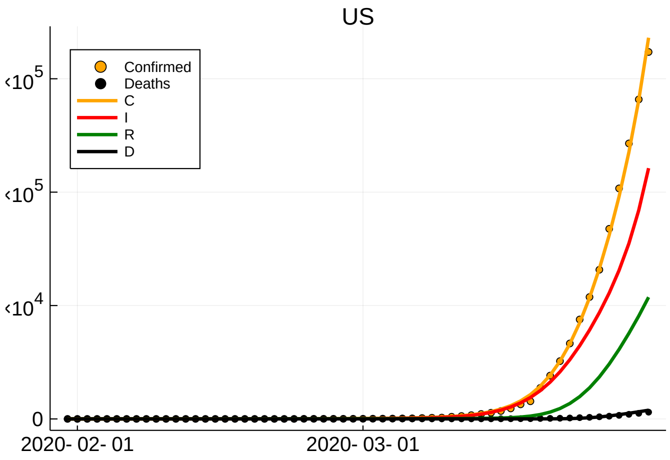


Fig. 10: Data from the US (dots) and assimilation (lines)

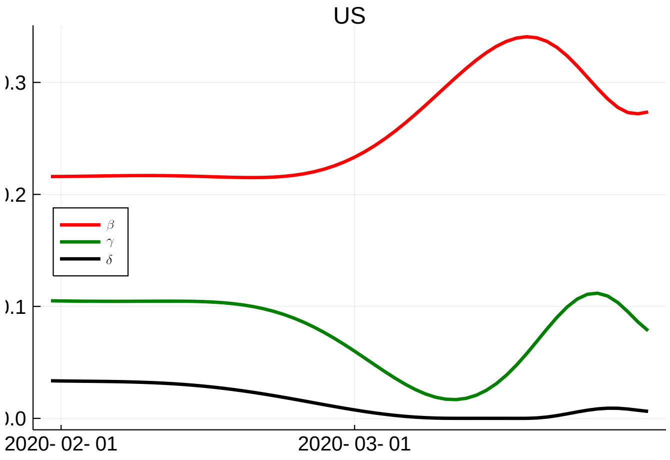
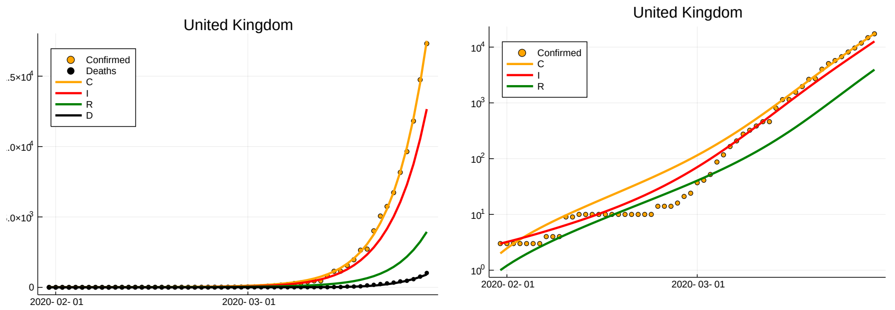


Fig. 11: Model parameters β, γ, δ for the US

3.2.5 United States

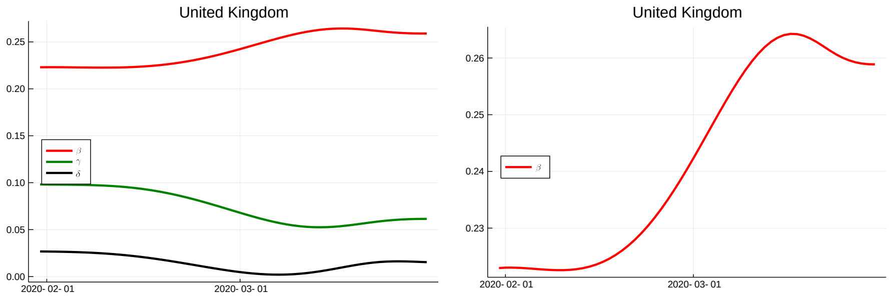
The United states have had ongoing cases prior start the start of the records such that the ramp up of the infection rate to $\beta = 0.24$ is not visible in the data. However, there was a second surge starting March 1st which lifted the value up to $\beta = 0.32$ which is well above what can be seen in European countries but below the Chinese peak value. There is evidence of a minor sucess in limiting the spread of the desease. It can also be observed that the recovered count is still far below the infected. This shows that the US is far from containing the virus and we have to expect the worst numbers from out of the US.



(a) Data (dots) and assimilation (lines)

(b) Data from the United Kingdom in logarithmic scaling

Fig. 12: The United Kingdom



(a) β, γ, δ for the United Kingdom

(b) β for the United Kingdom

Fig. 13: Model parameters β, γ, δ for the United Kingdom

3.2.6 United Kingdom

The case of the United Kingdom is akin to the US, but the rise is the first and hopefully only one, and the growth rate is still $\beta = 0.26$. From the logarithmic scaling in figure 11 one can see that the assimilation predicts much more infected people than reported by the source in the date range between February 8 and March 8 in order to be in accordance with the epidemiology model.

So far counter-measurements are visible only in the enlarged view of the data in figure 13b. Fortunately the level is substantially lower than the numbers seen for the US.

4 Prognosis

Based on the assimilated values of β , γ, and δ at the last instance where data is available and the correspondinng numbers of S, I, R, D, model calculations were made for the future. Examples are given for the case of Italy and Germany.

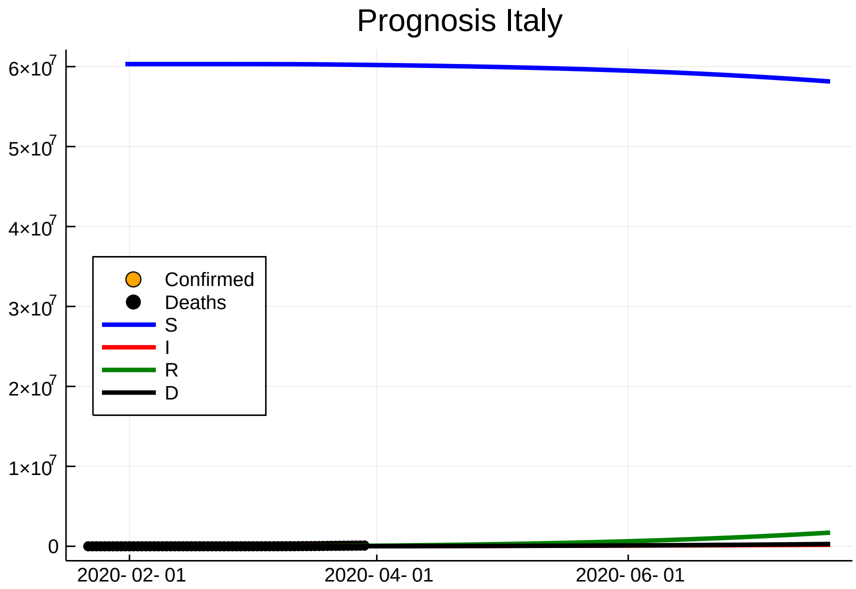


Fig. 14: Prognosis based on the values for Italy as of March 29th. Actual cases are to the left and their elevation is not visible in relation to the total numbers. This indicates the extent of not even a fully blown outbreak.

Italy is done with the outbreak if it can maintain the present values of the governing parameters. Germany is not at this stage yet.

The result for Germany shows, that (given the last values of the parameters which only partially reflect the effeciveness of the very recent goverment actions yet) will not limit the outbreak permanently, but delay it until June. But this is partly good news, because it shows, that the exponential growth is only slightly positive. It is expected that numbers within the next days will show the full extent of the government actions.

5 Conclusions

Data assimilation is able to fit a epidemology model to given data. The result is the recovery of the full model state S, R, I, and D, as well as the model parameters β, γ, and δ. In particular S, R, I, β, γ, and δ are difficult to obtain otherwise.

This gives a unique tool to interpret the data and assess the quality of governmental action or effect of crucial events like the end of the holiday season. This was demonstrated in particular by the values of β and their rise or drop.

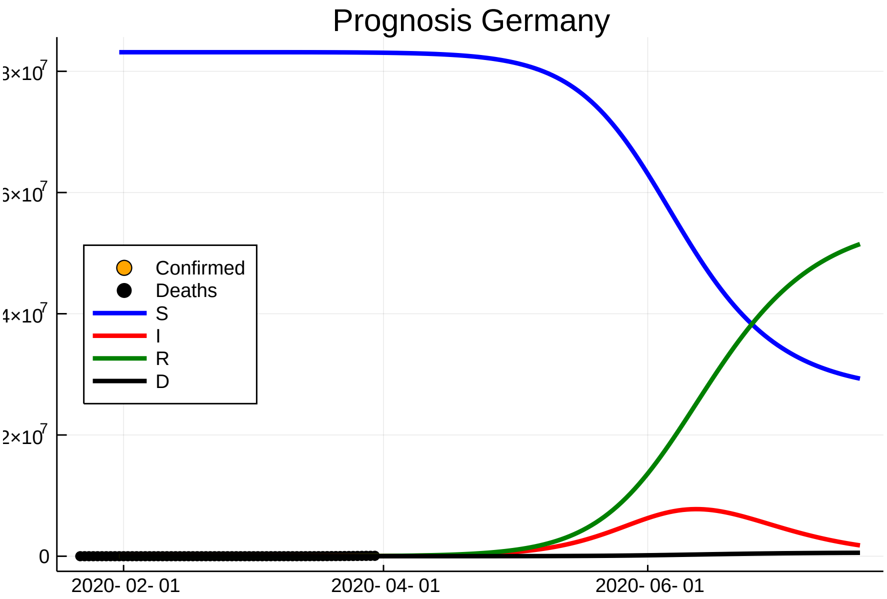


Fig. 15: Prognosis based on the values for Germany as of March 29th. Actual cases are to the left and their elevation is not visible in relation to the total numbers. This indicates the extent of not even a fully blown outbreak.

Government actions, not only in China, but also in Italy, Germany, and Bavaria are effective and can clearly be seen at an early state in the assimilation results.

The model can be exchanged by a better one as in use by University Institutions or governments. Feedback control is possible to implement, as well the coupling with for example economic models. The author is available for requests in that direction.

Conflict of interest

The author declares that he has no conflict of interest.

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