Term Paper - Research Case Study

Machine Learning Modelling of COVID-19

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Contents

Abstract

Background

It was the scenario the general public health community had feared for several years.The spread of coronavirus disease COVID-19 has increased day-by-day. World Health Organization declared its outbreak on 30th January 2020, recognizing the outbreak as a pandemic on 11th March 2020. As often said by politicians and scientific advisors, the target is "to flatten the curve" or "push the peak down" of the virus spreading. Mathematical models and data, played a crucial role in estimating the evolution of the amount of infected, recovered and deaths. The accuracy of the models is improved day by day by inferring the contact, recovery, and death rates from data (confirmed cases).

Methods

A data-driven model trained with both data and first principles is proposed. The model can quickly be re-trained any time that new data becomes available.

Data

John Hopkins University CSSE has been collecting global data from official organizations, such as the World Health Organization, Italy Ministry of Health, and others.

Results

The outputs of the analysis are the estimates of infected, recovered and deaths due to COVID-19, as well as the contact, recovery, death rates, basic reproduction number(R0) and doubling times. The subsequent case studies are analysed: Germany, Australia, India, Canada, Russia and China.

1 Introduction

In December 2019, a disease caused by single-stranded RNA coronavirus (Severe acute respiratory syndrome coronavirus 2,SARS-CoV-2) infected people in the city of Wuhan, the capital of Hubei province in the People's Republic of China. On 11th March 2020, the World Health Organization(WHO) declared the spread of the virus a global pandemic.

The disease caused by this virus has been named as COVID-19 (Coronavirus Disease 2019). Globally, as of 4:48pm CET, 2 February 2021, there have been 102,942,987 confirmed cases of COVID-19, including 2,232,233 deaths, reported to World Health Organization. To control the epidemic, aggressive measures have been implemented worldwide, for instance, self-isolation of confirmed and suspected cases, contact tracing and tracking, and social distancing. According to the data, the most extreme measures have managed (or are managing) to overcome the epidemic. Examples are the localised lockdown of the Hubei region in China (23rd-24th January 2020); and the national lockdowns of Australia(20th March 2020), Canada(9th March 2020); Germany(22nd March 2020), India(25th March 2020), among others.

Scientific advice typically relies on estimates of the contact, recovery and death rates. This information is summarized in the basic reproduction number, R0, which is the average number of new infections generated by a single infected person within a susceptible population. Estimates of COVID-19 R0 are variable due to the different methods, models and parameters employed, as well as the databases used. Flattening the curve or keeping the peak down, or similar wording, which have been extensively used by governments to level with a lay audience, can be achieved by either reducing the contact rate, β, or by increasing the recovery rate, γ. The objective of this paper is threefold. First, a model that optimally combines data from official databases and first principles of an epidemic model is proposed. Second, the model is applied to provide quantitative estimates on the contact, recovery, death rates; the basic reproduction number R0; the doubling times; and the evolution of the number of infected, recovered, deaths, and susceptible. Six cases are analysed: Germany, Australia, India, Canada, Russia and China. Third, predictions of future dynamics are provided. Although the results are consistent with the first principles and working assumptions used, they are affected by uncertainty because of biases in the data, such as errors in reporting, changes in case definition and testing regime, and modelling assumptions. The paper is structured as follows. The method is presented in Sec. 2 and the results are shown in Sec. 3.

2 Methods

2.1 Epidemic Model

In order to mathematically describe the behaviour of corona disease 2019 (COVID-19) as an epidemic, the population of interest, N, is divided into four disjoint groups: those who are susceptible (S), infected (I), recovered (R), and deceased (D). Deaths accounted for in this model are assumed to be caused by COVID-19. New births and number of unrelated deaths are considered to be insignificant in proportion to the entire population, and travel restrictions have been heavily enforced, thus N is assumed to remain constant over time (Magri and Doan, 2020). Each mutually exclusive group is assumed to have the same attributes, that is, the groups are homogeneous to one another. As well, it is assumed that there are no immune individuals existing, meaning every susceptible person has the same chance of contracting the virus. This method of compartmentalizing is known as the SIRD-epidemic model; the model used in this study will be referred to as the SIRD model for concision. Mathematically, the SIRD model can be written as:

$$N = S + I + R + D \tag{1}$$

The population N, which does not change over time, is the sum of the groups S, I, R, D, which do vary over time.

Initially, the entire population is reflected by the group of susceptible individuals, S. Subsequently, after the first COVID-19 case is recorded, the population will begin to move through the other appropriate compartments.

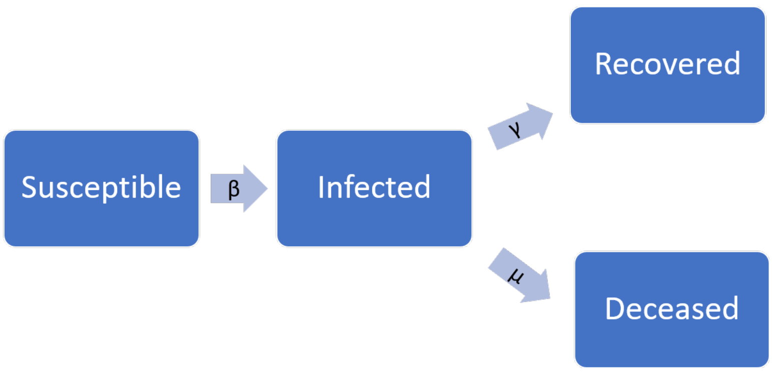


Figure 1: Flow through an SIRD model

The movement of people from one compartment to another over time, t, is expressed by the following four differential equations of the SIRD model:

$$\frac{dS}{dt} = -\beta \frac{I}{N} S \tag{2}$$

$$\frac{dI}{dt} = \beta \frac{I}{N} S - (\mu + \gamma) I \tag{3}$$

$$\frac{dR}{dt} = \gamma I \tag{4}$$

$$\frac{dD}{dt} = \mu I \tag{5}$$

which are subject to the initial conditions, denoted S_0, I_0, R_0, and D_0. From the above equations, interpretation has that $\frac{I}{N}$ is the probability of coming into contact with an infected individual, β is the average number of physical contacts per person per unit of time (contact rate), γ is the average number of recovered people per unit of time (recovery rate), and μ is the average number of COVID-19 related deaths per unit of time (death rate). The epidemic parameters are represented in the column vector

$$\boldsymbol{\alpha} \equiv [\beta, \gamma, \mu]^T, \tag{6}$$

and the state of a population at time t is found in the column vector

$$\boldsymbol{q} \equiv [S, I, R, D]^T \tag{7}$$

where

$$\boldsymbol{q} = \boldsymbol{q_0} \text{ at t=0.} \tag{8}$$

Using $\boldsymbol{F}$ to represent the SIRD model equations (2)-(5), the changes in $\boldsymbol{q}$ (derivatives at time t) are given by

$$\frac{d}{dt}\boldsymbol{q} = \boldsymbol{F}(\boldsymbol{q}; \boldsymbol{\alpha}). \tag{9}$$

Note that bold-faced symbols, such as $\boldsymbol{\alpha}$ and $\boldsymbol{q}$, are used to differentiate vector-valued quantities from their scalar equivalents, which are written in normal font: α, q.

2.2 Data Sources

It was found that inconsistencies exist in some of the data sets for certain countries, e.g. United Kingdom. Unreliability exists in the count of recovered individuals, R, due to the definition of recovery for COVID-19 and how the numbers are reported. The Center for Disease Control and Prevention

(CDC) outlines recovery status as having no COVID-19 symptoms for a minimum of 3 consecutive days (Schive, 2020). However, patients have reported persistent positive tests for COVID-19 even though they were symptom free for the minimum 3 days as mentioned (U.S. Department of Health & Human Services, 2020). The United Kingdom reports individuals hospitalized with and without a ventilator as well as the number of deaths that have occurred, but recovered individuals are not explicitly detailed[1]. Therefore, data is first screened for measurement consistency before being analyzed. Then, only the data on confirmed infected and deceased individuals is utilized, arranged into a single vector,

$$\boldsymbol{q_c} \equiv [I_c, D_c]^T. \tag{10}$$

The data used in this study was accessed through the publicly available repository from the Center for Systems Science and Engineering at the John Hopkin's University, CSSEGISandData/COVID-19, on GitHub[2].

2.3 Minimization Framework

The determination of a population's dynamics (7) and time-dependent parameters (6) through the course of the pandemic is regarded as a constrained optimization problem. The loss between the proposed solution of infected and deaths, (I, D), and the confirmed data, (I_c, D_c), is minimized, while being subject to the conditions of the epidemic model (2)-(5). The algorithm used for solving this minimization problem is discussed in detail in section 2.4.

2.4 Algorithmic Solution

The epidemic machine learning model is based on combining an ordinary differential equations (ODE) solver which advances the SIRD model equations (2)-(5) over time, and a feed-forward neural network (NN) which integrates the data with the epidemic model to learn the parameters, $\hat{\boldsymbol{\alpha}}$(t), and predict the state, $\hat{\boldsymbol{q}}$(t).

Before the training of the NN can take place, however, we need true parameters to compare our estimates to. Since we do not have this data readily available, a study is performed using Optuna, a hyperparameter optimization framework, to suggest the optimal $\beta_0, \gamma_0,$ and μ_0 using the Euclidean distance between the estimated and confirmed state as the objective function to be minimized (Akiba et al., 2019). Initially, parameters are suggested to be uniformly distributed with minimum 0 and maximum 1. The parameters are studied over the initial exponential growth time-period in the

[1] https://coronavirus.data.gov.uk/
[2] https://github.com/CSSEGISandData/COVID-19

respective country in order to reflect the behaviour of COVID-19 in a population before any governmental interventions or restrictions were introduced. After running 500 optimization trials, a constant set of the best parameters are obtained and cast as $\boldsymbol{\alpha_0} \equiv [\beta_0, \gamma_0, \mu_0]^T$. The NN is then initialized with weights randomly chosen from a standard normal distribution, a sigmoid activation function, and these parameters as output. The sigmoid function is often used as the activation function in shallow feed-forward neural networks and for probability prediction purposes, both relevant features of this study, and the reasons why it was chosen (Nwankpa et al., 2018).

The initialized NN receives as input the complete time series of confirmed infected and deceased cases for an individual country. The starting point, t_0, is that where the number of infected cases is no longer equal to zero (for the country of interest), and 180 days are studied thereafter. From the input data, the NN compiles the time evolution of the SIRD model, i.e. $\hat{\beta}(t)$, $\hat{\gamma}(t)$, and $\hat{\mu}(t)$, which are cast into the vector $\hat{\boldsymbol{\alpha}} \equiv [\hat{\beta}, \hat{\gamma}, \hat{\mu}]^T$ consistent with (6).

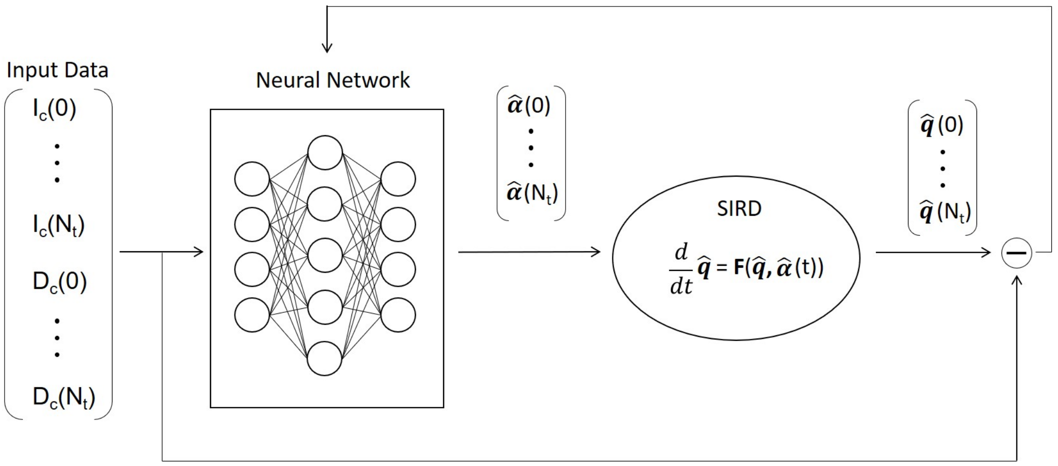


Figure 2: Pictorial representation of machine learning for epidemic modelling

Equations (2)-(5) are examples of first-order ordinary differential equations (ODEs) with given initial conditions, of which one can integrate to evaluate the system at a given time $t > t_0$ (Griffiths and Higham, 2010). The technique utilized to time-advance these equations for this NN is Euler's explicit method for solving ODEs with initial conditions (Asche and Petzold, 1998). "Explicit methods calculate the state of the system at a later time from the state of the system at the current time without the need to solve algebraic equations" (Bui, 2010). Euler's method is a numerical method used to approximate the solution to an initial value problem with a differential equation. Given the $\hat{\beta}(t)$, $\hat{\gamma}(t)$, $\hat{\mu}(t)$ values from the NN, and initial model values S_0, I_0, R_0, D_0, the state of the model at the next time step is estimated using:

$$\hat{\boldsymbol{q}}(t+1) = \hat{\boldsymbol{q}}(t) + \boldsymbol{F}(\boldsymbol{q}; \boldsymbol{\alpha}). \tag{11}$$

Thus, equations (2)-(5) are used together with Euler's explicit method to calculate the new state of our model, $\hat{\boldsymbol{q}}$(t+1), given the previously predicted state, $\hat{\boldsymbol{q}}$(t), and optimized parameters $\hat{\boldsymbol{\alpha}}$(t) (Griffiths and Higham, 2010).

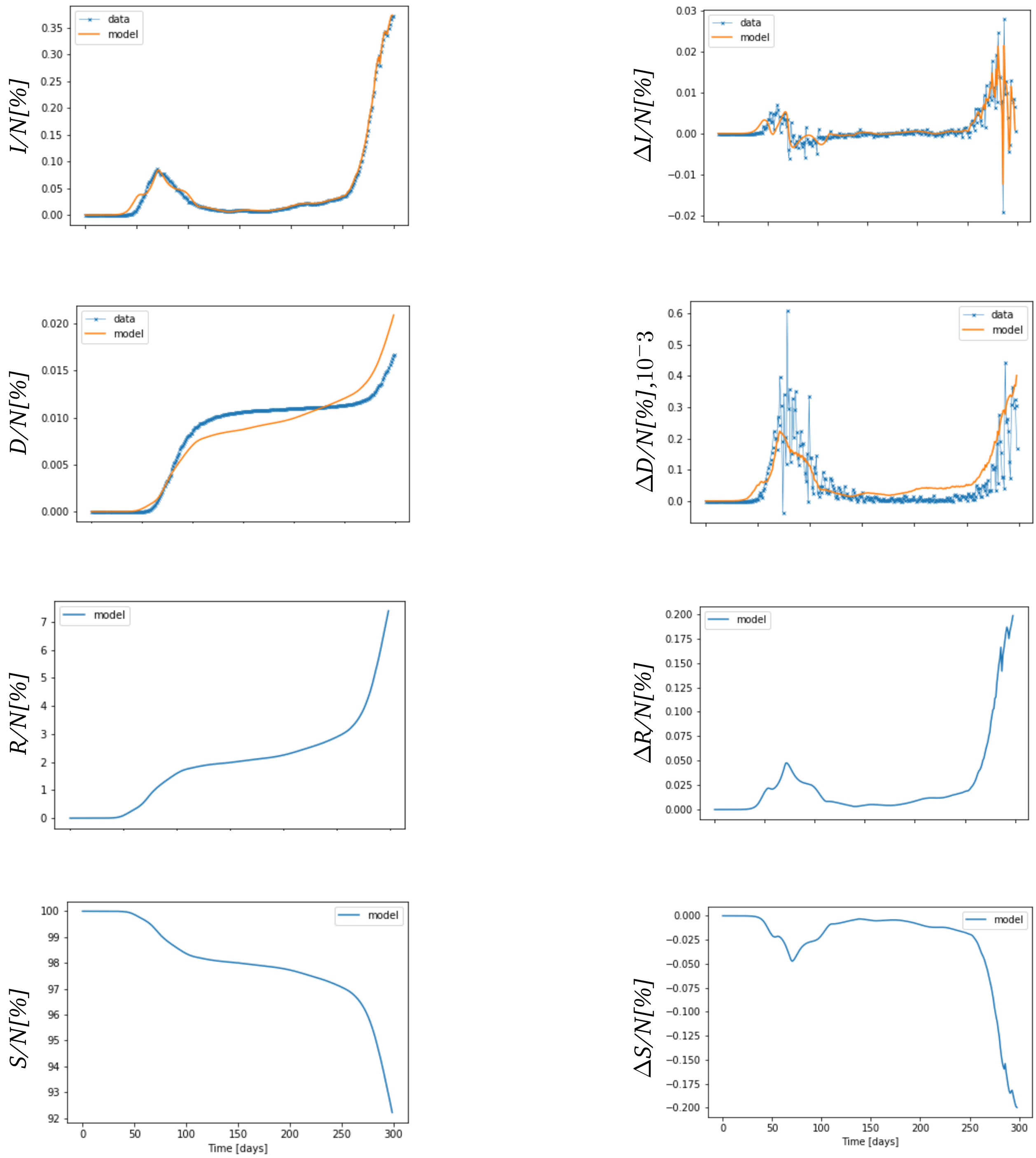
The loss function to be minimized is that proposed by Magri and Doan (2020), which aims to capture four sources of error: the error between the predicted and confirmed data (infected and deceased), both on a log and a linear scale, a regularization term for discontinuities in the time evolution of the SIRD parameters, and a term to constrain the initial values of $\hat{\boldsymbol{\alpha}}$ to be close to $\boldsymbol{\alpha_0}$.

The learning step is where the weights are updated based on a search method aimed at minimizing the aforementioned loss function such that the SIRD model holds with initial conditions $\boldsymbol{q_0} = [N_0 - I_0 - D_0, I_0, 0, D_0]^T$, where N_0 is the population of the country of interest, and I_0 and D_0 are the confirmed infected and deceased individuals at time t_0, respectively. A gradient search for the path of steepest descent with respect to the loss function is calculated and used to update the weights of the NN. In doing so, each subsequent parameter estimation will be calculated such that the loss function grows smaller.

This process is iterated through for each respective country, and finally summarized with graphical representations of the trends of the parameters, and of the S, I, R, and D population segments.

3 Results

3.1 Germany



(a):Cummulative quantites

(b):Daily rates

Figure 3: Germany (day 0 = 27th January 2020): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

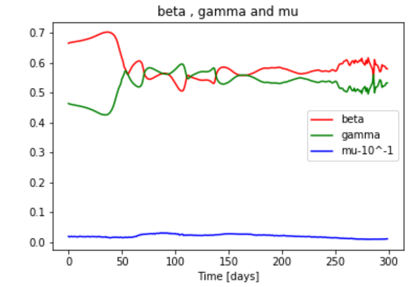
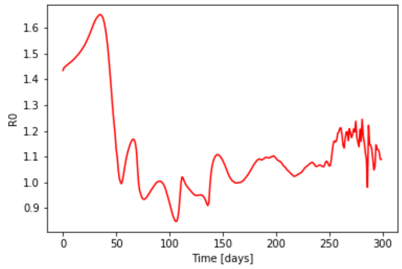


Figure 4: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 5: Germany (day 0 = 27th January 2020): SIRD parameters. Neural network trained with loss function.

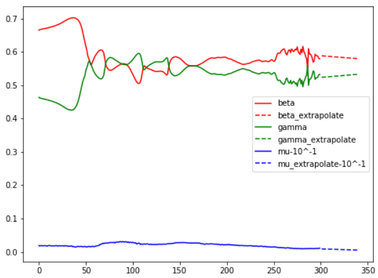


Figure 6: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

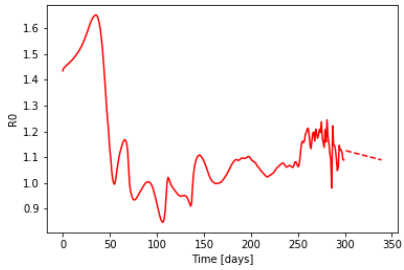
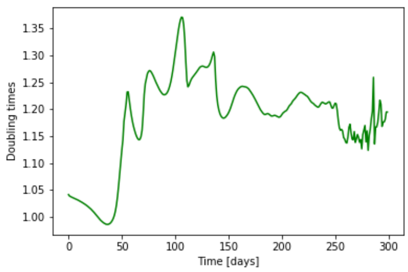
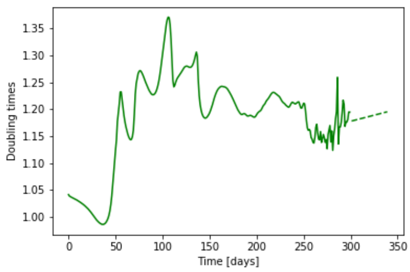


Figure 7: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 8: Germany (day 0 = 27th January 2020): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 9: Germany (day 0 = 27th January 2020): Doubling time with the log. The doubling time is calculated as t = $\log(2)/\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

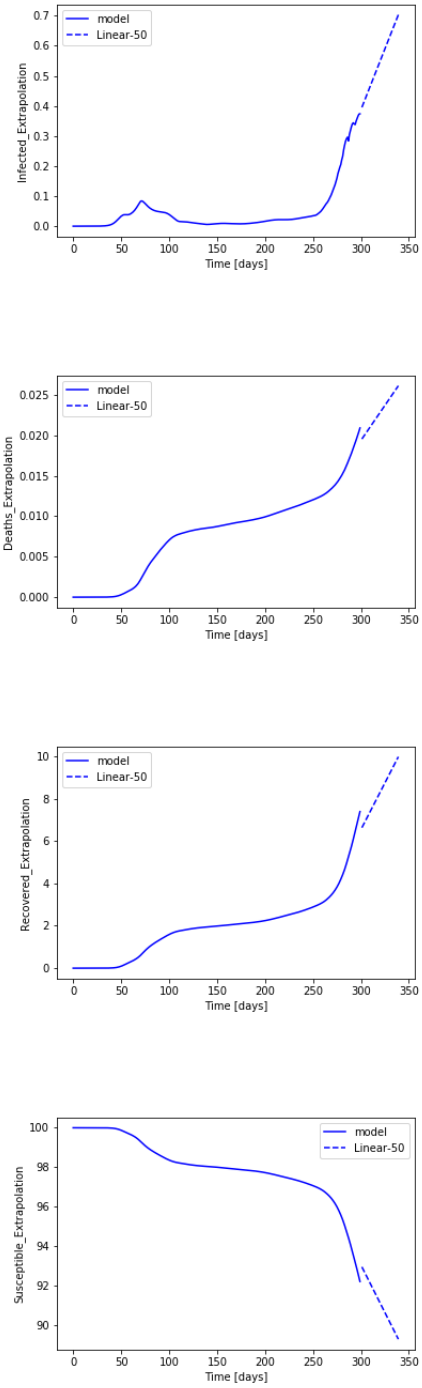
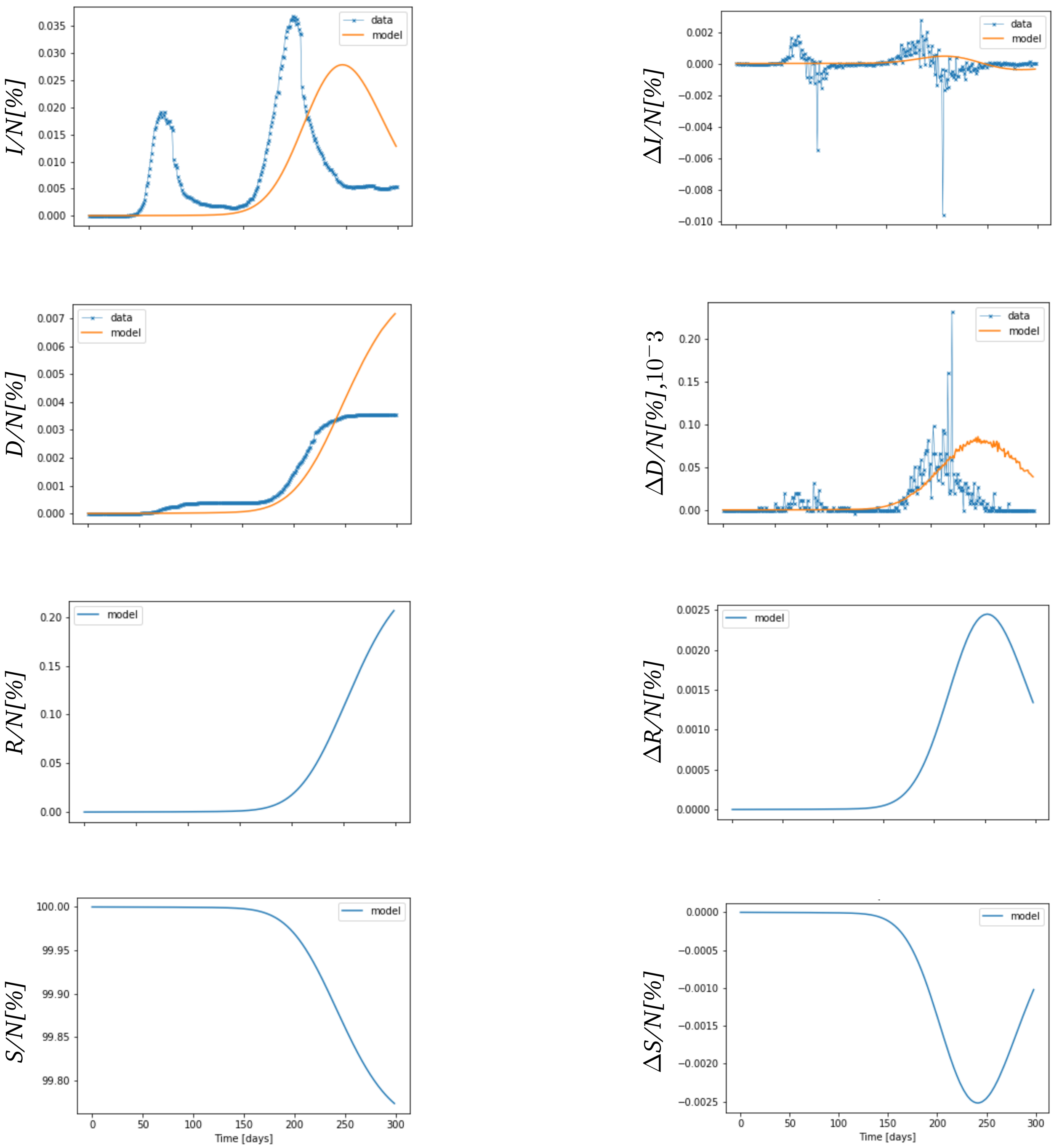


Figure 10: Germany (day 0 = 27th January 2020): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

3.2 Australia



(a):Cummulative quantites

(b):Daily rates

Figure 11: Australia (day 0 = 26th January 2020): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

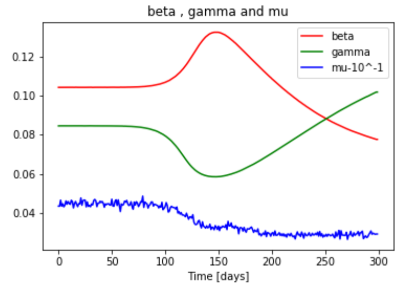
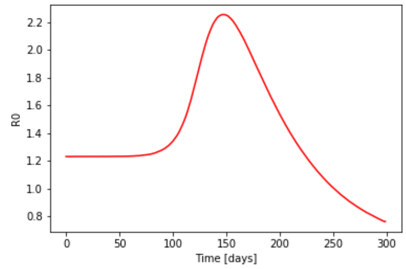


Figure 12: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 13: Australia (day 0 = 26th January 2020): SIRD parameters. Neural network trained with loss function.

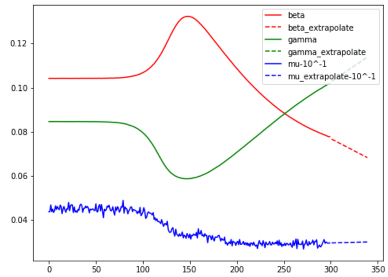


Figure 14: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

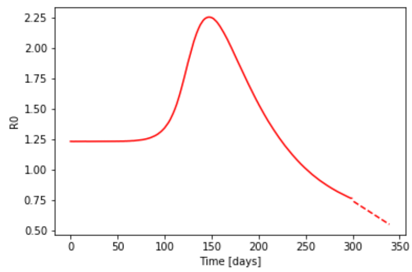
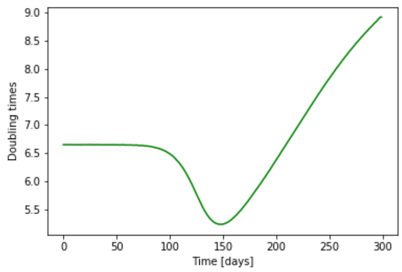
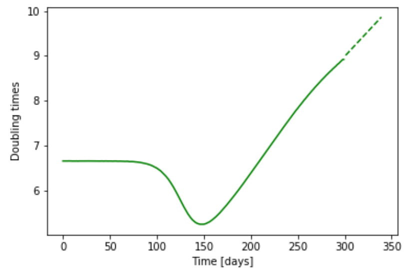


Figure 15: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 16: Australia (day 0 = 26th January 2020): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 17: Australia (day 0 = 26th January 2020): Doubling time with the log. The doubling time is calculated as t = $\log(2)/\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

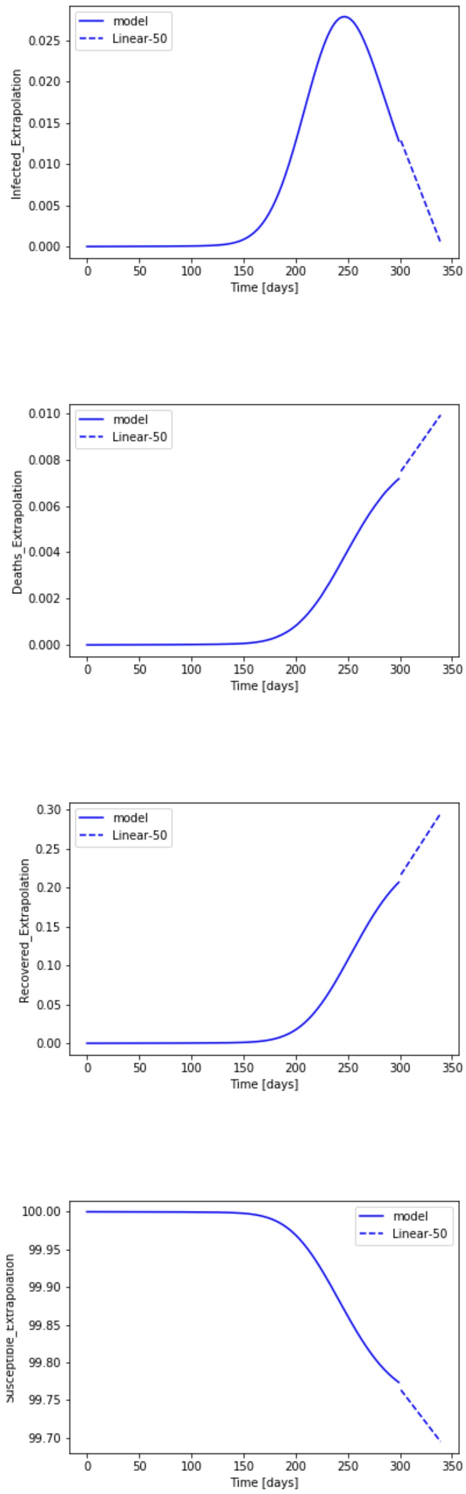
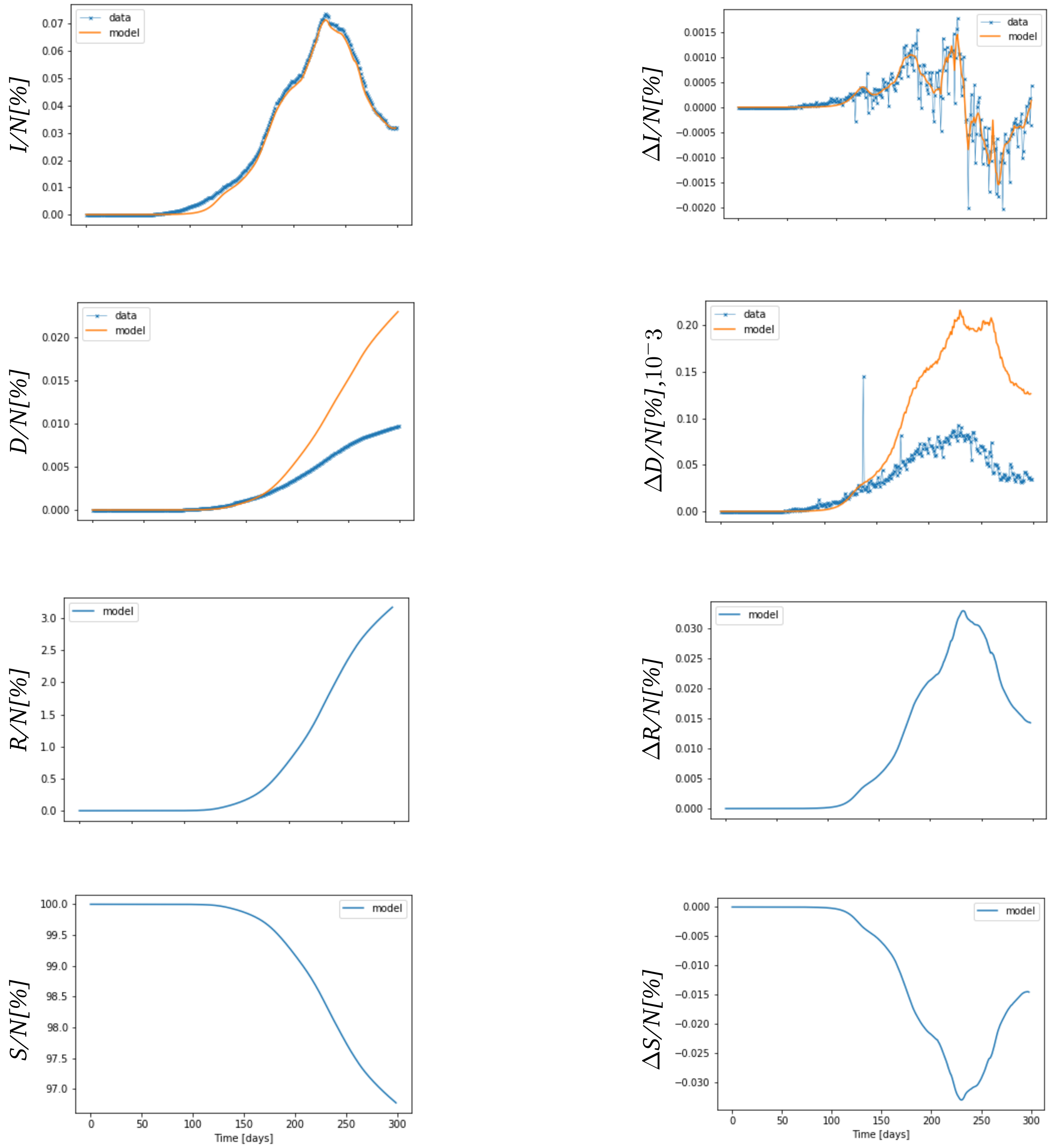


Figure 18: Australia (day 0 = 26th January 2020): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

3.3 India



(a):Cummulative quantites (b):Daily rates

Figure 19: India(day 0 = 30th January 2020): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

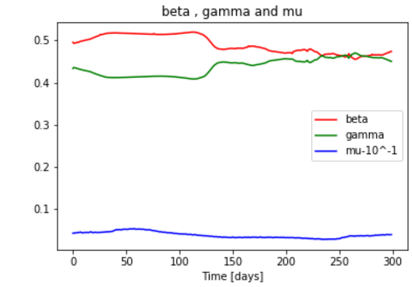
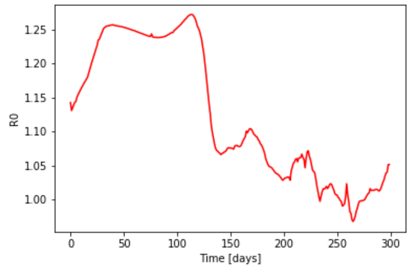


Figure 20: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 21: India (day 0 = 30th January 2020): SIRD parameters. Neural network trained with loss function.

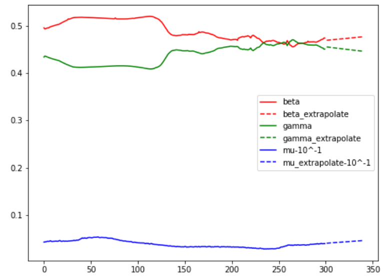


Figure 22: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

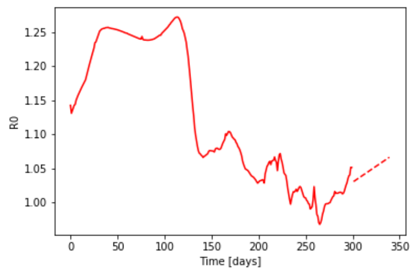
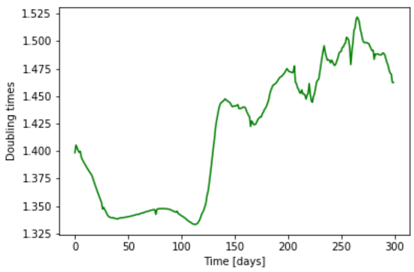
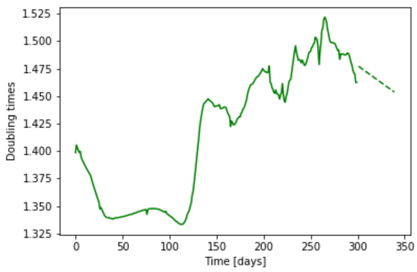


Figure 23: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 24: India (day 0 = 30th January 2020): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 25: India (day 0 = 30th January 2020): Doubling time with the log. The doubling time is calculated as t = $\log(2)/\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

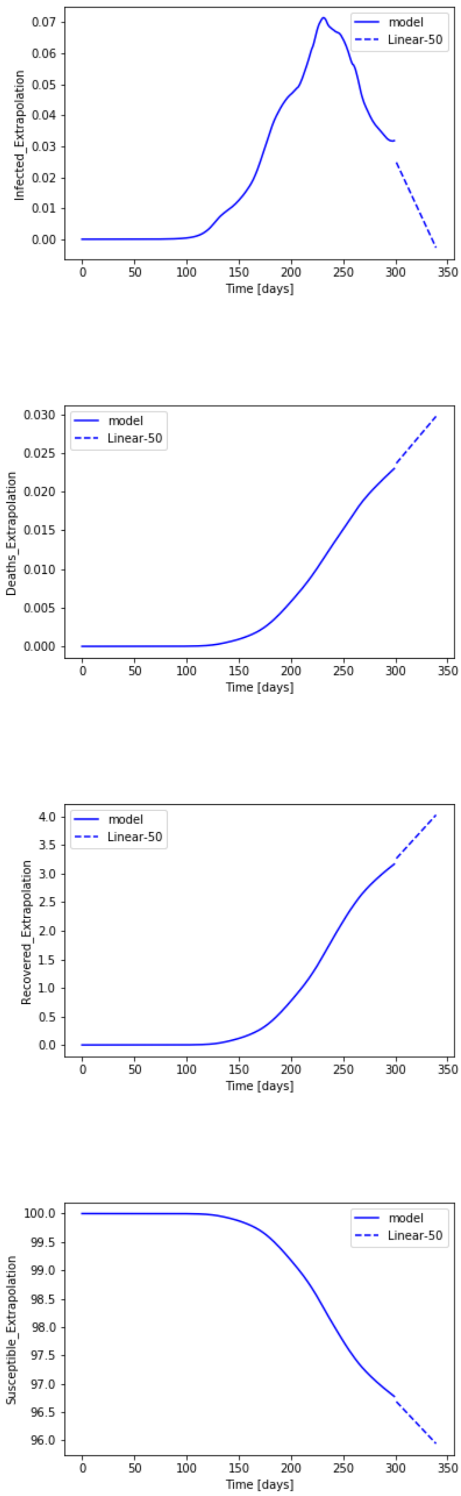
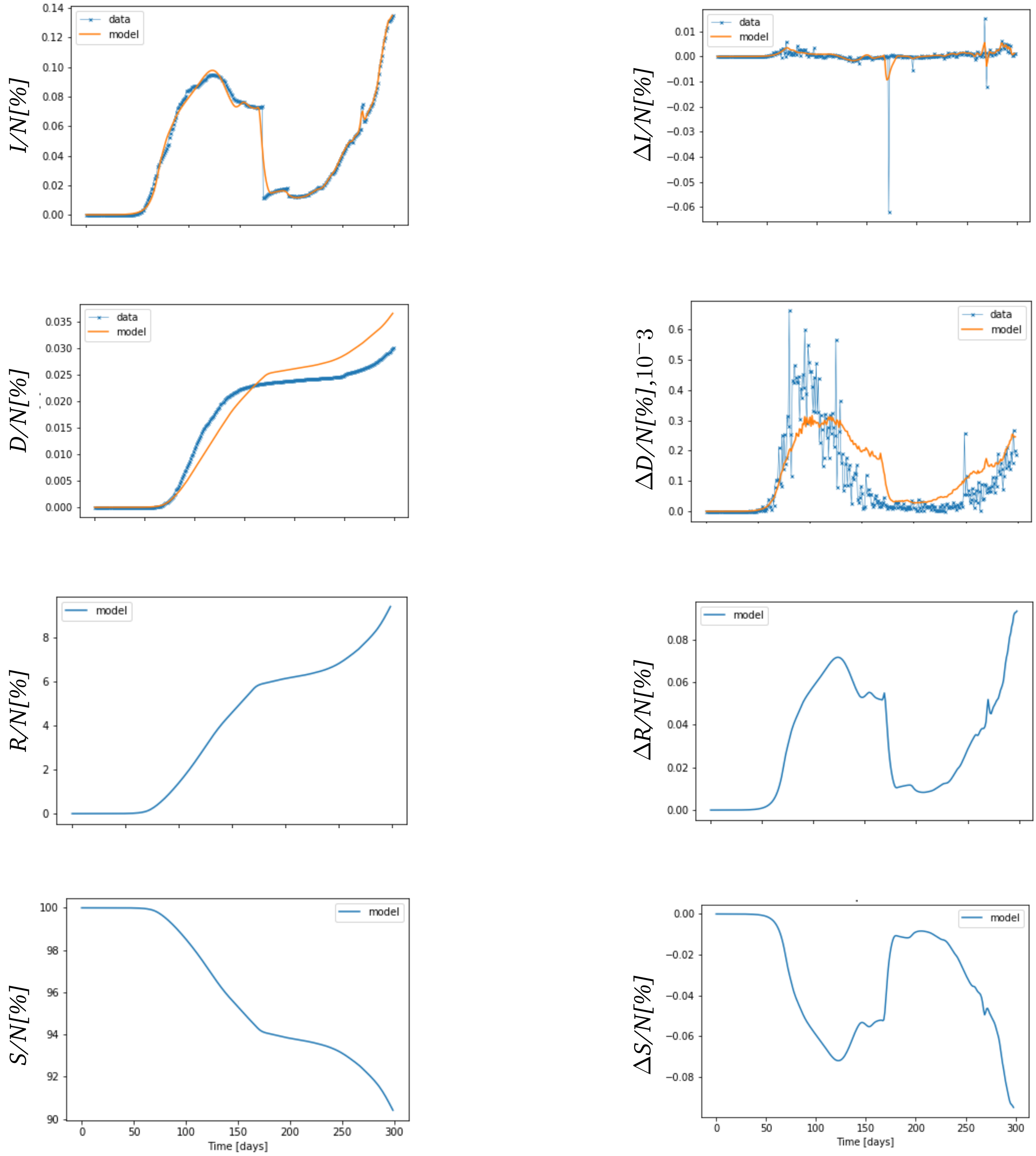


Figure 26: India (day 0 = 30th January 2020): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

3.4 Canada



(a):Cummulative quantites

(b):Daily rates

Figure 27: Canada (day 0 = 22nd January 2020): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

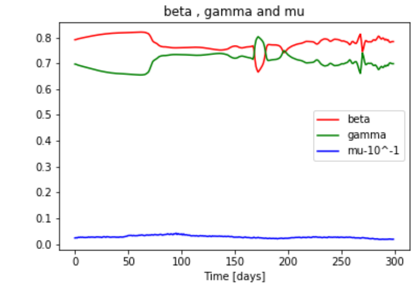
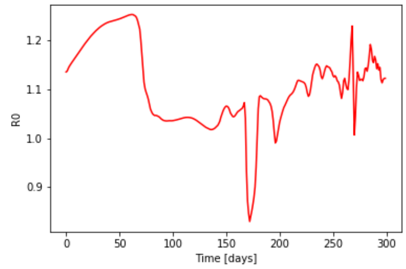


Figure 28: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 29: Canada (day 0 = 22nd January 2020): SIRD parameters. Neural network trained with loss function.

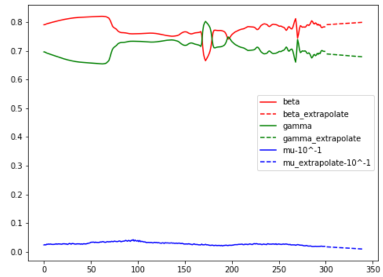


Figure 30: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

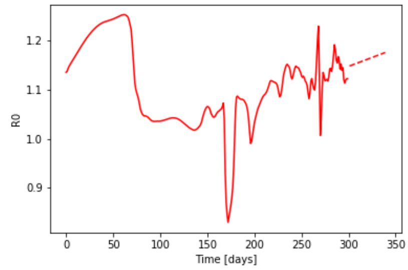
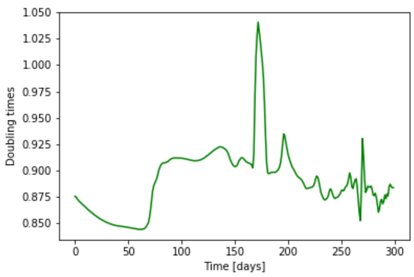
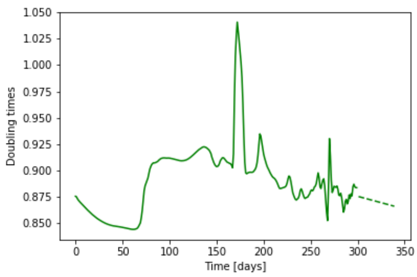


Figure 31: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 32: Canada (day 0 = 22nd January 2020): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 33: Canada (day 0 = 22nd January 2020): Doubling time with the log. The doubling time is calculated as t = log(2)/$\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

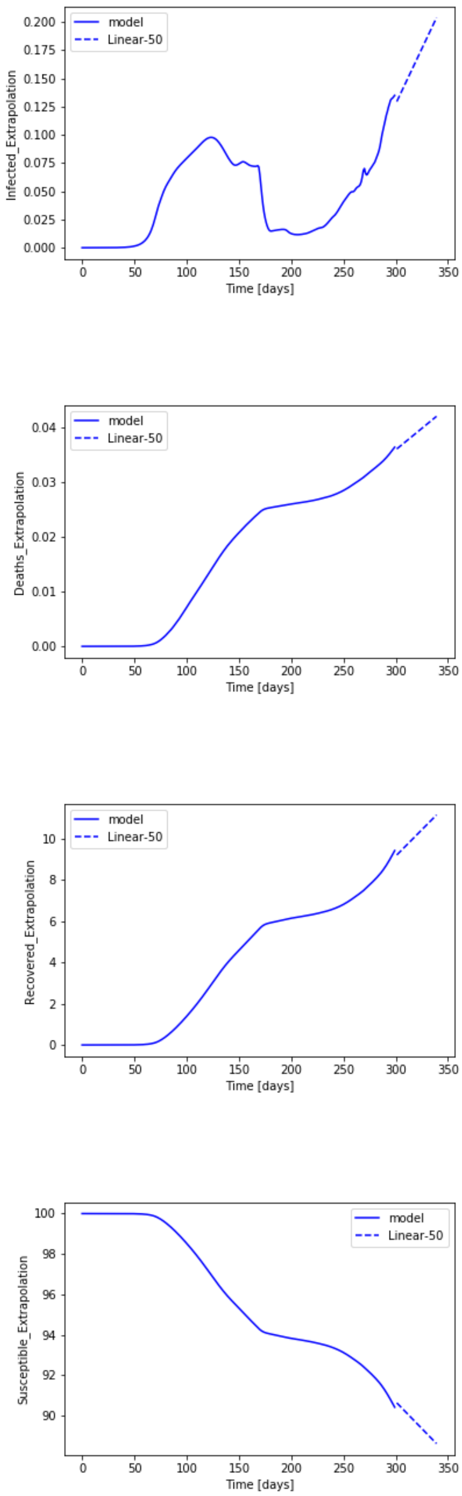
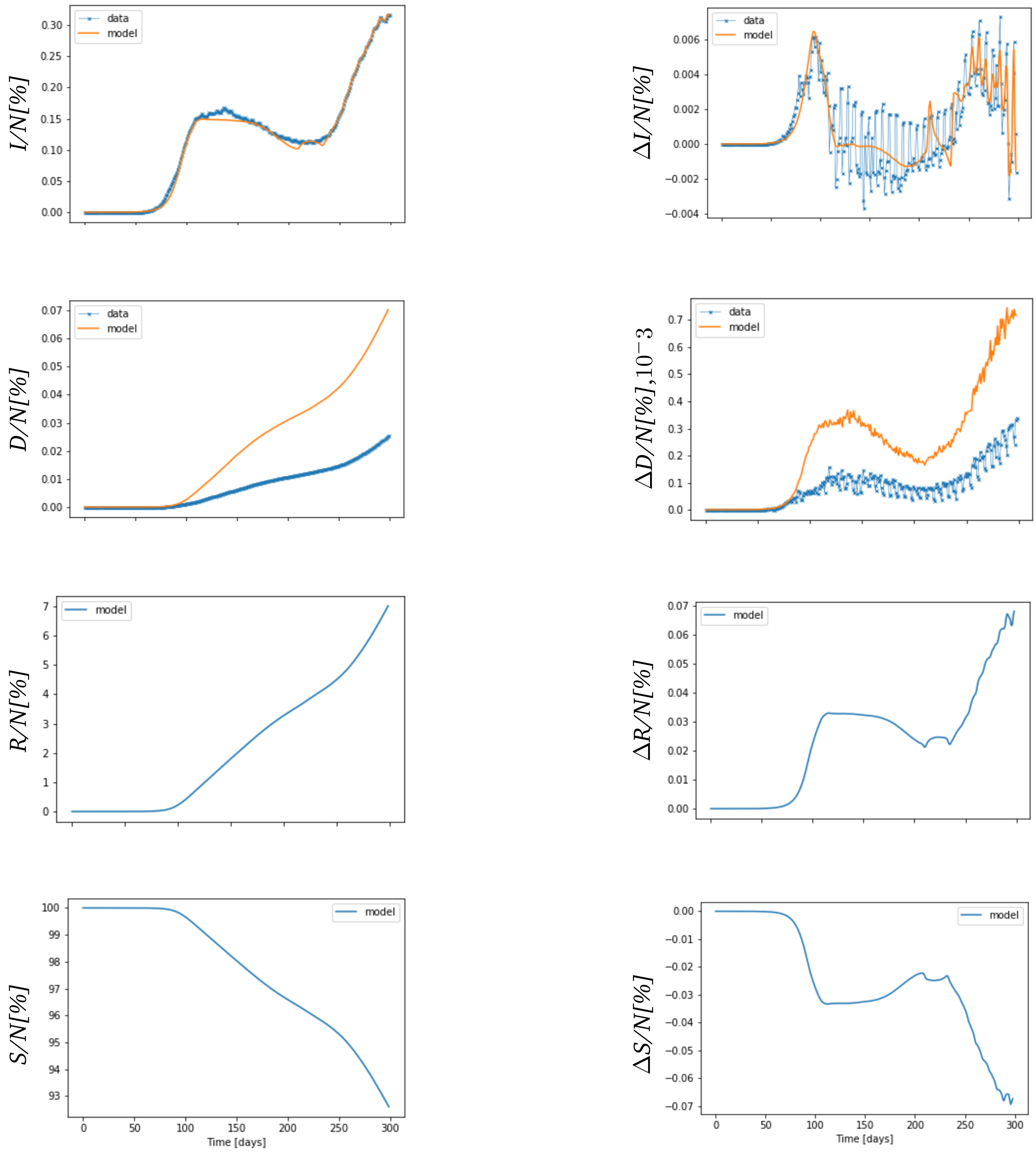


Figure 34: Canada (day 0 = 22nd January 2020): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

3.5 Russia



(a):Cummulative quantites

(b):Daily rates

Figure 35: Russia (day 0 = 31st January 2020): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

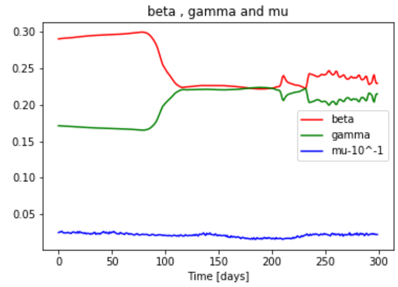
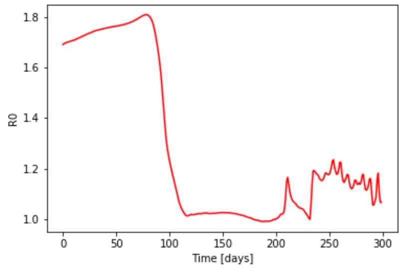


Figure 36: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 37: Russia (day 0 = 31st January 2020): SIRD parameters. Neural network trained with loss function.

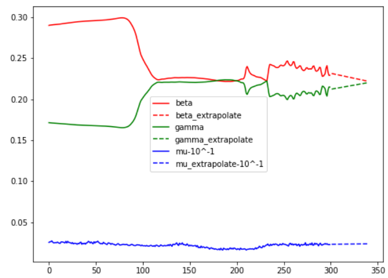


Figure 38: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

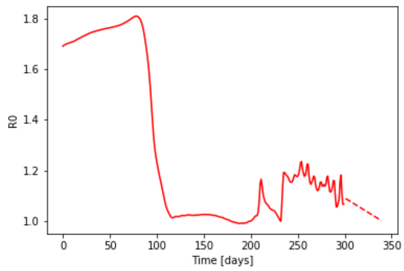
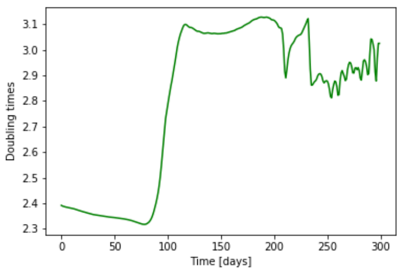
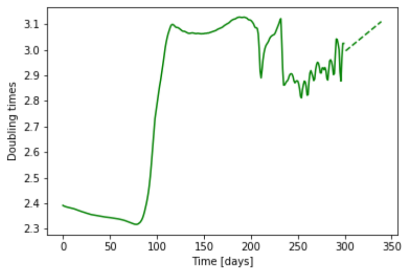


Figure 39: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 40: Russia (day 0 = 31st January 2020): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 41: Russia (day 0 = 31st January 2020): Doubling time with the log. The doubling time is calculated as t = log(2)/$\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

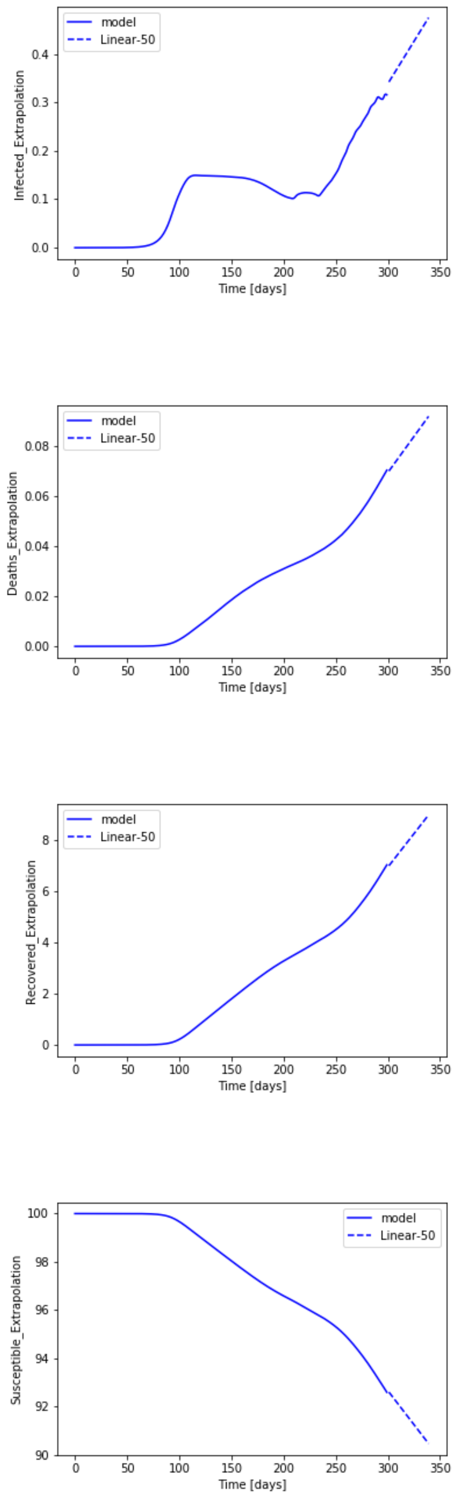
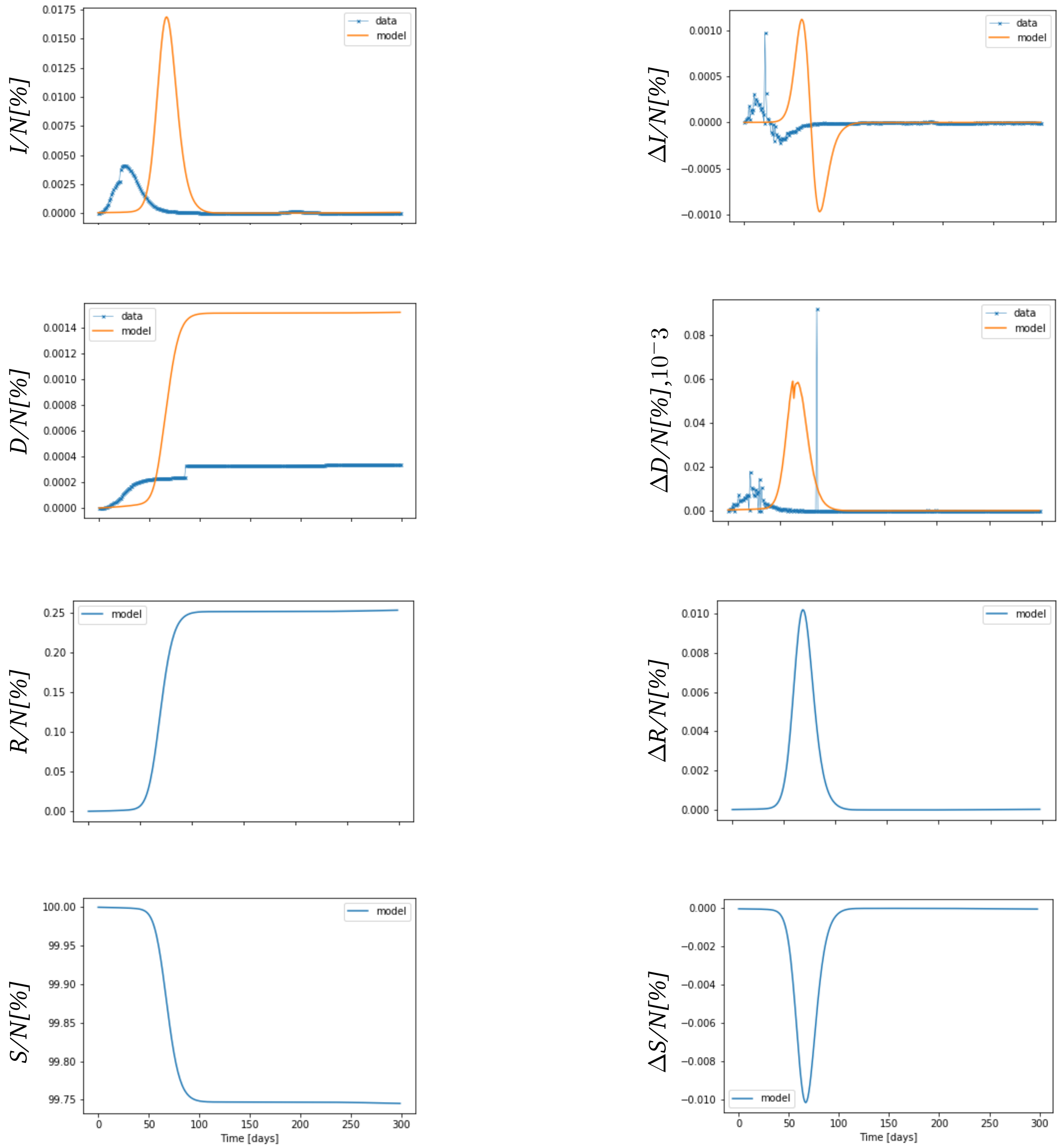


Figure 42: Russia (day 0 = 31st January 2020): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

3.6 China



(a):Cummulative quantites (b):Daily rates

Figure 43: China (December 2019): First and second rows: Validation of first-principles machine learning epidemic modelling. Third and fourth rows: Inference of recovered and susceptible.

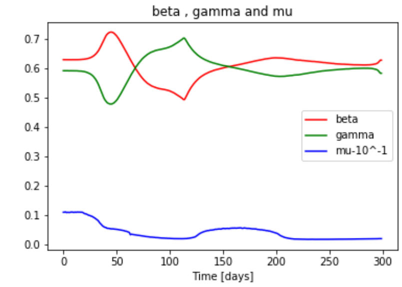
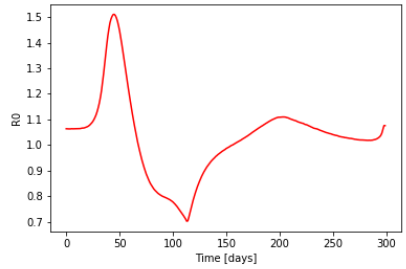


Figure 44: (a):Time-varying contact rate (β), recover rate (γ),and death rate (μ)..



(b) Basic reproduction number.

Figure 45: China (December 2019): SIRD parameters. Neural network trained with loss function.

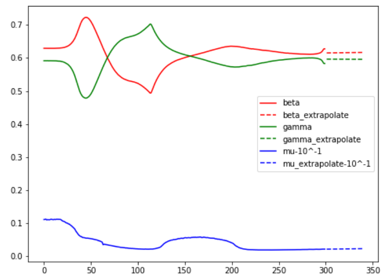


Figure 46: Extrapolated trends of the time-varying contact rate (β), recovery rate (γ), and death rate (μ) with average slope over the last fifty days(dotted lines).

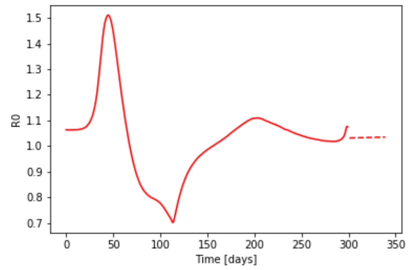
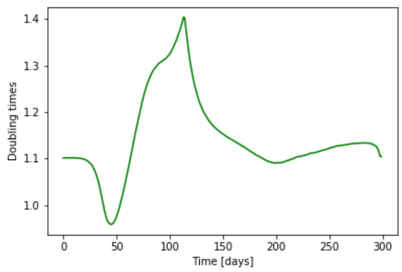
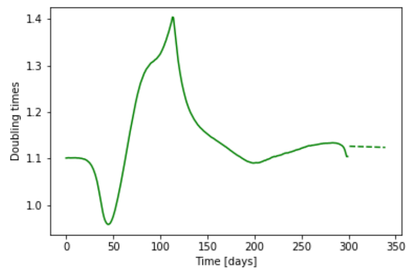


Figure 47: Extrapolated trend of the basic reproduction number with average slope over the last nine days(dotted lines)

Figure 48: China (December 2019): Extrapolated trends of the SIRD parameters.



(a) Doubling Time.



(b) Extrapolated Doubling Time.

Figure 49: China (December 2019): Doubling time with the log. The doubling time is calculated as t = log(2)/$\beta(t)$. (To take into account the time derivative of $\beta(t)$, semi-parametric methods can be used).

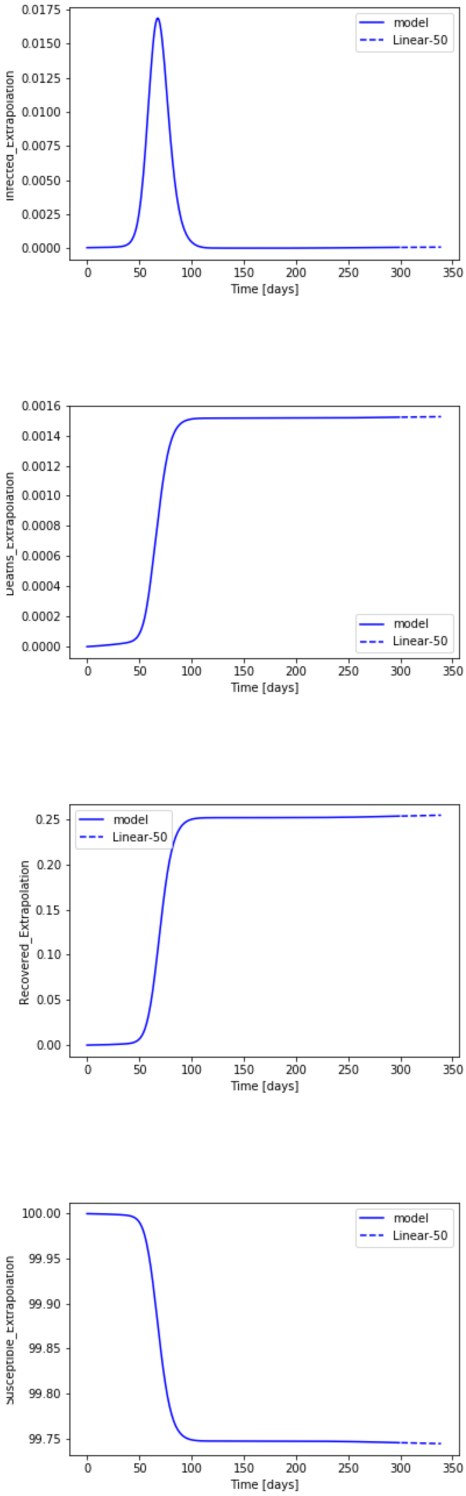


Figure 50: China (December 2019): From the top: Blue lines indicate the extrapolated trends of the percentage of infected, recovered, deaths, and susceptible. Estimates with average slope over the last fifty days (dotted lines).

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