

Modelling the Spread of COVID-19

Rada Böhning (12535303), Zaida Rivai (12124303)

I. INTRODUCTION

The respiratory coronavirus disease, in short COVID-19, caused by the SARS-CoV-2 virus, inducing a world-wide pandemic has lead to an aggravated loss of lives, congestion of national healthcare systems and complete shutdowns of entire countries, as there is thus far no vaccine available. To contain the spread of SARS-CoV-2, governments have adopted measures of restrictions ranging from social distancing advisements to national lockdowns.

This paper seeks to explore how different lockdown strategies affected case per capita in different countries. We will investigate the European countries Germany, Sweden and the Netherlands who had policy measures of varying restrictiveness in order to compare the effects of lockdown strategies on national case numbers and infection rates. In this research, we try to answer the question: *To what extent are restrictive lockdown measures effective in containing the spread of SARS-CoV-2?*

To answer this research question, a detailed review of related works will follow in Section II. Our hypothesis is that the more restrictive the lockdown measures are, the more successful a country will be in containing the SARS-CoV-2 spread, which will be seen in the number of infected individuals and the parameters of infections. The findings of this paper could provide an important insight in how to handle the future progression of the SARS-CoV-2 outbreak and ensure its containment and possibly aid the course of action for any future life-threatening disease that does not have a curative vaccine. The results of this paper can only be used as guidance and should not be used solely to base political decisions on.

II. THEORY

In order to compare containment strategies, the relative numbers of infections of a country before and after the introduction of new measures are to be compared. The increase of the infected population is dependent on the product of the number of infected and susceptible individuals [4][7]. Cooper et al. stress that early intervention is of great importance in the containment of a disease as this can prevent a positive feedback loop of new populations being added to the susceptible class,

which once infected can also introduce the disease to further previously unaffected groups. This spiral would result in an exponential increase of infections, whereas with lower numbers of infected individuals the number of infections increases slower [4]. An example of early and strong intervention in the COVID-19 pandemic can be seen in China where the peak was reached on the 16th of February 2020 after the Chinese government put the country in lockdown and manifested social distancing measures in place [4].

The same can be seen on an international scale, where the disease spread was slowed down by $\sim 80\%$ when a travel quarantine was put on the epicentre of the SARS-CoV-2 outbreak, Wuhan in the Hubei Region in China [3]. The travel ban delayed the national disease progression by 3 to 5 days. It was found that, although, the travel restrictions alone only had a moderate effect on the epidemic trajectory, the combination with significant restrictive measures within the Chinese mainland severely slowed down the spread of the virus [3].

A model that was developed to analyse, predict and visualise realistic simulations of epidemiological processes is the Global Epidemic And Mobility model, GLEAM [12]. It is used to model real-world data on global populations, on their mobility and individual based stochastic mathematical model of the infection dynamics [12]. GLEAM can be used to find interaction hubs within the population, and therefore, help adapt restriction measures to contain transmissions, as one way to minimise the spread of the disease is to reduce the number of infectious individuals, so that they do not transmit the pathogens within the population [11]. Further, new introductions of infectious individuals is essential to decrease the number of cases [9]. The rate of infection, β , depends on the probability that an infectious individual is in proximity of susceptible individuals and how many of the susceptible are infected per infected individual [8]. It is further depended on the biological characteristics of the virus such as its contagiousness, and furthermore, the political interventions that are being taken to contain the virus [8]. Finally, a reduction of susceptible through vaccination is a possible strategy [1]. However, for COVID-19, there is no curative vaccine in place at this time, therefore, the most effective way to contain the spread is via restrictive policies: Lockdown

policies are the first recommendation in order to lower the rate of infection [8].

III. METHODS

1) *Code*: The full repository can be found under the following link: <https://github.com/ga48nuq/intro-project-sir.git>. Instructions on how to access and run the code are given in the `README.md` file.

2) *The data*: The data used in this paper is from the European Centre for Disease Prevention and Control that provides for over 50 countries the daily cases for the number of infectious and death individuals since December 31st [5].

3) *Lockdown restrictions*: For the lockdown restrictions, data from the CoronaNet Research Project will be used. CoronaNet is a database that updates the global response to COVID-19 in real time [2]. We will analyse the response from several countries to the pandemic and the correlation between restrictiveness of lockdown policies and effectiveness of containment of the disease.

4) *Susceptible-Infected-Removed (SIR) model*: The following set of first order differential equations (ODEs) make up the basic SIR model:

$$\frac{dS}{dt} = -\beta SI \quad (1)$$

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

$$\frac{dR}{dt} = \gamma I. \quad (3)$$

The parameter of infection are described as β for the rate of infection and γ for the rate of recovery. The model can be described as $S + I + R = N$, where N stands for the population size [1][11][8]. The basic reproduction rate is written as $R_0 = \frac{\beta}{\gamma}$ [6].

5) *Python packages*: The python packages used in this paper are from scipy [10], to solve the ODEs from the SIR equations. To fit the real data and find the solutions for β and γ , we used the ODEs, Model and Data package from scipy. These packages solve the model using Orthogonal Distance Regression.

6) *Parameters*: We split up the timescale axis (x-axis) into two parts; the first 150 days that include, for all three countries, the first peak and the last 150 days. This is because the fluctuations could not be explained by the simple SIR model, hence splitting the x-axis and modelling the SIR model using different guesses for β and γ resulted in a smoothly fitted curve. According to literature, we chose β and γ to be approximately around 1 and 0.8 respectively [8] for the first 150 days for all three countries. For the last 150 days, β and γ were first

set to 0.9 and 0.8 for Germany and Sweden and to 0.9 and 0.5 for the Netherlands respectively.

IV. RESULTS

A. Three cases: The Netherlands, Sweden and Germany

Figure 1 shows the proportions of the number of infectious individuals for three countries: Germany, Sweden and The Netherlands. The figure shows the first peak for Germany (orange) and the Netherlands (blue) are found around day 100 and take about 50 and 40 days respectively. The first peak for Sweden (green) shows a delay compared to these countries, since the peak between day 150 and 200 was shown. There is no second peak found for Sweden, whereas a second peak for the Netherlands and Germany an increase in infectious individuals is found after day ~ 250 . Since, for both countries, the numbers of infectious individuals are still increasing, there is no second peak found yet. From this figure we can also conclude that, the proportion of infectious individuals for the Netherlands is much higher than for Germany or Sweden.

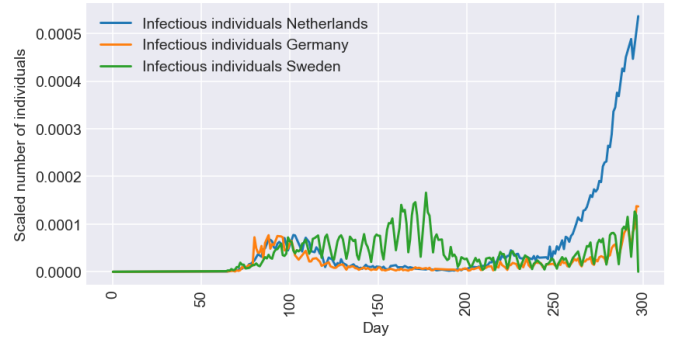
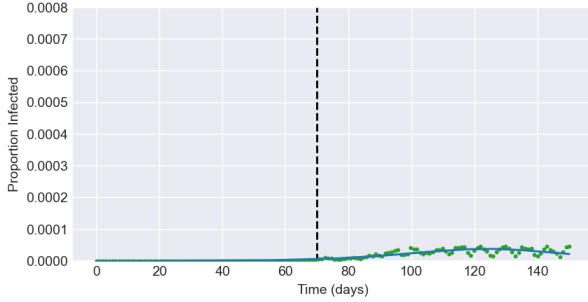


Fig. 1: Overview of infectious cases for the Netherlands, Germany and Sweden per day starting from 31st of December 2019 (Day 0) to 20th of October 2020.

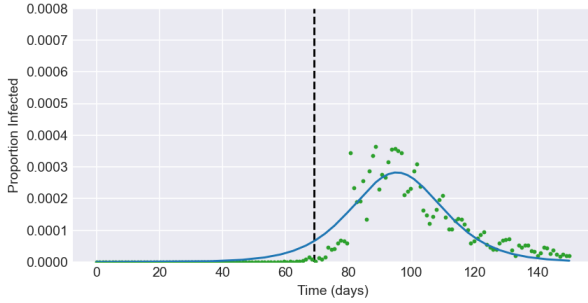
B. Lockdown Measures

Different countries decided to put different restrictiveness of lockdown measures into place at different time points. Figure 2 and 3 showed the dynamics of the number of infectious individuals, the proportions of infectious individuals and the time-point at which lockdown measures were taken into action. Only The Netherlands had a second lockdown in the second ~ 150 days at day 288. Shown is that the SIR model fits the real data, shown by green dots, well. It is also important to note that the restrictions had different levelled compliance such as Sweden only implementing a recommendation for social distancing but left national business open as usual, whereas Germany and the Netherlands shut down

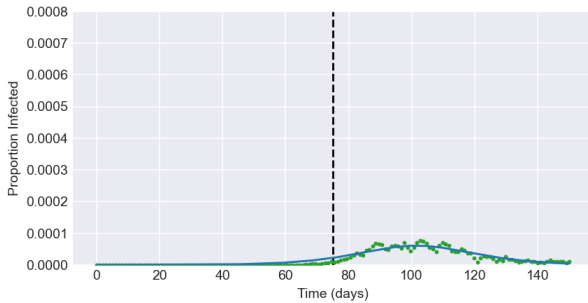
many industries [2]. Even between Germany and the Netherlands the rules were followed to different degrees and enforced or fined in different ways [2]. We expect that Germany manages to flatten the exponential growth the most, as the country had the strongest lockdown measures. The different lockdown measures are likely to have different effects on the curves. In Figure 4, we have therefore modelled predictions of the curves without lockdown measures to compare the effects of the policies.



(a) Sweden the first 150 days: β is 6.8 per day, γ is $\frac{1}{6.7}$ days.



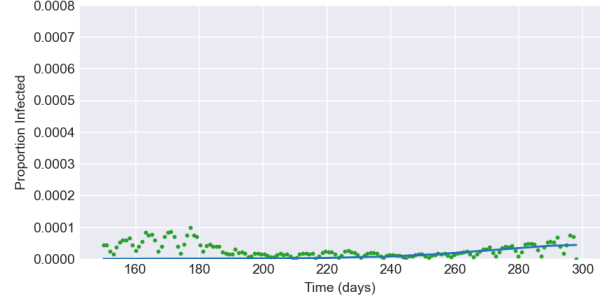
(b) Germany the first 150 days: β is 4.4 per day, γ is $\frac{1}{4.3}$ days.



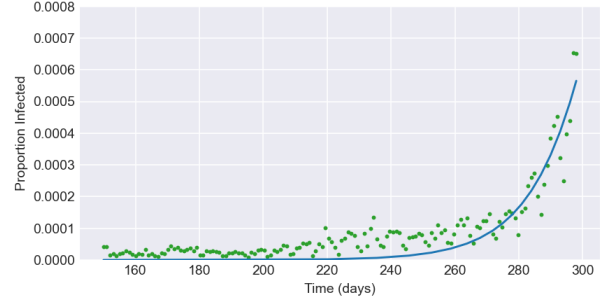
(c) The Netherlands the first 150 days: β is 7.5 per day, γ is $\frac{1}{7.4}$ days.

Fig. 2: Dynamics for (a-b) Sweden, (c-d) Germany and (e-f) The Netherlands. Starting day, day 0, is December 31st 2019 and the ending day is May 29th 2020. Black dotted vertical line indicate the date of the lockdown.

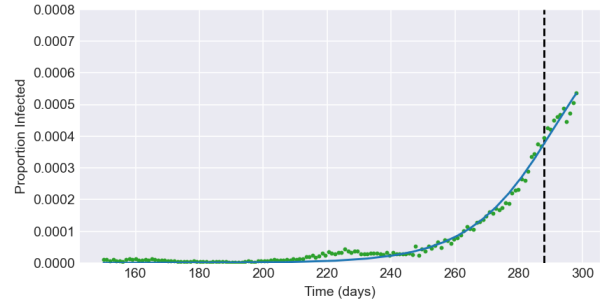
Different γ and β values that were calculated are shown in table I. Shown is that for all countries, higher β and γ values were found in the first 150 days compared



(a) Sweden the last 150 days: β is 5.3 per day, γ is $\frac{1}{5.3}$ days.



(b) Germany the last 150 days: β is 1.01 per day, γ is $\frac{1}{0.94}$ days.



(c) The Netherlands the last 150 days: β is 1.9 per day, γ is $\frac{1}{1.8}$ days.

Fig. 3: Dynamics for (a-b) Sweden, (c-d) Germany and (e-f) The Netherlands. Starting day, day 150, is May 30th 2020 and the ending day is October 20th 2020. Black dotted vertical line indicate the date of the lockdown.

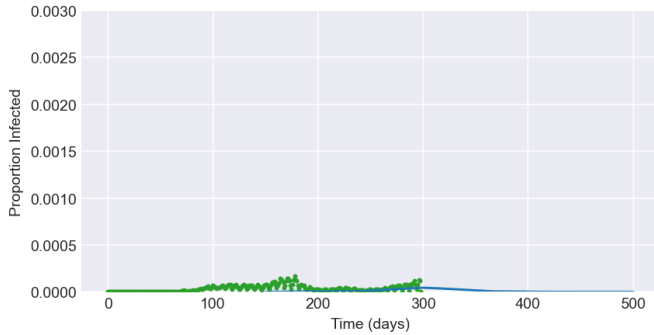
to the \sim last 150 days. This implies that the transmission rate and recovery rate changes over time and is lower after the first peak.

Timescale	Sweden [β, γ]	Germany [β, γ]	Netherlands [β, γ]
First 150 days	[6.8, 6.7]	[4.4, 4.3]	[7.5, 7.4]
Last \sim 150 days	[5.3, 5.3]	[1.01, 0.94]	[1.9, 1.8]

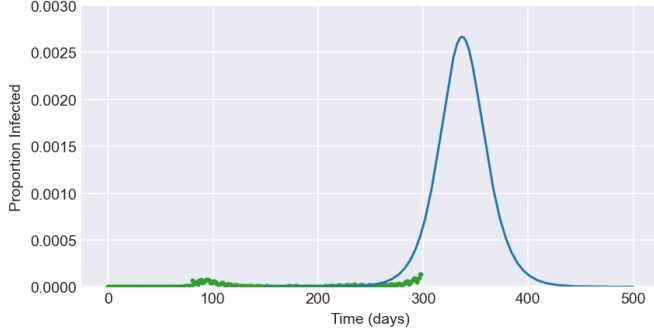
TABLE I: β and γ values predicted by the SIR model, for the first 150 days and the last \sim 150 days.

1) *Predictions of the proportions of infectious individuals:* Until now, we only have recent data until the 20th of October. However, it would be sufficient to predict or determine the amount of infectious individuals based on the previous results. Figure 4 shows the predictions for

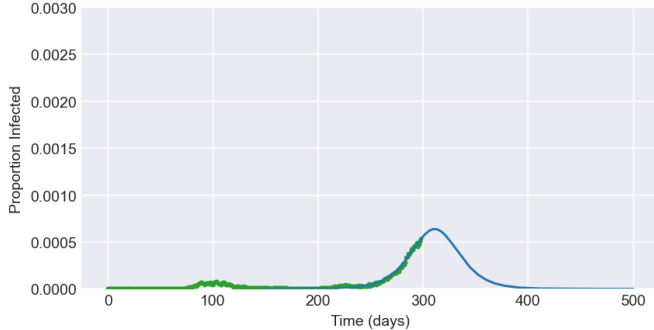
the number of infectious individuals starting from 29th of May until, 500 days later, 29th of April. Shown is that the SIR model fits the data pretty well, shown in green, and predicts a peak for The Netherlands and Germany. For Sweden, the dynamics are almost a flat line. The second peak for The Netherlands and Germany, will in total last ~ 100 Days, and 120 days respectively.



(a) Dynamics and proportions of the number of individuals in Sweden. β is set to 5.3 per day, γ is set to 1/5.3 days.



(b) Dynamics and proportions of the number of individuals in Germany. β is set to 1.01 per day, γ is set to 1/0.94 days.



(c) Dynamics and proportions of the number of individuals in The Netherlands. β is set to 1.9 per day, γ is set to 1/1.8 days.

Fig. 4: Proportions of the number of infectious individuals shown with green dots for (a) Sweden, (b) Germany and (c) The Netherlands. Starting day (day 0), 29th of May 2020. Solid blue line shows the dynamics of the number of infectious individuals predicted by the SIR model.

V. DISCUSSION AND CONCLUSION

According to the results, the β and γ values changed over time. Around the first peak these values were higher compared to the β and γ values of the second peak. According to the plotted proportions, it seems unreliable that the transmission rate and recovery rate, are lower for the Netherlands compared to the first peak, since the second peak is of much higher order than the first peak. This might be due to the social distancing measures and a lower R_0 , should one infectious individual infect less susceptible individuals as elaborated in Section II.

The predictions have shown that for both the Netherlands and Germany, the number of infectious individuals will increase for a while, but decrease after ~ 100 days. Compared to the first peak of Germany that lasted ~ 80 days and ~ 50 days for the Netherlands, this might be a reliable result, since the increase in number of infectious individuals is already higher and longer for both countries.

What could have been interesting to model is develop other extensions of the SIR such as the SUQR (susceptible-unquarantined-quarantined-removed) or the SEIR (susceptible-exposed-infectious-removed) model and see how the dynamics for the number of infectious individuals develop over time, with seasonality additionally incorporated for example and to analyse further details of the disease progression. Further research could look into the possibilities of only temporal immunity after infection and most removed individuals entering the susceptible class again after time as immunity research for SARS-CoV-2 is still outstanding and most models are based on the assumption of long-term immunity.

REFERENCES

- [1] Anas Abou-Ismael. Compartmental models of the COVID-19 pandemic for physicians and physician-scientists. 2(7):852–858.
- [2] Cindy Cheng, Joan Barceló, Allison Hartnett, Robert Kubinec, and Luca Messerschmidt. Covid-19 government response event dataset (coronanet v1.0). <https://www.coronanet-project.org>. 2020.
- [3] Matteo Chinazzi, Jessica T. Davis, Marco Ajelli, Corrado Gioannini, Maria Litvinova, Stefano Merler, Ana Pastore y Piontti, Kunpeng Mu, Luca Rossi, Kaiyuan Sun, Cécile Viboud, Xinyue Xiong, Hongjie Yu, M. Elizabeth Halloran, Ira M. Longini, and Alessandro Vespignani. The effect of travel restrictions on the spread of the 2019 novel coronavirus (covid-19) outbreak. *Science*, 368(6489):395–400, 2020.

- [4] Ian Cooper, Argha Mondal, and Chris G Antonopoulos. A SIR model assumption for the spread of COVID-19 in different communities. 139:110057–110057.
- [5] European Centre for Disease Prevention and Control. Download the daily number of new reported cases of COVID-19 by country worldwide. <https://opendata.ecdc.europa.eu/covid19/casedistribution/>, 2020. [Online; accessed 24-October-2020].
- [6] M.J. Keeling and P. Rohani. *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, 2007.
- [7] E. et al. Pardoux. Stochastic epidemic models with inference. Springer, 2019.
- [8] Ettore Rocchi, Sara Peluso, Davide Sisti, and Margherita Carletti. A possible scenario for the covid-19 epidemic, based on the sir model. 2(5):501–503.
- [9] K. Sasaki. Covid-19 dynamics with sir model. <https://www.lewuathe.com/covid-19-dynamics-with-sir-model.html>, 2020.
- [10] Scipy. Scipy. <https://www.scipy.org/>, 2020. [Online; accessed 24-October-2020].
- [11] et al. Smith D, Moore L. The sir model for spread of disease - the differential equation model. Convergence <https://www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model>, 2004.
- [12] Alessandro Vespignani and Vittoria Colizza. Global epidemic and mobility model, gleamviz. <http://www.gleamviz.org>, 2020.