

A model for the spread of SARS-CoV-2 between European states.

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1 Introduction

As of the 11th of March Dr. Tedros Adhanom Ghebreyesus, WHO's Director-General, announced that COVID-19 can be characterized as a pandemic.[6] Following his announcement the number of reported cases rose dramatically. In the European region alone it rose from over 20000 on the 12th of March to over 75000 cases just a week later.[9]. This outbreak has been unparalleled in the last decades and is already being compared to the 1918-19 H1N1 influenza pandemic, which according to reassessments in recent studies resulted in a total of 20 million deaths. [7]. In this report, we present an abstract epidemiological simulation of the spread of SARS-CoV-2 in Europe using a graph theoretical approach. It is based on a refined SIR model allowing for the solution in a network of latest intra-European travel data.

2 Model

The SIR model is a widely used system of differential equations which governs the epidemic spread of a disease, and has been adopted as the basic model for the spread of SARS-CoV-2 [5]. They put into relation three quantities within a population, namely: \mathbf{S} , the number of people susceptible to the disease; \mathbf{I} , the number of people infected by a disease; and \mathbf{R} , the number of people that have gone through the entire progression of the disease, i.e. either have recovered or died. We note that $\mathbf{S} + \mathbf{I} + \mathbf{R} = N$ is constant (representing, roughly, the total population). Furthermore, there exist constants R_0 , the expected number of persons an infectious person will infect supposing that no person in the population is immune against the pathogen, and T_r , the expected length of the disease progression. We can then write $\gamma = T_c^{-1}$ for the factor of recovery/death and $\beta = R_0/T_c$ for the factor of contagion (the average number of infected peo-

ple per time) and thus obtain the equations:

$$\begin{aligned}\frac{d\mathbf{S}}{dt} &= -\beta \frac{\mathbf{S}\mathbf{I}}{N} \\ \frac{d\mathbf{I}}{dt} &= \beta \frac{\mathbf{S}\mathbf{I}}{N} - \gamma\mathbf{I} \\ \frac{d\mathbf{R}}{dt} &= \gamma\mathbf{I}\end{aligned}$$

These are a surprisingly accurate in representing the spread of a disease within a secluded system. However, in the modern world states are by no means a secluded system, and the spread of SARS-CoV-2 is greatly influenced by the large-scale exchange of people between states. To account for this, we transferred this model from the frame of an isolated system to a Network of systems which influence each other.

Formally, let G be a weighted Graph, the nodes of which correspond states in a region; and the edges of which carry the value of the expected number of travellers between two states in one day. To maintain the constant population in each state, we assume that the number of people travelling from one state into another is equal to the number of those travelling in an opposite direction; we think of "exchanges" in population at a given day rather than of people commuting. Denoting by A the $n \times n$ -adjacency matrix of G , we hence set $A_{ij} = A_{ji}$ to be the mean of the expected numbers of people travelling from state i to state j and of those travelling from state j to state i . We assume further that the ratio of each group ($\mathbf{S}, \mathbf{I}, \mathbf{R}$) amongst travellers is representative of the population. Writing $\mathbf{I}_i, \mathbf{S}_i, \mathbf{R}_i$ and N_i for the number of infected, susceptible, recovered/dead and total people within a state i , we can conclude that on a given day, state i infects state j with $A_{ij} \frac{\mathbf{I}_i}{N_i}$ people, and a similar transfer happens of the groups \mathbf{S} and \mathbf{I} . The revised

equations then read:

$$\begin{aligned}\frac{d\mathbf{S}_i}{dt} &= -\beta_i \frac{\mathbf{S}\mathbf{I}}{N} + \sum_{j=1}^n A_{ij} \left(\frac{\mathbf{S}_j}{N_j} - \frac{\mathbf{S}_i}{N_i} \right) \\ \frac{d\mathbf{I}_i}{dt} &= \beta_i \frac{\mathbf{S}\mathbf{I}}{N} - \gamma_i \mathbf{I}_i + \sum_{j=1}^n A_{ij} \left(\frac{\mathbf{I}_j}{N_j} - \frac{\mathbf{I}_i}{N_i} \right) \\ \frac{d\mathbf{R}_i}{dt} &= \gamma_i \mathbf{I}_i + \sum_{j=1}^n A_{ij} \left(\frac{\mathbf{R}_j}{N_j} - \frac{\mathbf{R}_i}{N_i} \right)\end{aligned}$$

where β_i and γ_i are the constants of contagion and inverse disease length in state i . It is important here that these are neither global nor fixed in time - β describes how well the disease can spread, a factor that is influenced by social dynamic in these state and can be influenced by social distancing policies and hygiene; γ describes how long the disease lasts, which in turn can be influenced by the use of medication. In general, the higher $R = \beta\gamma$, the faster the disease spreads. SARS-CoV-2 has an initial R value of around $R_0 = 2.4$ [5] and the introduction of stringent policies can lower this factor. If R falls beneath 1, the spread ceases to be exponential, and hence, an epidemic.

We can evaluate this model for any quantities X using the simple time-marching method

$$X(t + \Delta t) = X(t) + \Delta t \cdot \frac{dX}{dt}$$

where we choose Δt to be one day. As we proceed in time, we can alter the values of β_i and γ_i within a state, corresponding to the introduction of social distancing measures, as well as the values of A_{ij} , which we can set to zero if states i and j shut their border. This completes the description of the model. An implementation can be found at <https://github.com/Julek99/BridgesOrWalls>.

3 Simulation

We created an interactive simulation of the model which allows users to run the simulation over time, and visualises results using a map of Europe (coloured by infections per capita) as well as a plot showing this value over time. As the simulation runs, the user can modify a "social distancing" factor F_i for any state i , which represents an amount of social distancing introduced in said state. For simplicity, F_i is taken as a percentage value between 0 and 100, which translates to $R_0 = \frac{(2.4-1)F_i}{100} + 1$ for purposes of the model. Moreover, the user can close or open the borders of each state at any point, which translates to altering the values in A . The simulation is available at <https://wallsbridges.appspot.com>.

The Data: For a realistic representation of the spread of the virus, accurate travel data is key. Fortunately

Regulation 692/2011 of the European Parliament and of the Council concerning European statistics on tourism provides for harmonised data collected by the EU-27 member states, Norway and Switzerland.[1] The data used for the simulation are from 2017. Recognising the important role of the UK in European travel its share is based on data from 2013, since there is no recent data available. In 2017 73.3% of the 1255 million trips made by EU-28 residents were domestic. Of the 26.7% of all outbound trips 20.6% were made to another EU Member State. [3] Therefore, trips within the EU-28 Member States account for 89.2% of all trips made. Considering Switzerland's 8% and Norway's 6% share of outbound trips made by EU-28 residents outside the EU-28, [3] we come to the conclusion that 90.0% of all trips made by EU-28 residents had a destination within the aforementioned countries: the EU-27 member states, Norway, Switzerland and the UK. This confirms the assumption that focusing on the travel between this 30 states and neglecting trips to other parts of the world, satisfies the need for accurate data in order to obtain realistic dynamics of the spread throughout Europe.

In order to reduce the complexity of calculations only the travel between the top 5 destinations of each countries were accounted for in the adjacency matrix. This is justified by the fact that 43.8% up to 78.7% of all outbound travel has one of the top 5 countries as destination with an of average 58.1%.

For the matrix to be symmetric, the average number of people traveling between two countries was taken, if both countries showed up in each other Top 5 respectively, or the value was assumed to be the same, as e.g Germany holds the largest share of outbound trips from Denmark, but Denmark does not show up in the Top 5 of Germany. In addition, it was assumed that travel is constant throughout the year and seasonal changes were neglected.

The knowledge of the starting point of an epidemic is crucial for a precise simulation. We chose the 12th of March 2020 and the number of reported cases for each country to the European Center for Disease Prevention and Control (ECDC) as the first infected Europeans as starting point for the spread of the pandemic. [2]

4 Results

The following is an evaluation of the model in a set of figures. In the unlikely event of no social policy and no change to travel habits of the European residents, we would expect a maximum of new cases per day after 45 to 60 days across all of Europe with a maximum of almost 20000 new infections in a single day in the most populous state, Germany, as seen in Figure 1. In this scenario we expect where the basic reproduction number stays constant at $R_0 = 2.4$, the new cases per capita rise up to about 0.23% of the total population, 2, and the ac-

cumulated infected per capita curves follow a generalized logistic growth model 3. Focusing on the UK specifically: It reaches it's maximum of newly infected per capita 61 days after the start of the simulation around the 15th of May 2020 in the event of no social policy. As the expected length of the disease is estimated to be 5 days, we can assume that following our simulation, the maximum amount of deaths per day would be at the end of May 2020. This in agreement with Neil M Ferguson [5], which found a date in early June 2020.

When measures in social policy are taken the aforementioned general course of the epidemic can be altered significantly, as our model shows. The effectiveness of two different policies, closing borders and introducing mitigation or suppression measures aimed at reducing R_0 can be evaluated with our model. The latter measures include, but are not limited to: home isolation of suspect cases and of those living in the same household, social distancing, ban on public events and closure of public buildings. If we introduce beginning with the 14th of May, the start of the simulation, mitigation and suppression measures in France and Italy, thereby reducing effectively the basic reproduction number to $R_0 = 1.4$ and close the borders of Austria and Bulgaria, we arrive at the situation presented in Figure 4. On the 14th of March, Austria had already reported cases of SARS-COV-2, whereas Bulgaria had not yet reported any cases. Not surprisingly the cases in Bulgaria stayed at zero. On the other hand the course of the epidemic in Austria followed a similar time evolution as the one in Germany and the UK, to borders, who we suppose do not take any sort of measures. Therefore, we conclude that closing borders is not an effective measure, when fighting an epidemic, as it may only decrease the amount of imported cases, but does not change the course within the country. This is supported by the findings of Matteo Chinazzi [4], who using a global metapopulation disease transmission model came to the conclusion that the the travel ban from Wuhan on 23 January 2020 “delayed the overall epidemic progression by only 3 to 5 days in Mainland

China”, as many infected had already traveled to other places within China. [4]

This evidence brings us to the conclusion, that using a graph theoretical approach to the SIR Model can be a valuable model for predicting the SARS-CoV-2 pandemic. In addition, measures mitigating or even suppressing the further course of the pandemic are an effective tool in combating the speed of the spread, which can reduce the ICU-demand drastically and thus save lives. Nevertheless, if the measures taken are not able to suppress the pandemic (reduce R_0 to a value below 1) in the end, the same amount of people get infected, but spread over a bigger time interval. This is not accounted for by our model.

5 Discussion

Although 90.0% of all trips made by EU-28 residents had a destination within the EU-27 member states, Norway, Switzerland and the UK, it should be mentioned that certain countries at EU borders have a notable share of their outbound trips going to none of the 30 countries. Such countries include Croatia, where 16.9% of outbound trips have Bosnia/Herzegovina as destination and Greece , where 16.1% of outbound trips go to Albania. This makes Bosnia/Herzegovina and Albania respectively the number one destination of residents from Croatia and Greece. Other noteworthy examples are Bulgaria with 10.1% to Turkey and 5.8% to Serbia, and Estonia with 9.5% to Russia. In these countries the actual dynamics might not be well represented by this model, considering that Croatia, Greece and Bulgaria are amidst the countries, who face the most dramatic fluctuations of number of trips over the year.

Also, it has to be mentioned that closing borders might aid indirectly in curbing the spread of the pandemic by motivating the population to take additional measures of social distancing, just as media reporting has been found to mitigate the spread of COVID-19 in the early phase of the outbreak by Wei-ke Zhou¹ and Aili Wang. [8]

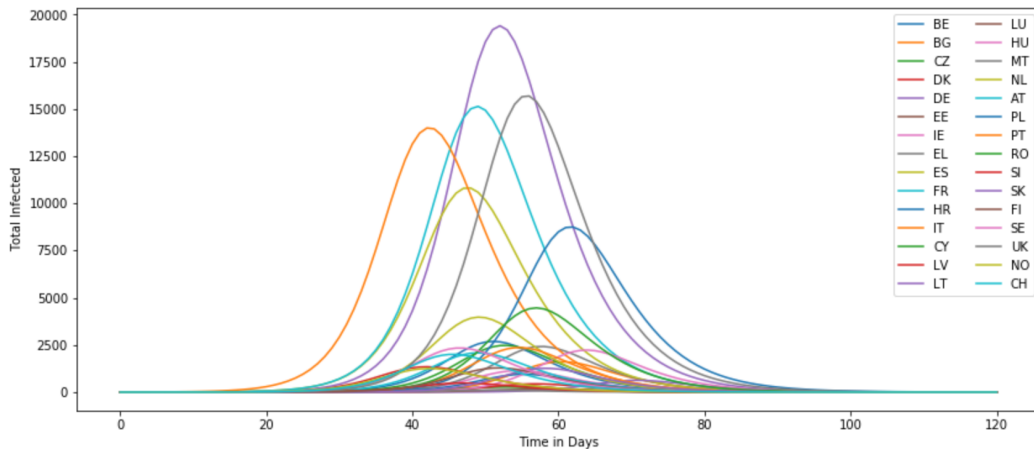


Figure 1: New cases per day in an unmitigated epidemic for the thirty European countries.

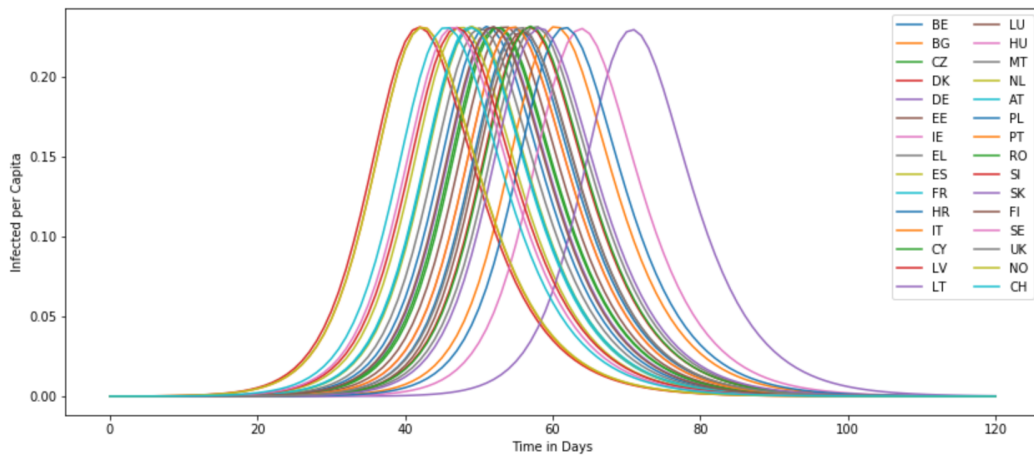


Figure 2: The accumulated infected per capita for the the European contries in an unmitigated epidemic. It rises up to 0.89 infected per capita.

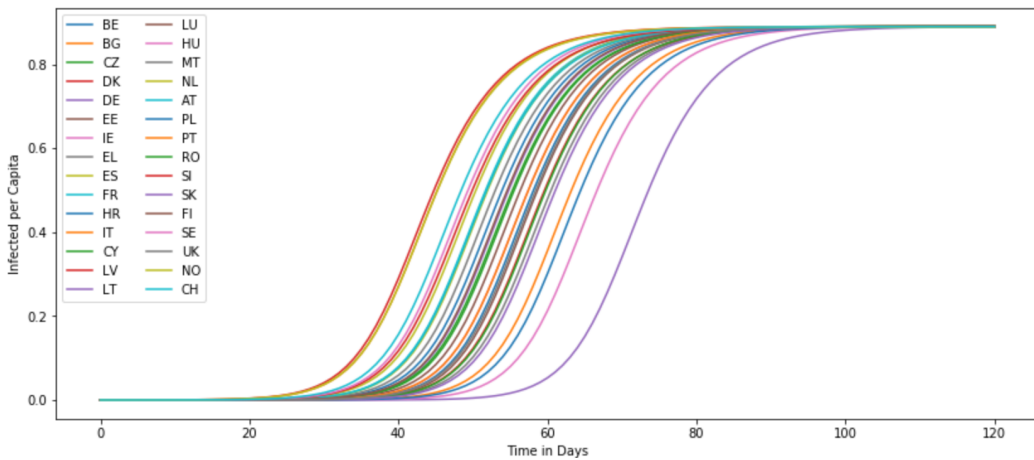


Figure 3: New cases per capita per day for the European countries in an unmitigated epidemic.

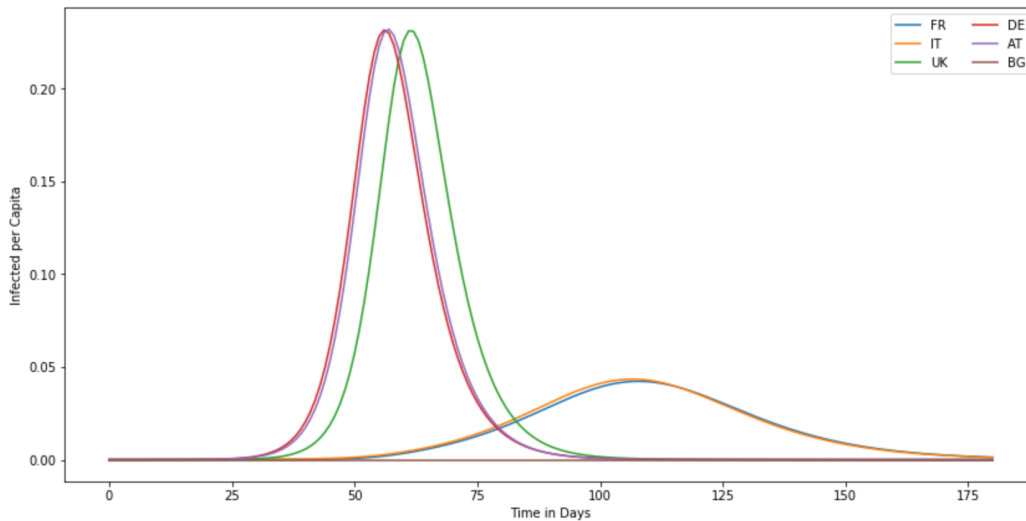


Figure 4: New cases per capita per day for the European countries in an unmitigated epidemic.

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