

Developing a Dynamic Network-Based Model for COVID-19

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We describe a dynamic network-based approach for modeling the spread of COVID-19. Building onto existing models, we introduce governmental measures in the form of quarantine in addition to data for the virus such as reinfection, death and vaccination rate. We found that the use of realistic parameters in our model resulted in a curve following a similar trend to that of real UK data for the virus.

Recently there has been a significant uprise in epidemiological modelling, as a natural response to COVID-19. Models of varying complexity and predictive power have been proposed to aid governmental decisions about every day life [1]. However, the reality of such models is that they are inherently imperfect, as they are sensitive to the data they employ and the assumptions they are built on [2].

A quintessential approach to epidemiological modelling are the so called compartmental models, which usually start by considering only three categories: Susceptible, Infected and Recovered (SIR) [3]. With this simple method modellers are able to explain the fundamental behaviour of a disease (e.g. [4]), yet fail to capture the response of society as a whole. Consequently, many approaches extend the SIR model in some way, for example with different compartments [5], statistical fitting to the observed data [6], or introducing the effect of geography [7]. However, even complicated compartmental models [4, 6] may fail to fit the data perfectly, and one possible explanation lies in the assumption that models are fixed over time. As an example, one may consider the number of confirmed cases in the UK during the early days of the pandemic. There is a steady rise in the number of new cases per day, which then leveled off slightly after 24 March 2020; the date when the first lockdown was announced. As a result, any epidemiological model calibrated to fit the circumstances and the data before the 24th of March needed to be readjusted to cater for the new rules.

Our goal with this study is to propose a sim-

ple dynamic model which alters its constraints based on the restrictions and policies present at a specific time. This time dependent model is better at picking up changes in the modelling environment, and thus can react to the changing rules in society.

Considering the many variations, extensions and inherent flaws regarding population homogeneity of compartmental models, we have decided to opt for a network-based approach. The core of our work was based on [8]. Throughout the analysis we have focused on the UK, which was picked arbitrarily.

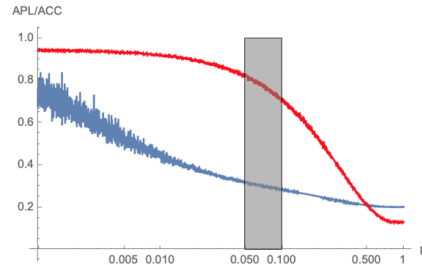


FIG. 1. Small-world Properties of Watts-Strogatz graphs with Varying p . The Average Path Length (APL - blue) is required to be low, while the Average Clustering Coefficient (ACC - red) is high. The highlighted gray area shows the recommended p values for small-world networks.

To model the spread of an epidemic through a population, we opted to use Watts-Strogatz random graphs [9], which posses the so called small-world property, given that the probability of rewiring p , is chosen correctly. Based on the experiments in [9] we concluded that a small

value for p is required, and in [8] p was taken to be 0.1. Based on these and on our own experiments 1 we have chosen p to be equal to 0.075, which was then used to generate communities for our model (e.g. Figure 2 and Figure 3).

We introduced simple demography to our model by assigning each node an age based on the age distribution measured in the UK [10]. To model the spread of the disease we assumed random recovery time ($r \sim \mathcal{N}(\mu(t), 3)$, where $\mu(t_0) = 10$) for each infected person and randomly selected a portion of our population to be infected (*initialInfected*). To give the virus a chance to spread, each person meets with n of their friends daily, where $n \sim \exp(\lambda(t))$ (exponential distribution) with $\lambda(t_0) = 1.2$.

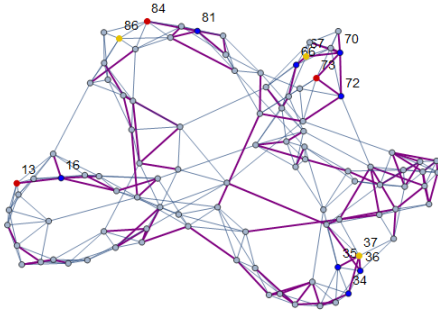


FIG. 2. Network representing the meetings between agents. Susceptible nodes are shown in blue and infected are the red (symptomatic) and yellow (asymptomatic) nodes. The meetings in the graph are shown by purple lines.

Diverging from our original source [8] even more we have introduced a chance of infection. At first, we considered to use an infection rate of 60% (upon meetings with infectious), based on the estimations derived from a set of studies done on the transmission of COVID-19 [11, 12]. When incorporating this into our model, however, we have tested a few values for the chance of transmission, including 60%, but found it too high. Instead, we have set this to 44% as the model proved to be more reliable and realistic. We have also set 84% of the infected to show symptoms based on [13], and the rest to

be asymptomatic.

As our start date for our simulation we have chosen 01/02/2020, since our evaluation dataset (Epidemic Data for Novel Coronavirus COVID-19 [14], reporting the number of confirmed cases and deaths per day) contains data starting from February. For the restrictions we used the dataset [15], which contained information about the governmental restrictions and the date they were issued on. However, as there was no data available on the duration of these measures, we have decided to enforce them only for 30 days. We have also assumed that each restriction in the same category affects the corresponding parameters by the same amount (*meetingMultiplier* = 1.2, *infectionMultiplier* = 0.8, *recoveryMultiplier* = 0.8). Additionally, we have made the following changes to our model:

Reinfection: Although there seemed to be no consensus whether reinfection with the coronavirus is possible [16] we decided to add a small chance for recovered people to be susceptible again. We choose the reinfection rate to be 0.001.

Death: The death rate of COVID-19 varies across ages, and thus we used the age distribution to distinguish the death rate between different age groups. The values for these were taken from [17], and normalised by the average recovery time.

Vaccination: Looking at the data provided by the UK Government [18], the average amount of daily 1st doses is around 300 000. If we take into account the 2nd doses, this average increases to 310 000, which accounts for 0.45% of the population. We also decided to prioritise vaccinating people of age.

Quarantine: Currently, the UK Government has set a 10 day quarantine. Studies show [19] that individuals may be infectious 1-3 days prior to showing any symptoms and that symptomatic individuals are most infectious during the first 7 days after symptoms begin [20]. Hence, in our model we assumed that after each symptomatic person has been in a 10 day quarantine, they are no longer infectious.

Communities: We have adapted the approach in [8] to generate a supergraph of smaller communities, based on demographic data of a given country. The mesh of a network of cities, with their population sizes is used to generate a larger structure representing a (part) of a country. We used Delaunay Triangulation and the country data available in Wolfram for this.

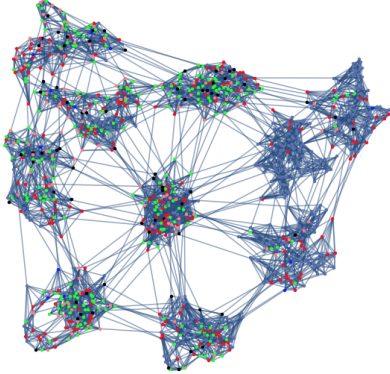


FIG. 3. A supergraph with Communities. Each cluster contains 100 nodes, and has 10 connections to neighbouring groups. Blue nodes represent susceptibles, red are infected (symptomatic and asymptomatic), black are dead and green have already been vaccinated.

To gain better understanding of how our model works, we compared how different parameters affect our UK Supergraph. The main three parameters we compared were: quarantining at earlier and later dates, changes in infection rates and changes in symptomatic rates.

Referring to our notebook’s evaluation, we could see that when quarantine was introduced earlier, there were less infected cases, and an increase in quarantined cases which resulted in a flattened curve of infection. We also saw that each time the infection rate doubled, the curve of infections steepened, resulting in a decrease in susceptible cases. This mostly followed our expectations, as a larger infection rate generated an increase in infected and recovered cases, with a decrease in susceptible. Lastly, as the symptomatic rate increased, the more cases

there were of people in quarantine. We have then compared our predictions with real data.

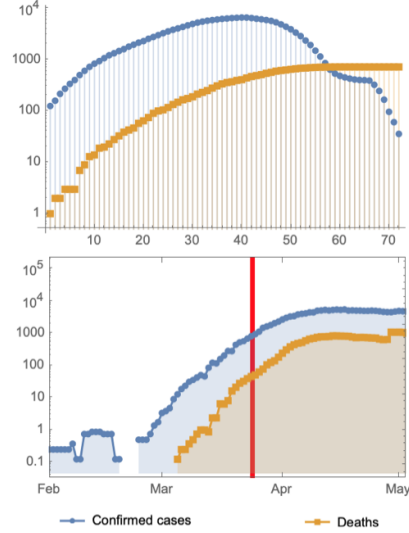


FIG. 4. Comparison between our model using realistic parameters (above) and real UK data (below). The red line indicates the introduction of the first lockdown in the UK.

Taking the same time frame from both graphs we could see extremely promising results. Our model followed a similar trend to that of real world data. Both the confirmed cases and the death followed an increasing curve until they flattened off. There were, however, multiple discrepancies. When quarantining was introduced in our model, at day 52, there was already a decline in confirmed cases, whereas in the real data, quarantining was introduced before the peak, which we can see flattened the curve of infections afterwards. Due to the small population size in our model, the confirmed cases declined from after day 40, which cannot be observed on the real data.

One of the main limitations in our model is its population size. We have found that when assessing a realistic start date of quarantining, our graph has already had its peak in infections due to its low population size. In a hope to fix this,

we tested how big of a population our graph could take. We calculated the vertex count of certain *Supergraphs* and found that the vertex count is low for 0.005, but too high for 0.1. However, as these values were too large to run, we set the scale factor for population to be 0.001, resulting in 26, 618 nodes in the graph.

Moreover, some of our biggest assumptions were regarding governmental measures. As we obtained no information on how long these measures were in place, we needed to resort to assumptions. Realistically, 30 days is far too short for most restrictions, but given the right data this could be easily solved. However, the exact effect of these restrictions on model parameters is far more difficult to assess, as it varies case-by-case. Tuning these hyperparameters can be key in a dynamic model.

The final main limitation was the number of deaths predicted by the model. We have observed less deaths present in our graphs regarding the number of infections, which must have been caused by our normalised death rate or population size.

In this study we have introduced a dynamic network-based model by adapting the work of [8], for predicting the spread of COVID-19. We have built onto this model by adding in: asymptomatic and symptomatic infection, vaccination, reinfection, quarantining, heterogeneous population, and geographic communities. When generating our final graph, we have been able to compare the results with real data and have found that our model followed the trend shown in the data. However, as aforementioned, there were some limitations to our model that we have come across when evaluating the different parameters we use. In future work, we hope to be able to reduce these limitations in order to obtain the most realistic model we can.

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