The comparison of trends in Spain and the Nederland: a Dynamical compartment model of the transmission of Coronavirus

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Abstract

Spreading of corona virus made many countries impose restrictions in order to control its dangerous effect on the citizens. We developed a theoretical dynamical model based on compartmental SIR system with additional adjustment taken from Flow network and Markov chain frameworks to illustrate the developments and trends based on publicly available data. Based on this Model a code in R was written and fed by publicly available data from Spain and Nederland, to compare their trends. Our results show that the ‘peak’ of infection is already behind us (in both countries), but also demonstrate that there is a danger of rebound of a spread. It is obvious that measures imposed are giving the results, but we should be precarious of near future practices and development, since the majority of population will be still susceptible to infection.

Introduction

The viral infection is raging around the world. Since its start in China in last quarter of 2019, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) which is causing the disease (COVID-19) spread all over the world in last three months (WHO). The first European country registering the person with COVID-19 was France, after which other countries followed. Among them, with very high speed of spread was Spain which probably already reached the ‘peak’ of number of infected citizens. In the Nederland the alarming level of infections was lagging after Spain; the first patient (infected during his recent travel to Lombardy) in the Nederland was confirmed on February 27th 2020. Very soon after outbreak the Website of John Hopkins University started updating publicly available data on number of infected, deceased and hospitalized persons in all affected countries and many scientific groups tried to employ their knowledge and already developed methods to answer various unknowns in connection to this epidemiologic phenomenon. Many research groups are working on similar problems and we wanted to stress here some of the most important findings so far. Friston published technical paper present on government website in UK (Friston et al., 2020) the Dynamical Causal Model of spread, shedding light on some parts of the mechanism. The same group published another paper (also as a preprint on ArXiv) aiming at estimating the susceptible part of population coming to the conclusion that less than 20% of EU countries population is infected, and that only 6.4% of those infected are gaining immunity. Since their posteriori estimate is suggesting that the majority of European population will stay without the immunity after this first outbreak, this
would eventually lead to another cycle of infections, resulting in consecutive peaks. They compared this situation with Spanish Flu pandemic from 2018, which had three peaks in total (Moran et al., 2020). Their result is important since it can inform further governmental actions to prevent loss of larger parts of European population due to the high infectivity of the corona virus. Researchers from the Nederland concentrated on testing of healthcare workers who became infected, concluding that more than half of them had mild symptoms and many of them kept on working while symptomatic (Kluytmans van den Bergh et al., 2020). Chinese researchers reported before about the mechanisms and levels of infectivity, as well as symptoms, but also used the epidemiological tools to predict outcomes (Prem, Liu et al. 2020). Several studies tried to forecast the future disease trajectories informing further management of hospitalization (Moghadas, Shoukat et al., 2020).

Although different countries adopted different approaches to solving the problem of massive infections, mainly by social distancing and lockdown, it can be seen that a similar patterns are present. We used an epidemiological compartments model originated from work of Kermack and McKendrick in 1927 (SIR) and used some characteristics from Markov chain and flow network in our work. Compartmental model is technique which simplify the mathematical modelling of infectious disease. One of the simplest compartment models is SIR model. It presumes that all the members of population are going through the three states/belong to three compartments: those who are susceptible (S), those who are infected (I), and eventually those who recovered (R-number of recovered or deceased). To represent that the number of susceptible, infected and recovered individuals may vary over time (even if the total population size remains constant), we make the precise numbers a function of time (t): S(t), I(t) and R(t). The model utilizes ordinary differential equations (ODE) which are deterministic, but the dynamics of the flow can become nonlinear, and therefore can be understood in stochastic framework. If the latter is the case the model becomes more realistic, but also much more complicated to numerically execute.

The first results of this work were publicly shared on LinkedIn pages of the authors (in consecutive days from the end of March and the first two weeks of April 2020), gaining valuable suggestions from colleagues on how to improve the model. After defining parameters and inferring unknown variables, the code in R was written and fed first by the publicly available data present on John Hopkins University Website (Dong et al., 2019). After the first week, we started using publicly available data present on the website of Spanish Ministry of Health (INE), after which we decided to start calculating the trends for the Nederland (from governmental RVO website) also with the difference in the data accessible. For example, the data about the numbers of recovered persons is not stated in RVO daily updates, it has to be inferred, although the disclaimer says that the number of deaths and hospitalization very often are cumulative for couple of days, especially around Easter holiday. The aim of this work is to compare trends in two European countries since the initial dynamics in one country can become similar in another one, which is lagging in numbers of hospitalized and infected people. It can already be seen that measures taken are affecting the dynamics and total numbers of affected people in both countries. Also, the aim of our work is to share the detailed theoretical model (especially how we determined transfer parameters between states) in order to help further balancing the future
model and managing the scarce resources, since we believe that another peak in infection is starting.

Methods

In this section we are describing the details of the model we developed and used, with ODE behind the SIR model (with additional adjustments from Markov Chain and Flow Network theory), and explained all the characteristic parameters added. We also describe the data we were using to get our results and report about the variables we took into account. Also, there is explanation of the R code written after the changes in the model, and the limitations we know our study has at the moment. But we need to stress here, that in our attempt to make our findings public as soon as possible, we decided to make it available to the readers in this not-perfect stage, since we believe others can use it for their work. It can be especially useful in smaller communities in case of future possible comebacks of a spread.

Data

First of all, we started from the information about the number of inhabitants of Spain as a publicly available number of 47 100 396 [www.ine.es] of which 17% are people older than 60 years (of whom 25% are over 80). For the Nederland, the National Statistics Office stated that the number of population (the data are from November 2019) is 17 424 978 [Centraal Bureau voor de Statistiek, CBS], and that 14.9% of them are persons older than 65.

According to the SIR model S are susceptible (the first compartment/nodes on a graph), who after being exposed change the compartment to be infected (I), after which part of them are admitted to the hospital (H) they might recover (R), go to the intensive care unit (ICU/U), or die due to the consequences of the infection (Lost/F). We will later explain the details of two models we considered before and after the Lockdown was proposed in both countries (in Spain a lockdown on 14-03-2020 but we have the data from 9-03, and in Nederland partial one on 23-03-2020).

During the first week we used data from a repository for the 2019 Novel Coronavirus at John’s Hopkins University Center for Systems Science and Engineering (JHU CSSE) were used (Dong, Du et al. 2020). After that initial week, we started using instead the official reports of Spanish (www.ine.es, www.datoscovid.es) and Nederland’s National Institute for Public Health (RVO/https://www.rivm.nl/en/novel-coronavirus-covid-19/current-information-about-novel-coronavirus-covid-19).

As described, from mentioned resources we collected daily the following figures important for the Model: the information about daily reported number of infected persons (INF/I), persons admitted to the hospital (H), people who deceased (Lost/F), latent persons (L) - people who are infected but not registered due to the lack of massive testing, active Healthcare workers (PS) and Healthcare workers infected (PSINFAC). We indirectly found the data about the number of people who are working even in this situation (TE) of the lockdown (beside healthcare workers, like drivers, those who deliver food, police etc.). We supposed that those who are in lockdown
(Q) in the situation like this are close to the number of inhabitants, since self-isolation in both countries was mandatory.

**Model**

Our model based on SIR (with additions taken from the theory of Markov chain and Flow Network) as a starting point, has two parts; before (left) and after (right graph) the lockdown.

**Figure 1.** Model based on SIR modified (in this figure for the Spain only) for the situation before (left graph) and after (the right graph) of the lockdown. Explanation in the text.

It can be seen on above graphical representation of the model that the nodes are symbolizing subpopulations of the number we begin with, the number of the whole population. Although it is an approximation of the reality (we simplify the problem in order to model it), the number from the beginning Q (those in lockdown/confined) and PS (active healthcare workers on the first line of primary care and in hospitals) are contributing to the next compartment L (Latent/Infected but not registered). On the version of Model after the lockdown we added TE (the working people, who are actively in transfer during the lockdown). Then, after the exposure (or after the incubation which can be according to WHO between 14 and 28 days) they gather in the compartment INF, which is Infected. Both L and INF can go directly to Recovered (R), but also those infected can die at home or die after admittance to the hospital (H). Those people who do recover (R) are coming from two different compartments, namely INF and H. Those who are treated in hospitals can develop life-threatening problems and be transferred to ICU; those from ICU can eventually become better after which they can be transferred to rehabilitation center or another department in hospital. The people who die (F, from Spanish Fallecidos) due to the consequences of COVID-19 are comprising of prior members of three different compartments: INF (those who die at home), H (those who die in the hospitals) and ICU (those who were on intensive care, probably on ventilators). The symbol A** represents those who, after being infected, recovered and develop the immunity on a corona virus (SARS-CoV-2). As we mentioned earlier it is still not clear from different sources of information, scientific literature included, whether the COVID-19 patients develop partial or full immunity, and whether re-infection is possible after recovery (we did not further specify this possible development in our model). Since we did not have reliable data about those who do have immunity on corona virus, and we cannot do this estimation, we considered in our model that two main end-nodes are R and F. The Objective functions we aimed to find in this research are the part of optimization, for which you need to introduce certain restrictions. For example, looking overall it is a question of in which relationship are Arrivals and Departures, and only if they are equal the system can be in
equilibrium; but that is not possible in reality. We consider this work as a trial of making balancing this model due to the knowledge of certain transfers of possible importance for further management of resources. Hospitals and ICUs are in any system so far bottlenecks, since they have limited capacities. To manage to circumvent such a bottlenecks administrator(s) of a system can try to optimize the flow by tackling the certain transfers we managed to define.

Another question visible on our left panel (the model before the lockdown) is illustrated in the arrows in the bottom grey one -those still in incubatory period and those with symptoms of the disease, and yellowish one- showing those who are latent, or asymptomatic/without symptoms and those who are already infective (have capacity to infect others), so they can transfer the disease further in their contacts. On John Hopkins Website it can be seen for example, that more than 80.2% confirmed patients were actually with very mild symptoms, sometimes believing it was the seasonal flu. The number of asymptomatic people is still not known, because that would require massive testing of the whole populations or at least a big sample to estimate that number.

The aim of all the measures applied at the moment is that the healthcare system and measures proposed would try to maximize the process/transfer/arrow leading from INF to R (and eventually to A**), and minimize the summary flow to F (Passed away/Deceased).

Another representation of Compartments leading us to the better understanding of the underlying dynamics can be seen on the Figure 2.

Figure 2. The scenario for the state of lockdown; SIR compartment model in combination with Flow network and Markov chain additions.
Here we are giving the meaning of all the parameters used in recurrent equations, since they are the arrows illustrating the flow between compartments, including all the possible interactions we could include at the moment. Beta (β) is the average number of contacts per person per time (here we are choosing the time of update is one day), and describes the transition from one compartment to another. We explored several scenarios to probe this. In case of our model, since we have three groups of susceptible persons, there are three transition parameters: probability of contagion/infection in isolation (for example members of household) $\beta_1$, probability of contagion for a person who is an active healthworker $\beta_2$, and probability of contagion of a person who works during the lockdown as a non-healthcare worker, $\beta_3$. The parameter Gamma (γ), the transition rate between infected and recovered (simply the rate of recovery or mortality, that is, number of recovered or dead during one day divided by the total number of infected on that same day, supposing "day" is the time unit). We did not mention the probability to change the state from latent to infective one (so one can transfer the disease) and on a final model there is not even an arrow between those two states. The parameters alpha are describing the probability of death: $\alpha_1$ - the probability of dying at home, $\alpha_2$-the probability of dying at hospital, and $\alpha_3$ - the probability of recovery at home. Parameter showing the probability of passing away in hospital (not in ICU) is described here as $\delta_1$, $\delta_2$ is probability of that one need a care in ICU, and $\delta_3$ is probability of recovering at hospital. Parameters signifying the probability of passing away in ICU ($\mu_1$) and $\mu_2$, the probability to leave the ICU and be transferred to another department in hospital (or another hospital for rehabilitation). Omega ($\omega_1$) signifies the probability to become infected for the second time (after the recovery) and $\omega_2$ signifies the probability of immunization (or of attaining the immunity to corona virus 2).
Here is the system of derivative equations we used from SIR model, and the most important are the following ones defining the changes of compartments (S, I and R) in time. From the definition of the states on day t+1 with respect to the previous day t, and using the derivative approximation, the system of differential equations is constructed. This idea simplified the complete diagram with 10 nodes to 3 nodes.

\[
\begin{align*}
S(t+1) &= S(t) - \beta_0 \frac{S(t)}{N} I(t) \\
I(t+1) &= I(t) + \beta_0 \frac{S(t)}{N} I(t) - \lambda I(t) \\
R(t+1) &= R(t) + \lambda I(t)
\end{align*}
\]

\[
\frac{x(t + \Delta t) - x(t)}{\Delta t} = x'(t)
\]

\[
\frac{\partial S}{\partial t} = -\beta_0 \frac{S(t)}{N} I(t)
\]

\[
\frac{\partial I}{\partial t} = \beta_0 \frac{S(t)}{N} I(t) - \lambda I(t)
\]

\[
\frac{\partial R}{\partial t} = \lambda I(t)
\]

**Figure 4.** Here is the system of derivative equations we used from SIR model, and the most important are the following ones defining the changes of compartments (S, I and R) in time. From the definition of the states on day t+1 with respect to the previous day t, and using the derivative approximation, the system of differential equations is constructed. This idea simplified the complete diagram with 10 nodes to 3 nodes.

**Parameter estimation and balancing**

\[
\beta_0(t) \quad \frac{\text{contagios}(t)}{[Q(t-1)]} + \epsilon_1(t)
\]

\[
\beta_1(t) \quad \frac{\text{contagios}(Q)(t)}{[Q(t-1)]} + \epsilon_2(t)
\]

\[
\beta_2(t) \quad \frac{\text{contagios}_Q(TE(t))}{[TE(t-1)]} + \epsilon_3(t)
\]

\[
\epsilon_1(t) \text{ factor of correction, can be set to zero for experimental purposes.}
\]

**Figure 4.** Estimation of Parameters used in recurrent equations important for balancing the Model.

On the Final Model Figure 2 it can be seen that the L and INF/I nodes have been merged as they are only joined by an arc, all passing through with greater or lesser viral load. According to the time windows, there is transit between the Q and TE nodes that are now Active Jobs outside the home. The model below does not study those immunized or infected in successive instances because they are residual or there is insufficient information. The model could be useful if applied to specific regions, such as a city or town. The Spanish state is very diverse and this makes estimates very unreliable (our opinion is that Madrid as such a big affected city/a focus, is contributing largely to the public figures, but it is a question how that applies to other areas like Almeria or Alhambra for example). Thus the model had to be tested further with a fresh data.

The model is very dynamic, the parameters require daily updates in order to obtain good quality results due to the constant introduction of political measures for the management of the
pandemic. It is also a very vulnerable system, any misuse can lead to radical changes, such as neglect or misuse of prevention measures. Based on above described model, a code in R is written and fed by the data from official sources mentioned in the Data section, which were updated daily. This yielded an evolution of the states cumulatively from early March to April 19th 2020 for Spain, and as a comparison similar output graphic representation for the Nederland. Both models are based on the data from 9. March to 19. April 2020.

Results

Our results comprise of two parts: the first one is the evolution of the spread in Spain from 9-03-2020 to 19-04-2020, with a special focus on a novel trend obtained in the third week of April, and the cumulative evolution of a spread in the Nederland, for the same period. Note that the proposed lockdowns were ten days apart. There are some specific remarks we can infer from those results:

- The model indicates that the probability of contagion is higher for active workers.
- Logically, those in isolation are the least vulnerable.

- As from Figure 2 it can be seen that for further optimization administrators have to minimize all the inflows to L and to maximize all the transfers to R. Hospitals and ICUs are bottlenecks due to a limited capacities.
- As a conclusion of this study, we could say that these data indicate a danger of rebound in the pandemic. As the first ‘peak’ of infections in Spain was behind us (reached on march 24th), people gradually start going out for work, but it is again giving rise to the number of newly infected ones and it can mean that another peak of spread is following.

**Figure 6.** Evolution and tendencies of COVID-19 for Spain (from 9 March to 19 April 2020)
The danger indicator: it can be seen that the ’peak’ of spread dynamics was on March 24th. But if we observe the difference between the inflow and output from this network, we can see at the far right part of the graph, that the another rise of infected persons is starting again.

Figure 8. The evolution and observed trends in the Nederland. Due to some missing data, we were not able to estimate the number of recovered persons, but it seems, as also stated on RVO website that the proposed measures of social distancing, self-isolation and working from home are giving the results.

Discussion

Our results show, by employing our Dynamical model fed with publicly available data, the SARS-CoV-2 (which cause the disease COVID-19) spread evolution and trends in Spain and in
the Nederland cumulatively from 9 March to 20 April 2020. It is clear that in both countries the recommended measures of social distancing and closing the public gatherings are giving the results; the ‘peak’ of new infections, admissions to hospitals and deaths already happened in both countries. We think that our dynamical model based on compartment SIR epidemiological model with modifications from Markov chain and network flow are giving the tool to those who want to optimize the management of resources especially in other than central areas. It is of importance since our results are also showing that another wave of infections is possible and that we would probably have another peak(s).

Our model is giving indications of future increase in infection which is in line with other researcher’s findings that only a fraction of population (6.4%) in any European country will have the antibodies necessary for later immunity on COVID-19 (Moran et al., 2020). It is still not clear whether those who recover after the infection are attaining partial or total immunity for COVID-19, since there are reports of sporadic re-infections in Asia. A study of Dutch blood donors has found that around 3% have developed antibodies against the new coronavirus; which change the insight in how many people were being sick below the radar of detection (Reuters). On a population of above 17 million, it is much more than the publicly available records. In the beginning of March an analysis of waste water around Amsterdam showed the presence of corona virus, illustrating the extent of spread of infection, which is probably larger than the detected cases (which is not strange since only around 17000 tests were performed in the Nederland). Our results are implying that active health workers have increased probability of contagion and that only those in isolation are safe, but that is defensive measure. Since the first vaccines can be expected in around a year (for safety reasons) the question here is how we are going to live, since the majority of population is not immune to the virus infection? Many will agree that life will have to change after this pandemic, significantly.

We are aware that our study has some limitations. We think that among limitations and restrictions (which should be taken in consideration) of our Model are the following:

- Model assumes a constant N population (no births or immigration, as any SIR)
- The population is not homogeneous, this study would be probably more useful for a small region (although, Moran et al., 2020 showed that the small city region model is less effective than the dynamical one)
- The parameters are estimated from the official data (which are sometimes aggregated)
- Q represents the quarantined and healthy node, i.e. one person may be incubating the virus and being in the quarantine, but that person is placed in the latent node L
- The strength of the infection and rate of recovery determine some transfers
- No pharmacological intervention (vaccines, drugs) exist at the moment
- Transmission is by random contact (all persons have the same probability) - after the state of Lockdown and within the corresponding population sector
• Infection capacity per infected person (2 to 3 people), some reports indicate =2.5 or somewhat less, and

• The initial values on the population Q(0), PS(0) and TE(0) are also estimates from the official data.

In conclusion, we can say that our results show that the dynamical trend in Nederland seems to follow a very similar pattern in the Spain, it is just lagging behind for less than two weeks. Due to the lack of R data on the Nederland side we can only estimate it from other present data. As a conclusion of this study, we could say that these data indicate a danger of rebound in the pandemic. Since the data show that Spain already reached the ‘peak’ of spread, it could mean that other ‘peaks’ are to follow, which can inform further preventive decisions from authorities.

In a documentary about pandemics in Netflix serial ‘Explained’, emitted before the onset of SARS-CoV 2 in Europe, a sentence from an expert epidemiologist from WHO stays a long time with us: ‘Mother nature is the biggest terrorist of all’. The narrative was (and now we all know) that the question is not ‘will the pandemic hit us’ but ‘when’. We hope that we can at least learn from the previous experience and make better optimization of our health care systems in next period.

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Additional: To those who would like to perform the same analysis on their regional data—please ask for the access to the R code from Victoria Lopez (vlopezlo@ucm.es).