Comparing Strategies to Slow Down the Spread of COVID-19 in Five Nordic Countries

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1   Abstract

This report examines the spread of the novel coronavirus SARS-CoV-2 (COVID-19) in five nordic countries: Sweden, Denmark, Norway, Finland and Iceland. Specifically, we aimed to understand the effects of the different mitigation strategies adopted by these countries. In contrast to its neighbors, Sweden applied less restrictive measures to stop the spread of the virus. Therefore, we expected Sweden to have a larger spread of COVID-19 relative to its population after other countries applied mitigation strategies. Conversely, we anticipated Sweden to have a lower spread after the other countries had lifted their restrictions, since it would have a larger proportion of immune individuals. To test these hypotheses, case data that have been collected since January 2020 were divided into three periods: Before countries other than Sweden closed educational facilities, while they were closed, and after they were reopened. Then, we fitted a metapopulation *SEIR(S)* model to the data in each of these periods. The model predicted exponential growth similar to the growth of total cases in the data for the first period. It overestimated the growth of total cases in the second period, except for Sweden, for which the growth was underestimated. Sweden did not have an increased spread compared to the other countries and thus our first hypothesis was not supported. For the last period, the initial growth was predicted by the model relatively accurate. Here, Sweden had a lower spread than the other nordic countries, supporting our second hypothesis.

2 Introduction

On 31 December 2019, news of unusual pneumonia cases emerged in Wuhan, the People's Republic of China [1]. A week after, the Chinese authorities informed the World Health Organization (WHO) that the cases were caused by a novel coronavirus. In the following weeks, what became known as the novel coronavirus SARS-CoV-2 (coronavirus disease 2019, COVID-19) rapidly spread across the globe. In response, the WHO declared the situation a global health emergency at the end of January 2020 and a pandemic on March 11, 2020. As of October 23, COVID-19 has caused over a million deaths globally [2]. Moreover, its global economic impact in 2020 alone is estimated at 5.6 trillion in lost GDP [3]. Given the enormous losses associated with the pandemic, the goal of this report is to explore the effects of different mitigation strategies on the spread of COVID-19. To achieve this aim, we compare the responses to the pandemic in five nordic countries: Sweden, Denmark, Norway, Finland, and Iceland. We expect this comparison to be informative due to the radically different response strategies adopted by these countries. Specifically, Sweden avoided lockdowns and border closures, instead relying on voluntary social distancing and self-isolation to slow down the virus [4]. In contrast, its neighbor Denmark imposed a nation-wide lockdown in which all non-essential travel was discouraged [5] and closed its borders for a month [6]. Likewise, Norway adopted strong measures such as closing businesses and imposing travel restrictions [7] and Finland imposed a lockdown on the capital Helsinki as well as the surrounding region for three weeks [8]. At the time of writing, there are approximately 10790 cases per million in Sweden with 587 deaths per million, compared to 6280 cases with 119 deaths in Denmark, 3035 cases with 51 deaths in Norway, 2446 cases with 63 deaths in Finland, and 12395 cases with 32 deaths in Iceland [2]. This prompts the questions: How have the different measures adopted by these countries influenced the number of cases they have today and what can be expected in the future?

2.1 Compartmental Models and the Dynamics of Infectious Diseases

The dynamics of an infectious disease can be described using *compartmental* models. A very simple case of a comparmental model is the *SIR* model. This model divides the population into three classes: *Susceptibles* (S), *infecteds* (S) and *recovereds* (R) [9]. The susceptibles are the *proportion* of the total population who have no immunity against the virus and thus can be infected with it. The infecteds are the proportion who have been exposed to the virus and can transmit it to the susceptibles. Finally, the recovereds are the proportion of the population who have recovered from the virus and have acquired life-long immunity (i.e., they are no longer susceptible). If one wishes to express the subpopulations as frequencies as opposed to proportions, the letters X, Y and Z are used to denote the susceptibles, infecteds and the recovereds, respectively. Compartmental models as the *SIR* can be used to estimate parameters than indicate the spread of a disease within a population. A common parameter is the basic reproductive ratio R_0, which indicates the number of secondary infections that arise from a primary infection [9].

The assumption of life-long immunity is important, since there are diseases against which humans do not acquire immunity at all (e.g., the common cold), and diseases against which there is only waning immunity (e.g., influenza) ([9, 10]. To account for this, we can extend the model with an S at the end, making it *SIRS* to indicate that the recovereds become susceptible again after a certain period [9].

In this report, we analyze the trajectory of COVID-19 under each assumption (i.e., life-long immunity versus waning immunity). Furthermore, it may be that individuals who are exposed to the virus become infectious only after a period of time. To account for the time period when an individual is exposed to the virus but not infectious yet, an *exposed* (E) compartment is added, leading to an *SEIRS* model [9]. Furthermore, it is possible that the contact between individuals is reduced as a consequence of social distancing measures. Indeed, this is what is expected of individuals during the current pandemic [11]. To consider this possibility, we constructed a second model with an additional parameter that represents the degree to which the level of contact in the population is reduced due to quarantining and isolation. As a result of the reduced contacts, fewer susceptibles can be infected.

In sum, our *SEIR(S)* model assumes the following: The whole population is susceptible to the virus before the epidemic. After the virus is introduced to a community, some people are exposed to the virus and become infectious after a period of time. Some of the exposeds isolate before they can transmit the virus and recover. The infecteds can transmit the virus to susceptible individuals, recover from the virus and may or

may not acquire life-long immunity. If they only acquire waning immunity, then they move back to the susceptible compartment after the immunity ends. The movement of individuals between these compartments is described by a set of ordinary differential equations (ODEs) that are detailed in the methods section. We now discuss a crucial factor that determines the extent to which a virus spreads within a community: Its interaction with other communities.

2.2 Metapopulation Models

Metapopulation models spatially divide a population into interacting subpopulations, each with independent dynamics [9]. For instance, the force of infection – which determines how fast the virus spreads and is determined by the connectivity between individuals – may be larger in one subpopulation than the other. However, since the subpopulations interact with one another through various means such as travelling on vacations, business trips, or migrations, the force of infection in one subpopulation is affected by the force of infection in the other. The exact relationship between the number of infected individuals in one subpopulation and the force of infection in another depends on two things: The level of connectivity between the two subpopulations and the relative number of infected individuals in one subpopulation to the total population size of the other [9]. In any case, the more strongly *coupled* two subpopulations are, the more similar their epidemic curves are. That is, the more they interact and the more the force of infection in one is affected by the other, the more similar the resulting dynamics are. In this study, we characterize each of the five nordic countries as a subpopulation who interact with each other.

2.3 The Present Study

In the following sections, we present a metapopulation *SEIR(S)* model to analyze the dynamics of COVID-19 in Sweden, Denmark, Norway, Finland and Iceland. Specifically, we examine the epidemic curves in these countries both before they introduced measures to slow the spread of COVID-19 and while the measures were being taken. Finally, we attempt to predict the number of infecteds in each population for the following months, taking the fraction of the population that have already recovered from the virus into account.

First, we hypothesize that the model will estimate higher spread of the disease (indicated by R_0) in the second period for Sweden compared to the other countries because it has taken less restrictive measures to stop the spread. Second, we anticipate that, if immunity is assumed, the model will predict lower spread of the disease (indicated by R_0) for Sweden in the third period and future predictions than its neighbors. With immunity, Sweden will already have more recovered individuals in the third period than the other countries (because more individuals got infected in the second period) and thus less susceptibles that can get infected.

3 Methods

3.1 Model Specification

We created two compartmental *SEIR(S)* models, one in which individuals are assumed to quarantine themselves and another one without this assumption. We also varied the assumption of immunity: in the first experiment life-long immunity was assumed. In the second, waning immunity was assumed. The model without assuming isolation due to social distancing is:

$$\frac{dX_i}{dt} = \mu_i N_i - \theta_i X_i - \mu_i X_i \tag{1}$$

$$\frac{dE_i}{dt} = \theta_i X_i - \mu_i E_i \tag{2}$$

$$\frac{dY_i}{dt} = \sigma E_i - (\gamma + \mu_i)\frac{Y_i}{(1-\epsilon)} \tag{3}$$

$$\frac{dZ_i}{dt} = \gamma Y_i - \mu_i Z_i, \tag{4}$$

where μ_i is the birth and death rate and N_i is the size of subpopulation i. The parameter θ_i is the force of infection in subpopulation i and is defined as:

$$\theta_i = \beta_i \sum_j^n \rho_{ij} \frac{Y_j}{N_i}, \tag{5}$$

which is the rate of transmission β_i multiplied by the sum of the interaction parameters ρ_{ij} and the number of infectious individuals Y_j/N_i from every country that infect individuals in subpopulation i [9]. Thus, the rates of transmission are scaled by the subpopulation size N_i. Furthermore, σ is the rate at which individuals move from exposed to infected, γ is the recovery rate, and ϵ is the infection-induced mortality rate. Importantly, this specification implies that we assume constant rates σ, γ, and ϵ. We justify this decision by assuming these parameters to be disease-specific and thus independent of the subpopulation. The other parameters are treated as country-specific and can thus differ for each subpopulation. Because we investigate a relatively short period of time (less than a year), we assumed birth and death rates to be equal. The basic reproductive ratio for this model is defined as:

$$R_0^i = \frac{\theta_i(1-\epsilon)}{\gamma + \mu_i} \tag{6}$$

If we assume waning immunity instead of life-long immunity, the global parameter τ is added to the equations of the susceptibles and the recovered, denoting the rate at which the recovered become susceptible again:

$$\frac{dX_i}{dt} = \mu_i N_i + \tau Z_i - \beta_i \sum_j^n \rho_{ij} \frac{Y_j}{N_i} X_i - \mu_i X_i \tag{7}$$

$$\frac{dZ_i}{dt} = \gamma Y_i - \tau Z_i - \mu_i Z_i \tag{8}$$

The model with isolation has the additional α_i parameter that represents reduced contacts in each subpopulation:

$$\frac{dX_i}{dt} = \mu_i N_i - (1-\alpha_i)\theta_i X_i - \mu_i X_i \tag{9}$$

$$\frac{dE_i}{dt} = (1-\alpha_i)\theta_i X_i - \mu_i E_i \tag{10}$$

$$\frac{dY_i}{dt} = \sigma E_i - (\gamma + \mu_i)\frac{Y_i}{(1-\epsilon)} \tag{11}$$

$$\frac{dZ_i}{dt} = \alpha_i \theta_i X_i + \gamma Y_i - \mu_i Z_i, \tag{12}$$

with the basic reproductive ratio:

$$R_0^i = \frac{\theta_i(1-\epsilon)(1-\alpha_i)}{\gamma + \mu_i} \tag{13}$$

The strength of the transmission from one subpopulation to another is epxressed in an interaction matrix of the following form:

$$\mathbf{A} = \begin{vmatrix} \rho_{11} & \cdots & \rho_{1j} \\ \vdots & \ddots & \vdots \\ \rho_{i1} & \cdots & \rho_{ij} \end{vmatrix},$$

were the rows of the matrix are receiving countries and the columns are the transmitting countries. The diagonals of the matrix are assumed to be $\rho_{i=j} = 1$, so that every country has its full transmission term plus fractions of the other countries tranmission terms as the force of infection.

3.2 Data and Parametrization

The data on COVID-19 cases, population sizes, and life expectancies (to estimate death rates) in Sweden, Denmark, Norway, Finland, and Iceland were obtained from the Our World in Data (OWID) database [12], which is publicly available on Git Hub (https://github.com/owid/covid-19-data/tree/master/public/data). Figure 1 gives an overview for the development of new and total COVID-19 cases in the five countries. The population sizes and estimated life expectancies for the nordic countries are displayed in Table 1.

We split the data into three periods based on data on restrictions as a response to COVID-19 publicly available from the Institute of Health Metrics and Evaluation at the University of Washington [13] (https://covid19.healthdata.org/denmark?view=daily-deaths&tab=trend): The first period was from the day on which the first COVID-19 case in any of the five nordic countries was reported (2020-01-29, in Finland) to the day when the first of the countries closed their educational facilities (2020-03-12, in Norway). We chose the latter date because all countries except Sweden closed their educational facilities within the same week. In contrast, Sweden did not close them at all. The total cases of COVID-19 for each period are displayed in Figure 1. The second period was from the end of the first period until the educational facilities were reopened in the first of the five countries (2020-05-04, in Iceland). The last period was from the day when the last of the five countries reopened their educational facilities (2020-09-20, in Denmark) until the last day where data was available (2020-10-19). We also made predictions for two months further than the available data.

To estimate the interaction between countries we used the number of nights spent in hotels with more than 10 beds by individuals from each country in 2019. The data was retrieved from the Nordic Statistics database [14] and is publicly available on their web page (https://www.nordicstatistics.org/foreign-trade/). The raw data is displayed in Table 2. To transform this data into an interaction matrix on the interval $[0,1]$, we normalized each row by dividing each cell by the number of guests of the host country:

$$\rho_{ij} = G_{ij}/G_{i=j}, \tag{14}$$

where G_{ij} is the number of nights spent by individuals from subpopulation j in hotels in subpopulation i. This normalization makes the diagonal become one. The transformed interaction matrix is shown in Table 3.

Table 1: Population sizes and estimated life expectancies (in years) per country.

	Sweden	Denmark	Norway	Finland	Iceland
N	5792203	5540718	341250	5421242	10099270
$1/\mu$	80.9	81.91	82.99	82.4	82.8

Table 2: Number of nights in hotels spent by individuals from Denmark, Finland, Iceland, Norway, Sweden (columns, in this order) in the same countries (rows, same order) in 2019.

$$
\mathbf{A}_{raw} = \begin{vmatrix}
12453347 & 173936   & 61784 & 1202408 & 1161120 \\
107530   & 12591720 & 32026 & 152212   & 442983   \\
113150   & 34476   & 438779 & 72608   & 79600   \\
429653   & 125653   & 21694 & 17964386 & 706311   \\
873011   & 501455   & 32026 & 1303392 & 34711796
\end{vmatrix}
$$

3.3 Parameter Optimization

We fitted the models to the total cases by minimizing non-linear least squares between the total cases from the OWID data set and the total cases produced by the model. The total cases produced by the model were obtained by integrating the number of infected individuals over time (also counting exposed individuals). We estimated the following parameters for the model without isolation: The β parameter (i.e., transmission rate) for each country and a single γ parameter (i.e., recovery rate). For the model with isolation, we estimated a β and α parameter for each country and one γ. The estimation for βs was bound between $(0, \infty)$, for γ between $[0.1, \infty)$, and for αs between $[0, 1]$. Starting values for the optimization were $\beta_{start} = 0.5$, $\alpha_{start} = 0.05$, and $\gamma_{start} = 0.1$. As the initial conditions for integrating the ODEs, we used the number of new cases at the start of each time period as the number of infected individuals Y_{ini} and the number of total cases 10 days before the start as the number of recovered individuals. For the other compartments we set $X_{ini} = 1 - Y_{ini}$, $E_{ini} = 0$, and $Z_{ini} = 0$.

For the least-squares optimization we used the `optimize` module of the `scipy` library (version: 1.5.3) [15]. From the same library we used the module `integrate` to integrate the ODEs of the models and make predictions, which builds on the Fortran library `ODEPACK` [16]. We created figures using the modules `pyplot` and `style` from the `matplotlib` library (version: 2.2.5) [17]. Furthermore, the libraries `numpy` (version: 1.16.6) [18] and `pylab` (also from `matplotlib`) were used for general calculations and operations.

Table 3: Estimated interaction matrix between Denmark, Finland, Iceland, Norway, Sweden (rows and columns, in this order) used in the models.

$$
\mathbf{A}_{norm} = \begin{vmatrix}
1   & 0.014 & 0.005 & 0.097 & 0.093 \\
0.009 & 1   & 0.003 & 0.012 & 0.035 \\
0.258 & 0.079 & 1   & 0.165 & 0.181 \\
0.024 & 0.007 & 0.001 & 1   & 0.039 \\
0.025 & 0.014 & 0.001 & 0.038 & 1
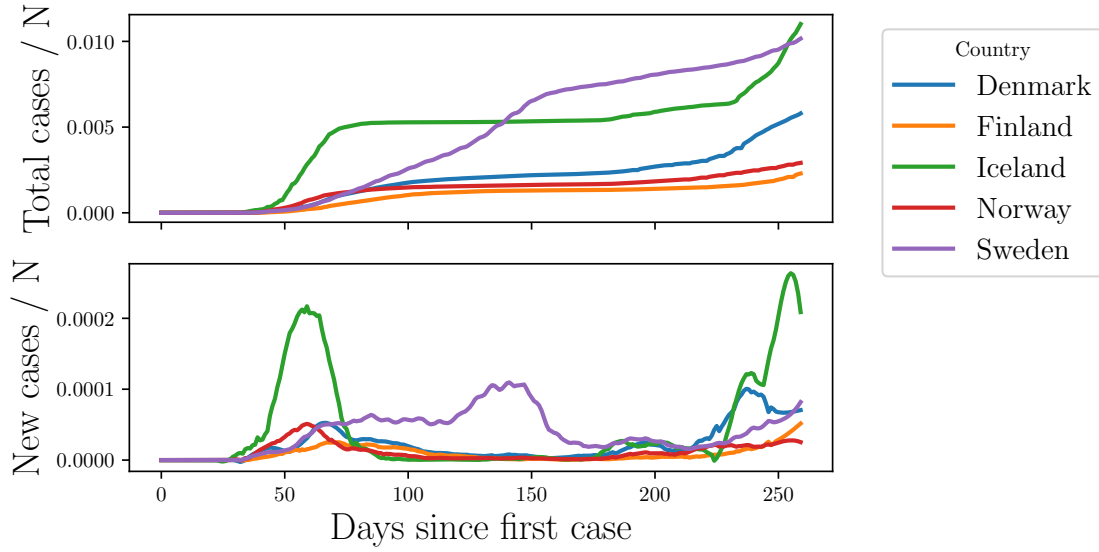\end{vmatrix}
$$

4 Results

Figure 1: The plots show the proportion of total cases (upper panel) and the proportion of new cases (lower panel) in each of the nordic countries for the number of days since the first case. Proportions rather than frequencies are depicted for comparability.
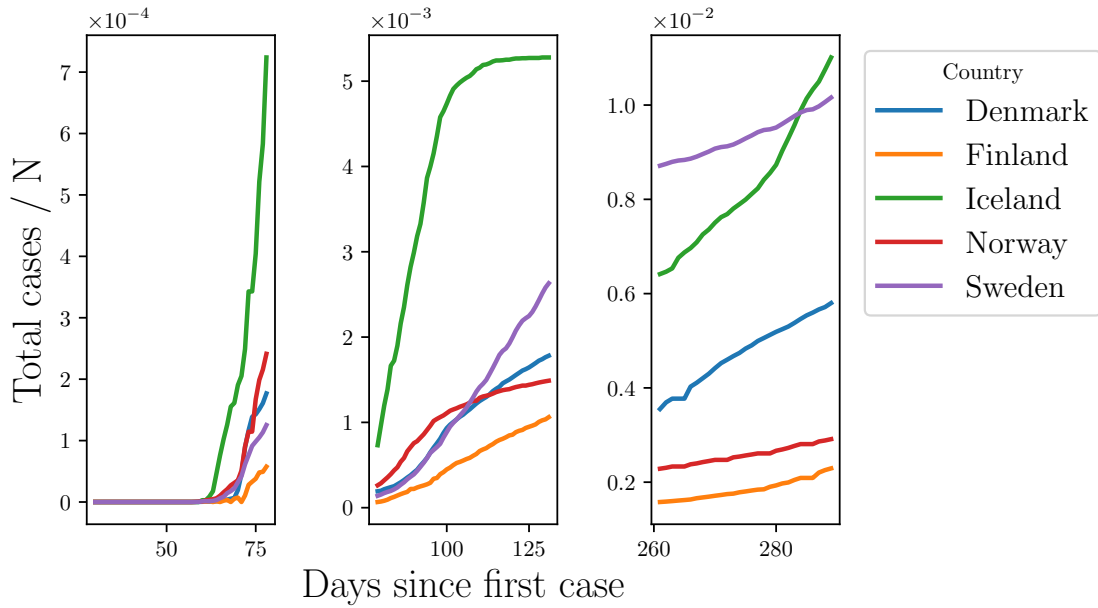

Figure 2: The figure shows the proportion of the total number of cases for the number of days since the first cases. Left panel: First period, before educational facilities in first country were closed. Middle panel: Second period from end of first period until first country reopened educational facilities. Right panel: Third period, from last country reopening educational facilities until end of data series. Colors represent different countries.
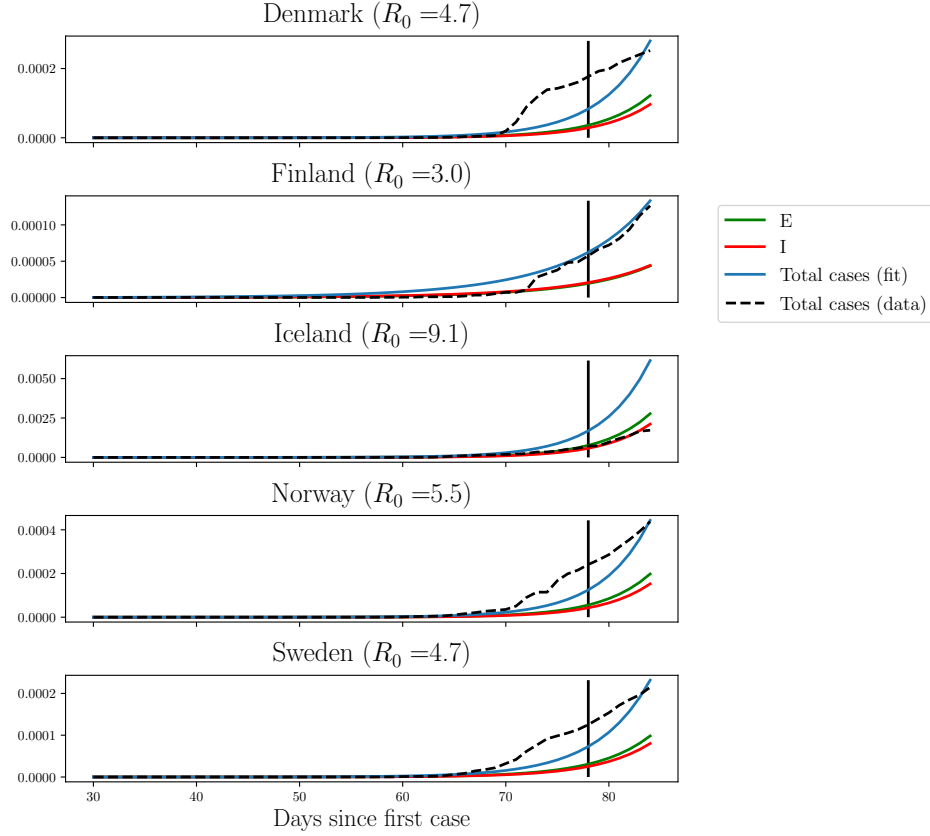
Figure 3: The figure shows the model fit for each of the five countries in the first period. The blue line depicts the total cases produced by the model, whereas the black dashed line represents the total cases in the data. The subpopulations are expressed as proportions of the total population in all the figures for clarity but the models were fitted with frequencies. The green and red lines are the proportion of exposed and infected people, respectively. The part of the curve after the vertical black line are predictions and were not included in fitting the model. The basic reproduction rates (R_0) are also estimated from model parameters.
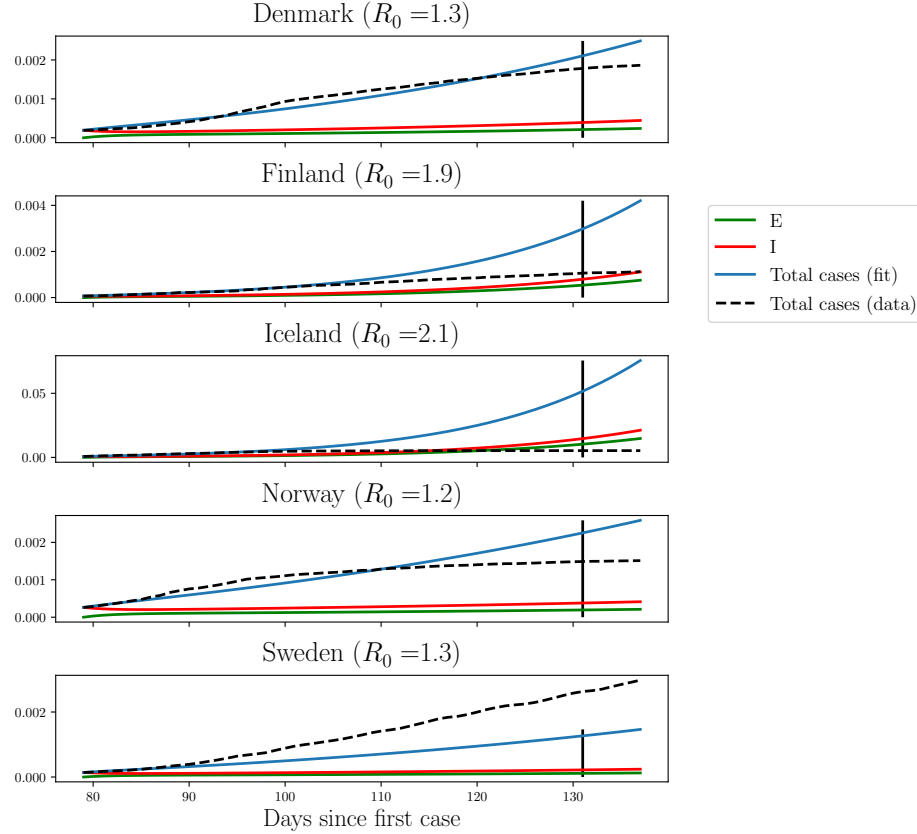
Figure 4: The figure shows the model fit for each of the five countries in the second period. The blue line depicts the total cases produced by the model, whereas the black dashed line represents the total cases in the data. The subpopulations are expressed as proportions of the total population in all the figures for clarity but the models were fitted with frequencies. The green and red lines are the proportion of exposed and infected people, respectively. The part of the curve after the vertical black line are predictions and were not included in fitting the model. The basic reproduction rates (R_0) are also estimated from model parameters.
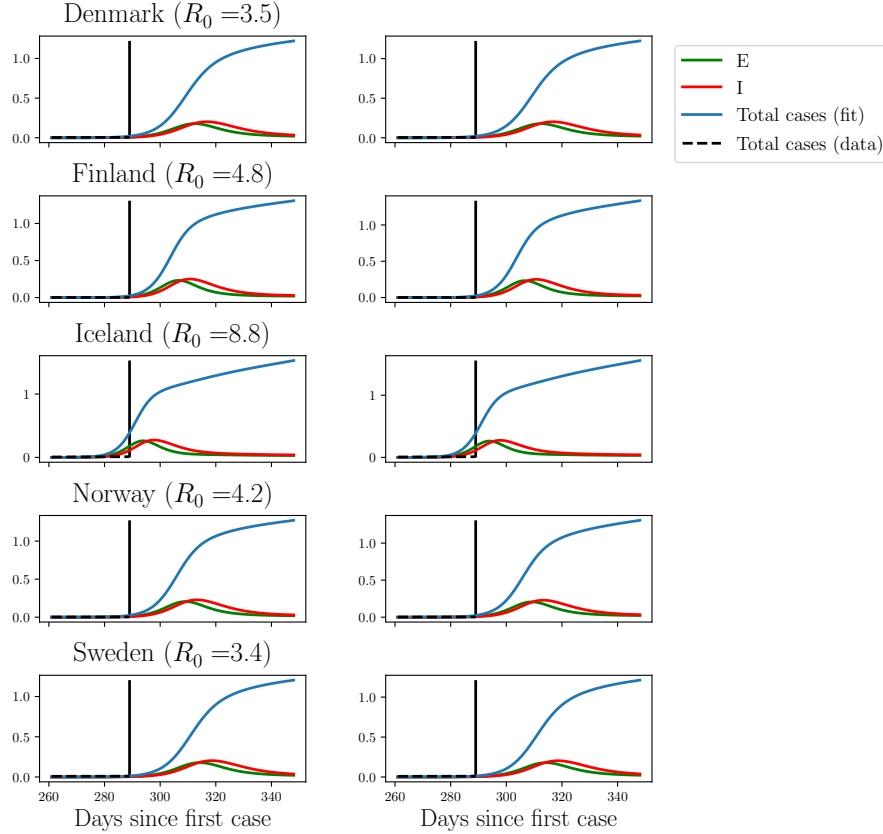
Figure 5: The figure shows the model fit for each of the five countries in the third period. The blue line depicts the total cases produced by the model, whereas the black dashed line represents the total cases in the data. The subpopulations are expressed as proportions of the total population in all the figures for clarity but the models were fitted with frequencies. The green and red lines are the proportion of exposed and infected people, respectively. The part of the curve after the vertical black line are predictions and were not included in fitting the model. Panels in left column represent model predictions with immunity and those in the right column predictions with waning immunity. The basic reproduction rates (R_0) are also estimated from model parameters.

For the first period, Figure 3 shows that the model captured the initial exponential growth observed in the data. All the basic reproduction rates were estimated to be above one. The best model fit was for Finland, whereas the worst fit was seen for Iceland. In the latter case, the cases were largely overestimated. For the other countries, the cases were underestimated. With regards to the predictions, they seem to be accurate for a week except for Iceland. We suggest that the enormous growth of cases in Iceland are due to the substantial interactions it had with the other countries. The interaction matrix shows that Iceland was the most connected of the studied countries (see Table 3).

Figure 4 shows that the model could approximately capture the slower growth in cases in Denmark, but overestimated the trend in Finland, Norway, and Iceland. Interestingly, the total cases were underestimated for Sweden. All basic reproductive ratios were still above one, but lower than in the first period. Our first hypothesis was not supported since Iceland and Finland had larger reproductive ratios than Sweden (although they were under-/overestimated). The overestimation of the model for three of the countries can be explained by their large population sizes: The model assumes a constant transmission rate and exponential spread until the critical threshold of susceptibles in the population is reached ($S < 1/R_0$). A decrease in infections can only occur beyond this threshold, which takes longer for large populations with many susceptibles.

For the third period, Figure 5 shows that, except for Iceland, the model captures the initial stages of the third

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period relatively well, when the cases slowly increase. For the two-month prediction period the model assumes fast exponential growth (due to reproductive ratios above one). However, it estimated a slightly lower reproductive ratio for Sweden than for the other countries, supporting our second hypothesis. Importantly, there was no difference between predictions were immunity was assumed compared to when immunity was expected to be waning.

5   Discussion and Conclusion

This report examined the trajectory of COVID-19 in Sweden, Denmark, Norway, Finland and Iceland between the end of January and late October 2020. Our goal was to compare the effectiveness of different mitigation strategies adopted by Sweden on one hand, and its neighbors on the other. Furthermore, we aimed to provide predictions for two months beyond the observed period. To achieve these aims, we divided the data into three periods, namely, before, during and after mitigation measures were taken (closing educational facilities). Then, we fitted a compartmental *SEIR(S)* model to the number of total COVID-19 cases. For period one, the model predicted exponential growth similar to the growth of total cases in the data. For the second period, it overestimated the growth of total cases, except for Sweden, for which the growth was underestimated. Sweden did not have an increased spread compared to the other countries and thus our first hypothesis could not be supported. For the last period, the initial growth was predicted by the model relatively accurate. Here, Sweden had a lower spread than the other nordic countries, supporting our second hypothesis.

That our model did not provide predictions confirming our first hypothesis can be explained by the fact that it overestimated the spread for countries other than Sweden, for which it underestimated the spread. Thus, there might have been larger spread of COVID-19 in Sweden during the second period, but the model did not capture this pattern. That predictions with immunity compared to with waning immunity were not different was unexpected, but could be due to the large population sizes and long waning periods. With those it could take a longer time than the disease needs to infect the majority of each population, before the waning immunity comes into effect.

In conclusion, our *SEIR(S)* model applied to COVID-19 cases in three different time periods did not support the hypothesis that Sweden has a larger spread of the disease because it has taken less restrictive measures than other nordic countries. However, the model supported our second hypothesis that Sweden has lower spread of infections after most countries have lifted their mitigations and cases started to rise again.

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