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COVID-19 interventions in some European countries induced bifurcations stabilizing low death states against high death states: An eigenvalue analysis based on the order parameter concept of synergetics

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A B S T R A C T
Taking a dynamical systems perspective, COVID-19 infections are assumed to spread out in a human population via an instability. Conversely, government interventions to reduce the spread of the disease and the number of fatalities may induce a bifurcation that stabilizes a desirable state with low numbers of COVID-19 cases and associated deaths. The key characteristic feature of an infection dynamical system in this context is the eigenvalue that determines the stability of the states under consideration and is known in synergetics as the order parameter eigenvalue. Using a SEIR-like infection disease model, the relevant order parameter and its eigenvalue are determined. A three stage methodology is proposed to track and estimate the eigenvalue through time. The method is applied to COVID-19 infection data reported from 20 European countries during the period of January 1, 2020 to June 15. It is shown that in 15 out of the 20 countries the eigenvalue switched its sign suggesting that during the reporting period an intervention bifurcation took place that stabilized the desirable low death state. It is shown that the eigenvalue analysis also allows for a ranking of countries by the degree of the stability of the infection-free state. For the investigated countries, Ireland was found to exhibit the most stable infection-free state. Finally, a six point classification scheme is suggested with groups 5 and 6 including countries that failed to stabilize the desirable infection-free low death state. In doing so, tools for assessing the effectiveness of government interventions are provided that are at the heart of bifurcation theory, in general, and synergetics, in particular.

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1. Introduction
The COVID-19 pandemic has produced within a six months period from the end of December 2019 to end of June 2020 more than 10,000,000 confirmed cases and more than 500,000 COVID-19 associated deaths [1]. As of July 2020, in some countries the local COVID-19 epidemic subsided. However, worldwide the pandemic is still rapidly evolving. The case numbers and the associated deaths are increasing. From a nonlinear physics perspective, the spread of the COVID-19 disease is a bifurcation away from an unstable fixed point characterized by zero infected individuals. Government intervention that aim at reducing the spread of the disease may induce a “reversing” bifurcation that stabilizes a new fixed point that in the idealized case exhibits again zero infected individuals. In view of the severity of the pandemic, a better understanding of this bifurcation perspective is desirable.
Mackey and Glass [2] motivated the notion that on the level of individuals diseases emerge via bifurcations. In clinical psychology, for example, mood disorders [3–6] and, in particular, schizophrenia [7] have been studied from this bifurcation perspective (for a short review see e.g. [8]). The healthy state of an individual is described in terms of an appropriately defined n-dimensional dynamical system and is given in terms of an attractor [8]. The disease makes the state unstable and a bifurcation to the disease state occurs [8]. Importantly, such bifurcations may exhibit a single eigenvalue that changes its sign from a negative to a positive value. If so, the eigenvalue comes with an eigenvector that describes the direction in the aforementioned n-dimensional state that dominates at least initially the disease dynamics. Within the framework of synergetics [8–10], it is pointed out that the eigenvector, its eigenvalue, and the dynamics along the eigenvector characterizes the overall dynamics. In this context, the eigenvector is called the
order parameter $\psi$ [8–12]. Mathematically speaking, the order parameter $\psi$ is the eigenvector related to the eigenvalue $\lambda$ that becomes positive at the bifurcation point. It has been suggested that this bifurcation perspective does not only apply to the emergence of a disease but also to the successful treatment of a disease. Accordingly, a treatment bifurcation takes place that brings the individual from the disease state either back to the original healthy state or to a new kind of healthy state [8].

This bifurcation perspective also applies to the emergence of infectious diseases such as COVID-19 and to interventions that aim at stopping the spread of the diseases. Fig. 1 illustrates two scenarios in this context. On the left, the healthy states affected by the virus are shown. In the very bottom part of Fig. 1, the state is characterized in terms of eigenvalues. In what follows, we will only consider the case in which there is a single eigenvalue that is positive. In fact, this case applies to the infection disease compartment model that will be discussed in Section 2. As mentioned above, the positive eigenvalue plays a key role for the infection disease dynamics. Note that the remaining eigenvalues are assumed to be negative but there might be some eigenvalues that equal zero. On the right, the final states of the two scenarios are shown. These states are assumed to be stable. They are characterized again by eigenvalues. For the stable states all eigenvalues are negative or zero. The healthy states shown on the left of Fig. 1 corresponds to the disease-free states with zero infected individuals [13–15]. If a population has been infected by a novel virus, typically, these disease-free states are unstable [13,14]. Consequently, as shown in the top part of Fig. 1 the infection dynamics evolve away from the unstable fixed point. In the context of COVID-19 infection dynamics, much research has been devoted to document the instability of the infected state on the basis of data from confirmed COVID-19 cases. To this end, the so-called basic reproduction ratio has been estimated. For example for various regions of China under various different scenarios values in the range from 1.7 to 4.7 have been derived [16–22]. Such values larger than one can be taken as evidence for an instability [13,14]. Without intervention, the COVID-19 epidemic in a country under consideration would claim more and more cases and there would be an dramatic number of COVID-19 associated deaths. This scenario is depicted in the top part of Fig. 1 and will be described in somewhat more detail in Section 2. The stable fixed point of the COVID-19 infection dynamics under this scenario is referred to as a high death state. In contrast, when governments enforce intervention measures that aim to reduce the spread of the disease, the intervention scenario shown in Fig. 1 is likely to take place. While initially the infection dynamics evolves towards the high death state, after a certain period the intervention measure show an effect. In particular, they are assumed to affect the positive eigenvalue and shift it towards a negative value. Consequently, a treatment or intervention bifurcation takes place in which the infection dynamics converges to a state that features a relative low number of COVID-19 cases and, importantly, a relative low number of COVID-19 associated death. In Fig. 1 this stable state is referred to as low death state.

Taking this bifurcation perspective, it would be desirable to track and estimate the eigenvalue of the order parameter over time to support the validity of the intervention scenario shown in Fig. 1. In fact, attempts in this direction have been conducted for the aforementioned basic reproduction ratios [23]. In Section 2 an extended SEIR model will be introduced. For the model the order parameter and its eigenvalue will be determined. It will be shown how to track and estimate the eigenvalue through time by decomposing the course of a given COVID-19 epidemic into three stages. In Section 3 eigenvalues will be determined for COVID-19 infection data observed in 20 European countries. Time constants related to those eigenvalues will be determined as well. The countries will be compared with respect to the characteristics of their COVID-19 epidemics given in terms of eigenvalues and time constants. Importantly, it will be shown that the hypothesized sign change from a positive to a negative eigenvalue (see the intervention scenario in Fig. 1) can in fact be observed at least for some of the investigated countries.

2. Infection disease modeling, order parameter, and eigenvalue

2.1. Extended SEIR model and high death state

The SEIR model [13,15] is an extension of the Kermack-McKendrick SIR model [24] and involves the populations of susceptible (S), exposed (E), and infected (I) individuals. Traditionally, the population denoted by $R$ describes recovered individuals [15]. In line with various studies on COVID-19 infectious dynamics [17], $R$ will be interpreted in a more general sense as removed individuals in the sense that they cannot infect others. In this context, the following sub-populations that all belong to the group of removed individuals are introduced: exposed individuals recovered ($R_e$), infected individuals recovered ($R_i$), individuals diagnosed with COVID-19 and removed (e.g., hospitalized or quarantined) but not recovered or deceased ($R_{e0}$), diagnosed individuals recovered ($R_{i+}$) and diagnosed individuals deceased ($R_{i-}$). Accordingly, the evolution equations for the extended SEIR model reads

\[
\begin{align*}
\frac{dS}{dt} &= -\beta_1 \frac{ES}{N} - \beta_2 \frac{IS}{N} \\
\frac{dE}{dt} &= \beta_1 \frac{ES}{N} + \beta_2 \frac{IS}{N} - (\alpha + \gamma_2)E \\
\frac{dI}{dt} &= \alpha E - (\gamma_1 + \gamma_3)I \\
\frac{dR_e}{dt} &= \gamma_2 E \\
\frac{dR_i}{dt} &= \gamma_1 I \\
\frac{dR_{e0}}{dt} &= \gamma I - (a + b)R_{e0} \\
\frac{dR_{i+}}{dt} &= aR_{i+} \\
\frac{dR_{i-}}{dt} &= bR_{i-} \\
\end{align*}
\]

(1)

Here $N$ is the population size defined by the sum of the individuals of all populations except for the deceased individuals: $N = N + IS + I + R_e + R_i + R_{e0} + R_{i+}$. Consequently, we have $N(t) + R_{i-}(t) = N_0$, where $N_0$ is constant. In Eq. (1) we follow recent sug-
gestions according to which both exposed and infected individuals can infect susceptible individuals [17]. All parameters \( \beta_1, \beta_2, \alpha, \gamma, \gamma_c, \rho, b \) are semi-positive and \( t \) denotes time. We have contact rate between exposed and susceptible individuals \((\beta_1)\), contact rate between infected and susceptible individuals \((\beta_2)\), rate of progression from being exposed to being infected \((\alpha)\), recovery rate of exposed \((\gamma_e)\) and infected \((\gamma_I)\) individuals, diagnoses rate \((\gamma_C)\), and finally recovery rate of diagnosed individuals \((\alpha)\) and death rate of diagnosed individuals \((b)\). The total population of individuals diagnosed with COVID-19 is \(N_t = R_{C,0} + R_{C,1} + R_{C,2} \ldots\). From Eq. (1) we obtain \(dP_C/dt = \gamma_C I\). The healthy state of the whole population under consideration corresponds to a fixed point of the model defined by \(S_t = N_0\) and all other variables zero. The case is considered in which the population is perturbed out of the healthy state due to the SARS-CoV-2 virus. Importantly, the healthy state is considered to be an unstable fixed point [13,14] such that the perturbation increases in the amount leading to an epidemic in the country under consideration. As mentioned in the introduction this evolution away from the unstable fixed point may be considered as a disease bifurcation [25] in analogy to diseases on the level of individuals that have been studied as bifurcations [2,8]. In general, the disease dynamics converge to a stable state (not necessarily an asymptotically stable state) with \(S_t = (1 - x)N_0\), \(I_t = E_t = 0\), \(R_{C,0} = 0\), and \(R_{C,1} + R_{C,2} + R_{C,3} + R_{C,4} \ldots = N_0\) with \(x \in (0, 1]\). Without government intervention the parameters \(\beta_1, \beta_2, \gamma_C\) are assumed to be constants like \(\beta_1 = \beta_{1,0}, \beta_2 = \beta_{2,0}, \gamma_C = \gamma_{C,0}\). In this case, the number of individuals deceased due to COVID-19 is given by \(R_{C,\ldots} = \rho_0 N_0\) with \(\rho_0 \in [0, 1]\). This state will be defined as the high death state mentioned in Fig. 1.

2.2. Impact of government interventions and three stages of infection dynamics

Government interventions are assumed to affect transmission parameters \(\beta_1, \beta_2\) and the diagnosis rate \(\gamma_C\) like \(\beta_1 = \beta_{1,1} < \beta_{1,0}, \beta_2 = \beta_{2,1} < \beta_{2,0}\) and \(\gamma_C = \gamma_{C,1} > \gamma_{C,0}\). That is, the contact rates decay, for example, due to measures like physical distancing (social distancing) and wearing face masks and the diagnoses rate increase, for example, due to increased COVID-19 testing. These parameter changes imply that the disease dynamics converges to a stable fixed point with \(R_{C,\ldots} = \rho_0 N_0\) and \(\rho_0 < \rho_0\). This state will be referred to as low death state, see Fig. 1 again.

In what follows, a parsimony approach will be pursued. Accordingly, the focus is on the fact that the stability of a fixed point is determined by eigenvalues. Therefore, while it is of interest to study how interventions change specific model parameters such as \(\beta_1, \beta_2, \gamma_C\) in the present study, the focus is on the change of eigenvalues. As will be shown in the subsequent section, Section 2.3, this is motivated by the fact that the eigenvalues of interest depend, in general, on the SEIR model parameters and, in particular, on the parameters \(\beta_1, \beta_2, \gamma_C\). In this context, infection dynamics will be split into three stages and the eigenvalues in these stages will be determined. The stages will be defined using a data-driven approach. Accordingly, we define stages on the basis of epidemiological data, namely, the number of individuals diagnosed with COVID-19 in a country of interest. These reported COVID-19 cases correspond in the model to the variable \(P_C\). The graph of cumulative COVID-19 cases frequently follows a sigmoid curve [26]. Consequently, stage 1 will be defined as an approximately exponential increase (i.e., a first bend) of \(P_C\) as function of time \(t\). Stage 2 will be defined as linear increase of \(P_C\). Finally, stage 3 will be defined as the convergence towards the low death stationary state (which means that the \(P_C(t)\) graph exhibits a second bend) with \(dP_C/dt > 0\) but \(d^2P_C/dt^2 < 0\).

2.3. Extended SEIR model, eigenvalues, and intervention bifurcation

In order to determine eigenvalues from reported COVID-19 case data and use a semi-analytical approach, we will make two simplifying assumption. In this section, we address the first simplifying assumption. The second assumption will be discussed in Section 2.4. The first assumption is that \(S \approx N \approx N_0\) holds. That is, the change of the number of susceptible individuals over the observation period of interest due to the infection dynamics can be neglected in a first approximation. For example, Germany with a population of approximately 80,000,000 has reported about 200,000 COVID-19 cases beginning of July 2020 [27]. Although the number of 200,000 COVID-19 cases within a relative short period of less than half a year is a dramatic number, using these two approximative numbers (80,000,000 and 200,000) the COVID-19 cases correspond only to 2.5 permille of the whole population. Therefore, in a first approximation, the number of susceptibles may be considered to be constant. In a similar vain, the difference between \(N\) and \(N_0\), which is given by the number of COVID-19 associated deaths \((P_{\ldots})\), may be neglected in a first approximation. Taking the example of Germany, about 9000 deaths have been reported on July 2, 2020 [27]. Again, this is indeed a tragic number. However, if we put initially \(N = N_0 = 80,000,000\) then the decay of \(N\) due to those COVID-19 cases can be neglected in a first approximation. In line with those considerations, we put \(S = N\). In this case, from Eq. (1) it follows that the disease dynamics for \(E\) and \(I\) reads

\[
\frac{d}{dt}E = \beta_1 E + \beta_2 I, \quad \frac{d}{dt}I = \alpha E - \gamma_I I
\]

with \(\beta_1 > (\alpha + \gamma_E)\) and \(\gamma_I = \gamma_I + \gamma_C\). The eigenvalues of the dynamical system defined by Eq. (2) read

\[
\lambda_{1,2} = \frac{\beta_1 - \gamma_I}{2} \pm \sqrt{\left(\frac{\beta_1 - \gamma_I}{2}\right)^2 + \frac{(\beta_1 - \gamma_I)^2}{4} + \beta_1 \gamma_I + \beta_2 \alpha},
\]

where \(\lambda_1\) and \(\lambda_2\) refer to the upper (+) and lower (−) sign. Note that \(\lambda_{1,2}\) are real. Introducing the effective contact rate \(\beta_{eff} = \beta_1 + \alpha \beta_2 / \gamma_I\), a detailed calculation shows that the following stability properties hold. For \(\beta_{eff} > \alpha + \gamma_E\) we have \(\lambda_{1,2} > 0, \lambda_2 < 0\) and the fixed point \(E = I = 0\) is a saddle point. In contrast, for \(\beta_{eff} < \alpha + \gamma_E\) we have \(\lambda_1 < 0, \lambda_2 < 0\). That is, \(E = I = 0\) is a stable node. Consequently, for \(\beta_{eff} < \alpha + \gamma_E\) we have \(\lambda_1 < 0, \lambda_2 < 0\) and the infection dynamics system is at the bifurcation point between an unstable and stable fixed point.

From those considerations it follows that changes of the COVID-19 disease parameters \(\beta_1, \beta_2, \gamma_C\) due to government interventions affect the value of the effective parameter \(\beta_{eff}\). We will show in Section 3 that consistent with reported COVID-19 cases data, one can make the assumption that \(\beta_{eff}\) changes due to the impact of interventions from \(\beta_{eff} > \alpha + \gamma_E\) to \(\beta_{eff} = \alpha + \gamma_E\) to \(\beta_{eff} < \alpha + \gamma_E\). This implies that \(\lambda_1\) goes from \(\lambda_1 > 0\) to \(\lambda_1 = 0\) and \(\lambda_2 < 0\). If so, according to the infection dynamics model considered in the present study, government intervention induce a bifurcation that stabilizes the fixed point \(E = I = 0\) and causes the disease dynamics to converge to the fixed point of the low death state defined above.

2.4. Eigenvalue parameter estimation for three stages

Using the theory of self-organization [28], in general, and synergetics [8,9], in particular, the dynamics of the variables \(E\) and \(I\) can be expressed in terms of the eigenvectors \(v_1\) and \(v_2\) of the fixed point \(E = I = 0\) like

\[
\begin{align*}
E(t) \\
I(t)
\end{align*} = A_1(t) v_1 + A_2(t) v_2
\]
The eigenvectors $v_1$, $v_2$ exhibit components along the axes $E$ and $I$ like $v_1 = (v_{1E},v_{1I})^T$ and $v_2 = (v_{2E},v_{2I})^T$. For an explicit definition of the components in terms of model parameters $\beta_1, \beta_2, \alpha, \gamma^*$ see e.g. Ref. [29]. The time-dependent variables $A_1$ and $A_2$ are referred to as amplitudes [8,9]. From Eq. (2) it follows that

$$\frac{d}{dt} A_j = \lambda_j A_j$$

(5)

for $j = 1, 2$ holds, where $\lambda_j$ are defined by Eq. (3). Since $\lambda_1 > \lambda_2$ holds, we neglect the impact of $A_2$ in Eq. (4). Let us dwell on this issue. First of all, within the framework of synergetics, the variable $A_1$ is the dominant amplitude and $v_1$ is called order parameter and describes the dominant direction in which the $E - I$ dynamics evolves [8,9]. In this context, neglecting $A_2$ in Eq. (4) means to take only the dominant amplitude into account. Second, from a data fitting perspective, neglecting $A_2$ in Eq. (4) implies that we describe $E$ and $I$ by simple exponential functions rather than by a sum of two exponential functions. Therefore, neglecting the contribution of $A_2$ can be regarded as a parsimony approach for data fitting purposes. The COVID-19 case trajectories that will be discussed in Section 3 are relatively short trajectories with approximately 100 daily observations. This total observation period is decomposed into three stages and in each stage data fitting will be conducted separately. From a data fitting perspective, taking only $A_1$ into account, means that we do not attempt to capture much details of the trajectories under consideration in view of the fact that the trajectories are relatively short, in particular, when considering the fractions of the trajectories in each stage. In summary, the second simplifying assumption is that we can focus only on the contribution of the (order parameter or dominant) amplitude $A_1$ that is associated with the eigenvalue $\lambda_1$ that changes it sign from stage 1 to stage 3. Neglecting $A_2$ in Eq. (4), we obtain

$$I = gE$$

(6)

with $g = v_{1I}/v_{1E} > 0$. Consequently, the effective SEIR model dynamics reads

$$S = N_0, \quad \frac{d}{dt} E = \lambda E, \quad I = gE, \quad \frac{d}{dt} R = \gamma I = g^* E$$

(7)

with $g^* = gy_C$. Note that in Eq. (7) we dropped the index 1 of $A_1$. In what follows, the eigenvalue of the infection dynamics is understood as the eigenvalue of the order parameter or dominant dynamics (i.e., $\lambda_1$). Our two assumptions have the benefit that the COVID-19 cases function $P(t)$ can be described explicitly in all three stages. Let us denote the three stages by S.1, S.2, and S.3. From Eq. (7) we obtain

S.1. \quad t \in [t_0, t_1], \quad \lambda = \lambda_{S.1} > 0:

$$P(t) = P(t_0) + \frac{\gamma_{S.1} t(t_0)}{\lambda_{S.1}} (\exp(\lambda_{S.1}(t - t_0)) - 1)$$

(8)

S.2. \quad t \in [t_1, t_2], \quad \lambda = \lambda_{S.2} = 0:

$$P(t) = P(t_1) + \gamma_{S.2} t(t_1) (t - t_1)$$

(9)

S.3. \quad t \in [t_2, t_3], \quad \lambda = \lambda_{S.3} < 0:

$$P(t) = P(t_2) + \frac{\gamma_{S.3} t(t_2)}{\lambda_{S.3}} (1 - \exp(\lambda_{S.3}(t - t_2)))$$

(10)

3. Application to COVID-19 data of some European countries

3.1. Data and data fitting

The COVID-19 epidemic data from 20 European countries was analyzed: 19 countries belonged to the European Union. In addition, data from the United Kingdom was included in the analysis. The 19 European Union countries were selected as those countries that had a population of more than 5,000,000. Ireland was included in the list of 19 countries although the population of Ireland (approximately 4,900,000) was slightly below the 5,000,000 mark. In total, the following countries were considered: Austria, Belgium, Bulgaria, Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Italy, Ireland, Netherlands, Poland, Portugal, Romania, Slovakia, Spain, Sweden, and United Kingdom. Data from January 1, 2020, to June 15, 2020, was considered. June 15, was used as end date because around June 15, the countries of the European Union started to open their borders within the European Union [30]. Daily, cumulative reported COVID-19 cases were used as reported by the John Hopkins University [26].

For each country, COVID-19 cumulative cases were fitted to Eqs. (8)–(10) using a standard nonlinear fitting algorithm (S.1 and S.3) and linear regression analysis (S.2). In particular, $\lambda_{S.1}$ and $\lambda_{S.3}$ were estimated and the corresponding confidence intervals (CIs) were determined. If a confidence interval of a stage 3 eigenvalue $\lambda_{S.3}$ included zero, then the eigenvalue $\lambda_{S.3}$ was not significantly different from zero. Consequently, the country failed to stabilize in stage 3 the low death rate (at least up to June 15, 2020). For Bulgaria a negative value for $\lambda_{S.3}$ could not be determined because the COVID-19 trajectory followed a three stage pattern with an exponential increase (S.1), linear increase (S.2), and another exponential or at least nonlinear increase (S.3), see also Section 3.2. Therefore, Eq. (10) was replace by: $\lambda = \lambda_{S.3} > 0 : P(t) = P(t_0) + \gamma_{S.3} t(t_0) (\exp(\lambda_{S.3}(t - t_0)) - 1)/\lambda_{S.3}$, similar to the stage-1 equation. As far as the time points $t_0, t_1, t_2$ were concerned the following procedure was used. The time point $t_0$ of the beginning of stage 1 was defined as the time point for which there was at least 1 new reported infection on every day of the two weeks period following $t_0$. That is, $t_0$ was the first time point for which in the following two weeks a monotonic increase of COVID-19 cases was observed. The time points $t_1$ and $t_2$ were varied with the constraint $t_2 > t_1 > t_0$ and for each pair $t_1, t_2$ the model was fitted to the data. The final values of $t_1$ and $t_2$ were selected as those time points that produced the best fit to the data as measured in terms of the root-mean-square error.

3.2. Results

Fig. 2 shows the COVID-19 cases reported in the 20 European countries under consideration as functions of time (gray circles) and the model fits $P(t)$ (solid black lines) as obtained from Eqs. (8)–(10). For illustration purposes, the countries have been divided into four groups shown in panels A,B,C,D. The countries within a group showed similar numbers of COVID-19 cases as of June 15, 2020. Note that the graphs differed in total duration because in general the parameter $t_0$ varied across countries. Panel A shows the five countries with the highest numbers of reported COVID-19 cases as of June 15, in the range from 200,000 (France and Germany) to 270,000 (UK). The second group of countries is presented in panel B with diagnosed COVID-19 cases as of June 15 in the range from 30,000 (Poland) to 60,000 (Finland). Panel C shows the graphs for the third group of countries with 8000 (Austria) to 25,000 (Ireland) cases. Panel D shows the remaining five countries that reported on June 15, between 2000 (Slovakia) and 7000 (Finland) cases. On the scales presented in panels A, B, C, D the model fits $P(t)$ (solid lines) captured the characteristic features of the observed trajectories (at least by visual inspection). In particular, the third stages with the deaccelerating increase of cumulative cases was visible for various countries. Exceptions in this regard were Poland, Sweden, and Portugal (panel B) as well as Romania (panel C) and Bulgaria (panel D). The four countries Poland, Sweden, Portugal, and Romania exhibited still a linear increase of the cumulative COVID-19 cases in the weeks preceding June 15, (panels B and C). Bulgaria showed an exponential or nonlinear increase in this period (panel D).
**Table 1**

| Country     | Eigenvalues [1/d] | Time constants [d] |
|-------------|-------------------|-------------------|
|             | Stage 1 CI        | Stage 3 CI        | Stage 1 | Stage 3 |
| Austria     | 0.15 [0.140,0.17] | −0.035            | [−0.038,−0.032] | 6.62    | 28.46   |
| Belgium     | 0.12 [0.110,0.14] | −0.041            | [−0.042,−0.039] | 8.10    | 24.66   |
| Bulgaria    | 0.014 [0.010,0.018] | 0.10 pos.        | [0.090,0.11]   | 72.41   | 10.27   |
| Czech R.    | 0.14 [0.130,0.15] | −0.012            | [−0.013,−0.010] | 7.28    | 86.95   |
| Denmark     | 0.054 [0.050,0.059] | −0.040           | [−0.041,−0.039] | 18.38   | 24.95   |
| Finland     | 0.046 [0.042,0.051] | −0.046           | [−0.048,−0.043] | 21.51   | 21.83   |
| France      | 0.051 [0.043,0.059] | −0.035           | [−0.038,−0.032] | 19.75   | 28.67   |
| Germany     | 0.18 [0.170,0.19] | −0.045            | [−0.046,−0.044] | 5.47    | 22.31   |
| Greece      | 0.04 [0.03,0.05]  | −0.027            | [−0.029,−0.024] | 25.21   | 37.65   |
| Hungary     | 0.062 [0.075,0.089] | −0.034           | [−0.036,−0.033] | 12.23   | 29.16   |
| Ireland     | 0.064 [0.058,0.069] | −0.063           | [−0.064,−0.061] | 15.69   | 15.98   |
| Italy       | 0.124 [0.117,0.131] | −0.045           | [−0.046,−0.044] | 8.06    | 22.19   |
| Netherlands | 0.128 [0.123,0.133] | −0.028           | [−0.030,−0.026] | 7.83    | 35.21   |
| Poland      | 0.115 [0.105,0.120] | −0.0006 n.s.     | [−0.005,0.003] | 8.72    | N.A.    |
| Portugal    | 0.086 [0.075,0.097] | −0.0002 n.s.     | [−0.002,0.002] | 11.64   | N.A.    |
| Romania     | 0.15 [0.140,0.16]  | −0.0007 n.s.     | [−0.003,0.002] | 6.79    | N.A.    |
| Slovakia    | 0.045 [0.040,0.049] | −0.032           | [−0.036,−0.028] | 22.42   | 31.52   |
| Spain       | 0.089 [0.078,0.099] | −0.030           | [−0.033,−0.027] | 11.29   | 33.43   |
| Sweden      | 0.081 [0.077,0.084] | −0.011 n.s.      | [−0.034,0.011] | 12.41   | N.A.    |
| UK         | 0.15 [0.140,0.16]  | −0.0365          | [−0.0371,0.0358] | 6.66    | 27.41   |

Table 1 presents the eigenvalues and their confidence intervals for stage 1 and 3 for all countries. As mentioned in Section 3.1, if for a stage 3 eigenvalue the confidence interval included zero, then the eigenvalue was regarded as not to be different from zero in a statistically significant sense. This is indicated in Table 1 by “n.s.”. The inverse of an eigenvalue describes a time constant that provides a more appealing measure of speed of the infection dynamics as the eigenvalue itself. For stage 1 a small time constant (large eigenvalue) means a quick exponential increase. For stage 3 a small time constant (large eigenvalue) means a good stabilization of the desirable low death state and a fast approach of the infection dynamics toward that fixed point. Table 1 presents those time constants in the two final columns.

Most importantly, columns 2 and 4 of Table 1 include the sign of the eigenvalues in stages 1 and 3. For all countries eigenvalues were positive in stage 1, as expected. For most countries eigenvalues were negative in stage 3, consistent with the notion that in those countries government interventions caused a stabilization of the low death state with $I_d = E_d = 0$. Table 1 supports the discussion made above in the context of Fig. 2 about countries in which interventions failed to stabilize the fixed point $I_d = E_d = 0$ as of June 15. Accordingly, the infection dynamics in Bulgaria showed a statistically significant positive eigenvalue in stage 3. The COVID-19 dynamics in the three countries Poland, Portugal, and Romania showed negative eigenvalues that were much smaller in the amount than those of the remaining countries. The confidence intervals indicate that those eigenvalue $\lambda_{5,3}$ were not statistically significant different from zero. This implies that as of June 15, the infection dynamics still followed a linear increase. The eigenvalue $\lambda_{5,3}$ for Sweden was negative and in the same range as the eigenvalue $\lambda_{5,3}$ of the Czech Republic ($−0.011/d$ versus $−0.012/d$). However, while for the Czech Republic the eigenvalue was statistically significant different from zero, this was not the case for Sweden. Stage 3 time constants were not reported for countries that
showed a linear increase in stage 3 in the sense of an eigenvalue \( \lambda_{33} \) being not statistically significant different from zero (i.e., for Poland, Portugal, Romania, and Sweden).

Fig. 3 presents a graphical way the stage 1 and 3 eigenvalues for all countries. Countries were sorted according the amount of their stage 3 eigenvalues. Recall that the larger the eigenvalue is in the amount, the more stable is the desirable fixed point \( I_0 = E_0 = 0 \) of the low death state. The country with the most stable fixed point was Ireland. Fig. 3 documents in a graphical way the presence or absence of an intervention bifurcation. An intervention bifurcation means that the positive eigenvalue \( \lambda \) from stage 1 becomes negative in stage 3 presumably due to the intervention measures enforced by a government (and not due to a decay of the number of susceptible individuals, see our discussion about the assumption \( S = N_0 \)). Fig. 3 illustrates that the countries listed in-between Ireland and the Czech Republic (including those two countries) were able to induce intervention bifurcations. As far as Sweden is concerned, although in line with Table 1, Fig. 3 shows a switch from a positive stage 1 to a negative stage 3 eigenvalue, the statistical analysis reported above suggests that the infection dynamics in Sweden did not exhibit an intervention bifurcation up to June 15. Furthermore, Fig. 3 illustrates that the COVID-19 disease dynamics in Romania, Poland, and Portugal did not exhibit an intervention bifurcation. The epidemic in Bulgaria showed a switch back to a stage 1 like dynamics with a positive eigenvalue in stage 3.

The discussion so far allows us to classify the countries qualitatively and quantitatively. Qualitatively, we can distinguish between countries whose infection dynamics exhibited or did not exhibit a bifurcation. Quantitatively, we may use the stage 3 time constant in order to group those countries with bifurcation into classes. Table 2 suggests a classification along those ideas. Accordingly, groups 1 to 4 are countries that were able to stabilize by the time of June 15, the low death state \( E_0 = I_0 = 0 \). Groups 1 to 4 are distinguished by the magnitude of stabilization as measured by the stage 3 time constant. For the first group of countries with time constants smaller than 20 days only one country qualified: Ireland. In the second group featuring longer time constants between 20 and 30 days we found nine countries (see Table 2). In the third group with even weaker low death fixed point attractors as characterized by time constants in the range of 30 to 40 days we found four countries (see Table 2). The Czech Republic is considered as its own group, group 4, because of its extremely weak attractor \( E_0 = I_0 = 0 \), which comes with an extremely long time constant of about 87 days. Groups 5 and 6 are the countries in which interventions were not able to stabilize the fixed point \( E_0 = I_0 = 0 \) of the low death state by the time of June 15 (at least as suggested by the analysis presented in the present study). Countries of group 5 exhibited as of June 15, a linear increase suggesting an eigenvalue close to zero. Four countries of this kind were identified. Finally, Bulgaria with its nonlinear increase in COVID-19 cases in the weeks around June 15, is its own group: group 6.

4. Conclusions

COVID-19 infection dynamics was discussed from the perspective of bifurcation theory and in line with the notion of the emergence of diseases and the successful treatment of diseases as bifurcations [2,8]. Accordingly, the initial stage of a local COVID-19 epidemic was considered as a bifurcation away from an unstable healthy state of zero infected individuals. Without interventions the disease dynamics would settle down in a stable fixed point with a high number of COVID-19 cases and related to that a high number of COVID-19 associated deaths. In contrast, it was argued that that government interventions may induce a second (“reversing”) bifurcation such that the disease dynamics converges to a stable fixed point with relatively low numbers of COVID-19 cases and COVID-19 associated deaths. Simplifying an appropriately defined infection dynamics compartment model, the key eigenvalue was identified that changes its sign at such an intervention bifurcation. The eigenvalue was estimated for the epidemics observed in 20 European countries on the basis of reported COVID-19 cases. Evidence was found that in 15 of those 20 countries the interventions successfully induced a bifurcation and stabilized the desirable fixed point of the low death state. As a by-product the countries whose infection dynamics exhibited an intervention bifurcation could be ranked as shown in Fig. 3 on the basis of the degree of stability of the desired infection-free fixed point. Ireland was the leading country in this regard. The quasi-continuous ranking also allowed us to suggest a classification into groups as presented in Table 2. While the suggested specific values for the group boundaries are open for debate, the overall grouping of the countries is not much affected by the choice of the boundaries in view of the quasi-continuous ranking illustrated in Fig. 3. Future research may be devoted to identify predictors for the ranking based on eigenvalue stability parameters. Such predictors could be used to improve the effectiveness of government interventions. In particular, they might be used to deal with second wave COVID-19 outbreaks.

The bifurcation theoretical perspective does not replace the traditional epidemiological perspective that puts emphasize on the basic reproduction ratio [13,15]. Rather, the bifurcation theoretical perspective presented in the present study supplements traditional perspectives. It sketches a universal framework according to which diseases both on the level of individuals and populations satisfy similar principles. Identifying such overarching common principles.
seems to be as important as understanding the peculiarities of a specific disease or a specific virus epidemic/pandemic at hand.

**Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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