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On Parameter Identifiability in Network-Based Epidemic Models

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Abstract

Modelling epidemics on networks represents an important departure from classical compartmental models which assume random mixing. However, the resulting models are high-dimensional and their analysis is often out of reach. It turns out that mean-field models, low-dimensional systems of differential equations, whose variables are carefully chosen expected quantities from the exact model provide a good approximation and incorporate explicitly some network properties. Despite the emergence of such mean-field models, there has been limited work on investigating whether these can be used for inference purposes. In this paper, we consider network-based mean-field models and explore the problem of parameter identifiability when observations about an epidemic are available. Making use of the analytical tractability of most network-based mean-field models, e.g. explicit analytical expressions for leading eigenvalue and final epidemic size, we set up the parameter identifiability problem as finding the solution or solutions of a system of coupled equations. More precisely, subject to observing/measuring growth rate and final epidemic size, we seek to identify parameter values leading to these measurements. We are particularly concerned with disentangling transmission rate from the network density. To do this, we give a condition for practical identifiability and we find that except for the simplest model, parameters cannot be uniquely determined, that is, they are practically unidentifiable. This means that there exist multiple solutions (a manifold of infinite measure) which give rise to model output that is close to the data. Identifying, formalising and analytically describing this problem should lead to a better appreciation of the complexity involved in fitting models with many parameters to data.

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1 Introduction

Differential-equation-based models are widespread in modelling population dynamics be that in problems arising in ecology, evolution or epidemiology (Anderson and May 1992; Blasius et al. 2007; Diekmann and Heesterbeek 2000; Kiss et al. 2017). Such systems are relatively straightforward to set up and the theory of dynamical systems offers tools to analyse them. Over the past two decades, differential-equation-based models have gained a lot of popularity in modelling epidemics on networks (Porter and Gleeson 2016; Kiss et al. 2017). Such models, often referred to mean-field models, aim to approximate the expected behaviour of some quantities of interest (e.g. expected number of infected individuals in time) and rely on closure assumptions which are needed to produce tractable systems.

The major difference between mean-field models arising from modelling epidemics on networks and classic compartmental models is that in the former the assumption of homogeneous random mixing between individuals can be relaxed. This sometimes comes at the expense of having to keep track of multiple variables, such as the number of nodes with different number of contacts (Pastor-Satorras and Vespignani 2001) and different disease status or write down differential equations for all nodes in the network (Van Mieghem et al. 2008). The complexity of such network-based mean-field models is highly dependent on the heterogeneity in the contact network and how the modelling is performed. For example, the edge-based compartmental model (Miller et al. 2012) is able to retain all the information about the distribution of contacts in the form of the corresponding probability generating function and the resulting system consists of one single differential equation. While such models have been studied extensively and have provided the means to understand the impact of contact heterogeneity on the epidemic threshold, final epidemic size and other epidemic characteristics, there has been relatively little work on using such models for inference purposes. For example, often information about the network of contacts is not available or patchy. Hence, placing such models in an inference framework where network parameters are inferred along disease dynamic parameters may reveal important information about the underlying contact network which can be used for the design and implementation of control measures.

Many of the network-based mean-field models provide explicit or implicit analytical expressions for quantities such as the basic reproduction number (or leading eigenvalue based on the linear stability analysis around the disease-free steady state), timing and/or peak prevalence, final epidemic size etc. Hence, given a synthetic or real epidemic and being able to measure a number of the aforementioned quantities, it is of interest to investigate whether parameters of the epidemic model, including that of the contact network, that generated the data can be inferred or determined. In this paper, we focus on the pairwise (Keeling 1999) and the edge-based compartmental model (Miller et al. 2012). These choices are motivated by the popularity and wide use of the pairwise model and the compact nature of the edge-based compartmental model.

Fitting epidemic models to synthetic or real-world data is of great interest as it allows us to infer model parameters which in turn helps us to (i) learn more about the disease, (ii) implement and test control scenarios via simulations, and (iii) make short- or long-term predictions about the epidemic (Chowell 2017; King et al. 2015). In many
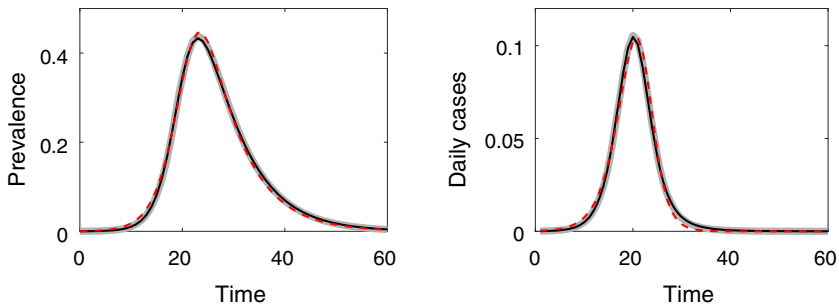
Fig. 1 (Color Figure Online) Illustration of how distinct pairs of average degree and transmission rate, (n, τ), lead to almost indistinguishable time evolution of the prevalence and daily new cases. Baseline values of the parameters are: average degree $n = 6$, $\tau = \gamma R_0/((n-1) - R_0) = 0.1429$, with $R_0 = 2.5$, rate of recovery, $\gamma = 1/7$, number of nodes $N = 10000$ and epidemic started with one infected individual, with the corresponding output shown by the thick grey lines. The black and red-dashed lines correspond to $(n, \tau) = (8.46, 0.09)$ and $(n, \tau) = (2.454, 1.091)$, respectively

cases, such models can and will be used for parameter estimation and prediction and can suffer of the well-known problem of parameter redundancy and unidentifiability (Cole 2019; Villaverde et al. 2016; Gallo et al. 2022). This problem has also been highlighted in network-based epidemic models, for example in Britton and O'Neill (2002). This problem is not model specific. For example, in Fig. 1, we show that for the pairwise model, Eqs. (3)–(6), it is possible to find distinct sets of parameters whereby the time evolution of prevalence and daily new cases are near indistinguishable. Of course this also implies that the initial growth rate and final epidemic size are also close. We note that this figure is for illustration purposes only. The pairwise model is discussed in the main body of the paper, and its full understanding in the context of the figure is not necessary.

Parameter identifiability can be considered in two different ways. On the one hand, different parameter values may lead to identical observations, which is called structural, or a priori unidentifiability (Anstett-Collin et al. 2020; Villaverde et al. 2016). On the other hand, the observations belonging to two sets of parameters can be very close to each other, referred to as practical unidentifiability, see e.g. (Wieland et al. 2021). Structural identifiability has been studied in several epidemic models. For example, in Roosa and Chowell (2019), the authors consider the problem of parameter identifiability in a number of increasingly complex compartmental epidemic models. As the number of states in the model increases so does the number of parameters. While the parameters remained identifiable, in particular the basic reproduction number, the uncertainty around the estimate increased in models with more parameters. The paper (Massonis et al. 2021) relates the identifiability problem to observability in a higher dimensional augmented system, and investigates structural identifiability in more than fifty compartmental epidemic models by using the formalism of observability-identifiability conditions. On the other hand in Gallo et al. (2022), the authors provide a framework to quantify how the uncertainty in the data affects the determination of the parameters and the evolution of the unmeasured variables of a given model. Their approach allows them to characterise different regimes of identifiability and argue that in some

cases, such as COVID-19 the lack of identifiability may prevent reliable predictions of the epidemic dynamics. Finally, in Villaverde et al. (2016), the authors argue that structural identifiability in every model should be checked before using the model for inference. But this is seldom done since it involves either complex analytical or numerical calculations.

In this paper, we show that practical unidentifiability is present in a number of network-based epidemic models. This is, however, not due to hidden or unmeasured variables. Moreover, our inference is making use of available analytical formulas for leading eigenvalue, or equivalently growth rate, and final epidemic size. While many of the previous works are concerned with local changes, that is, quantifying change in observations induced by a small local change in parameter values, we show that in our models varying the parameters globally leads to small local changes in measurement.

The paper is structured as follows. In Sect. 2, we describe the general mathematical approach and suggest some definition and ways to formalise the identifiability problem. In Sect. 3, we start with simple models such as the well-mixed susceptible-infected-recovered (SIR) compartmental model, followed by more complex models such as, the pairwise (Sect. 4), and the edge-based compartmental model (Sect. 5). We show that except for the simplest of models, there are clear parameter identifiability problems which we map out and explain analytically, where possible. In models with a larger number of parameters, it is often the case that many different combinations of the model parameters (with many individual parameters being far from their true values) result in output which is consistent with the true epidemic. Finally, we provide some discussion and future directions of research.

2 General Approach

We are given a system of ODEs involving some parameters:

$$\dot{x}(t) = f(x(t), \mu),$$

where $x(t) \in \mathbb{R}^n$ is the state vector of the system and $\mu \in \mathbb{R}^k$ is the vector of parameters. We observe a derived quantity (e.g. final epidemic size, growth rate) for which data is available. This is given by an observation function $h : \mathbb{R}^n \to \mathbb{R}^m$, i.e. the observation y is

$$y(t) = h(x(t), \mu).$$

The goal is to solve the inverse problem, namely to determine the parameter μ based on the observation $y(t)$; note that the observation does not need to be time dependent. This is line with the formulation of a general inverse problem, see (Cole 2019).

Our question here is parameter identification, namely to understand whether it may happen that the observations y and $\overline{y}$ corresponding to different parameters μ and $\overline{\mu}$ are identical or very close to each other. The first one is called structural (or a priori) unidentifiability, while the second one is referred to as practical unidentifiability, see

e.g. (Wieland et al. 2021). Our main focus here is practical identifiability, and hence we deal with structural identifiability only briefly.

The main idea of investigating structural identifiability can be explained as follows. Since the observation $y(t)$ is known for all time values in an interval, its derivatives are also known (measured). Differentiating the equation of the observation function and substituting $t = 0$ yields

$$\dot{y}(0) = h'(x(0), \mu) f(x(0), \mu)$$

that is an equation for the $n + k$ unknowns: the coordinates of $x(0)$ and those of μ. Hence we need further equations to determine the parameters. Differentiating $y(t)$ $n + k - 1$ times leads to $n + k$ equations for the $n + k$ unknowns. (Note that the zeroth-order derivative can also be used.) These derivatives are called the Lie derivatives of the output along the trajectories of the governing dynamical system. This system of equations is nonlinear, and hence its unique solvability is determined by the Jacobian matrix containing the partial derivatives with respect to the coordinates of $x(0)$ and those of μ. This matrix is called the Observability-identifiability Matrix, see e.g. (Massonis et al. 2021). The application of the implicit function theorem yields that the parameters can be locally uniquely determined if this matrix has full rank, i.e. the Observability-identifiability Condition (OIC) holds. More detailed approaches lead to slightly different definitions, the relationships of which are studied in Anstett-Collin et al. (2020). The OIC condition has been studied in the case of many compartmental epidemic models. An exhaustive summary is presented in Massonis et al. (2021). As an illustration of the results derived there, we mention that the traditional SIR model is structurally identifiable when the observation is the number of infected individuals, $I(t)$. However, in the more realistic case when one can observe only an unknown proportion of the infected individuals, $qI(t)$, the parameter q is not structurally identifiable. It is important to note that the definition of structural identifiability is related to Kalman's observability condition in an augmented system (where the phase space is extended by new artificial variables representing the parameters), see e.g. (Villaverde et al. 2016).

Let us turn now to the main focus of our study, practical identifiability, when significantly different parameter values yield observation which are almost identical. Generally speaking, defining practical identifiability, we use some ε accuracy of the observation. The accuracy of the observation can be measured in two different ways. The first is when the time dependence of the observation is known for all time values, or at least for an observation time-window and accuracy is defined as some norm of the difference of the two functions, see e.g. (Gallo et al. 2022; Wieland et al. 2021). The second is when we have formulas for some characteristic quantities of the observation. For example, the derivative of the quantity being observed at the initial instant, $\dot{y}(0)$, or its limit for large time, $y(\infty)$. These formulas typically involve the unknown parameter values and hence define a system of equations for them. We note that structural identifiability can be defined in this case as well, namely the parameters can be identified by the model, if this system can be uniquely solved for the parameters. We speak about practical unidentifiability when clearly distinct parameter values satisfy the above system of equations but with some small error.

This can be formulated as follows. Let the system of equations for the parameters take the form $F(\mu) = 0$. We call the problem structurally unidentifiable if the system of equations $F(\mu) = 0$ has more than one (typically infinitely many) solution. The problem is called practically unidentifiable if the system $|F(\mu)| < \varepsilon$ is satisfied by a large set of μ values for any $\varepsilon > 0$. In fact, we will show that in our cases the set of μ values solving $|F(\mu)| < \varepsilon$ has infinite measure. We note that this does not exclude that the equation $F(\mu) = 0$ has a unique solution.

This notion of unidentifiability is related but not identical to the question of sensitive dependence on parameters, which is a notion of local nature. That is expressed in terms of the Jacobian of F at the solution of $F(\mu) = 0$. The problem fits into the framework of error analysis and sensitivity analysis that are widely studied important fields of parameter inference. We refer the interested reader to Stigter and Molenaar (2015) and to the books (Cacuci et al. 2005; Einarsson 2005), in which both the introduction to the topic and elaborated examples are available.

Comparing our definition to those in Gallo et al. (2022), Wieland et al. (2021), the main novelty in ours is that the inequality $|F(\mu)| < \varepsilon$ holds globally in the parameter space. Another difference between our definition and previous ones is that both (Gallo et al. 2022; Wieland et al. 2021) infer parameters from the time dependence of the solutions, while we use exact (not numerical) formulas for some characteristic quantities (leading eigenvalue and final epidemic size). Hence, the parameter inference is done by solving a system of equations instead of fitting to time-dependent curves.

We apply this general theory to the SIR compartmental, pairwise and edge-based compartmental models when the observations are the leading eigenvalue at the disease-free steady state and the final epidemic size. We note that the leading eigenvalue of the disease-free steady state results from the linear stability analysis around it. The largest eigenvalue of the resulting Jacobian is the leading eigenvalue. For the three different models analysed in this paper, these are given in Eqs. (1), (7) and (18). The parameters to be determined, given these observations, are the infection rate τ, the recovery rate γ and the average degree of the underlying network, n. We will show that for these models (in fact for several other models as well) the leading eigenvalue can be expressed in terms of these parameters as

$$\lambda = \tau l(n) - \gamma,$$

where $l(n)$ is a linear function depending on the model. We will derive an implicit equation for the final epidemic size in each case. It will turn out that this implicit equation contains the parameters τ and γ linearly and n in a nonlinear way. The equation can be written in the form

$$\tau = A(n)\gamma$$

for all cases, where $A(n)$ is a nonlinear function.

The problem of parameter identification can be formulated as follows. Depending on the choice of the model, i.e. the choice of the functions $l(n)$ and $A(n)$, can the parameters be recovered by solving the two equations above? Since we have two equations for three parameter values, it is obvious that one of the parameters has to be

assumed to be given. The recovery rate is more appropriate for being a known value since it depends on epidemiological characteristics. While τ and especially n are more dependent on the behaviour of the agents and on the network, these are more difficult to determine. Our goal will be to solve the above equations for τ and n with a given value of γ and also with given initial conditions. (We note that the initial conditions could also be considered as parameters which makes the problem even more complicated in a real-life situation.)

These equations define two curves in the (n, τ) parameter plane. The parameter values leading to the desired values of the final size and leading eigenvalue can be obtained as the intersection point of the two curves. The main novelty of the paper is the observation that these curves are very close to each other, and hence relatively different parameter values may yield very similar final size and leading eigenvalue. Thus, noisy data may preclude the correct identification of the values of these parameters.

The above system is linear in τ and γ when n is considered to be known. Hence its solvability is easy to check by computing the determinant. For the sake of completeness, this will also be carried out below in each case.

3 Identifiability in the Compartmental SIR Model

The well-known SIR compartmental model takes the form

$$\dot{S} = -\tau n I \frac{S}{N},$$
$$\dot{I} = +\tau n I \frac{S}{N} - \gamma I.$$

Simple differentiation at the disease-free steady state ($S = N$, $I = 0$) yields that the leading eigenvalue is $\lambda = \tau n - \gamma$. On the other hand, the final epidemic size is given by the solution of the following implicit equation $R_\infty = N - S_0 \exp\left(-\tau n R_\infty / N \gamma\right)$ as it is given in (4.12) in Kiss et al. (2017). Let us assume, for sake of simplicity, that $S_0 = N$, that is, initially there are very few infected and recovered nodes. Then the final size equation can be rearranged to $-\tau n r_\infty = \gamma \ln(1 - r_\infty)$, where we introduced the fraction $r_\infty = R_\infty / N$.

Thus the system relating the measured characteristic quantities λ and R_∞ to the parameters, τ, γ and n takes the form

$$\tau n - \gamma = \lambda, \tag{1}$$
$$\tau n r_\infty + \gamma \ln(1 - r_\infty) = 0. \tag{2}$$

This system is linear in τ and γ, and hence apart from exceptional cases it has a unique solution for τ and γ if n is known and the characteristic quantities of the epidemic, λ and R_∞, are measured. That is, knowing/measuring the leading eigenvalue and final epidemic size, it is possible to uniquely determine τ and γ. However, the parameters τ and n cannot be obtained from this system, since only their product is determined by the equations. That is, knowing/measuring the leading eigenvalue and final epidemic

size, it is not possible to determine the infection rate τ and average degree n. This is the case of structural unidentifiability when the system of equations has infinitely many solutions (if it has a solution at all).

4 Identifiability in the Pairwise SIR Model

The pairwise model focuses on a hierarchical construction where expected number of nodes in state A at time t, $[A](t)$, depends on the expected number of pairs of various types (e.g. $[AB]$) and then, these in turn depend on triples such as $[ABC]$. Here the counting is done in all possible directions meaning that [SS] pairs are counted twice and and that [SI] = [IS]. With this in mind, the pairwise model becomes (see e.g. in Kiss et al. (2017))

$$[\dot{S}] = -\tau[\text{SI}]; \quad [\dot{I}] = \tau[\text{SI}] - \gamma[I]; \quad [\dot{R}] = \gamma[I],$$
$$[\dot{SI}] = -(\tau + \gamma)[\text{SI}] + \tau([\text{SSI}] - -[\text{ISI}]); \quad [\dot{SS}] = -2\tau[\text{SSI}].$$

This system is not self-consistent as pairs depend on triples and equations for these are needed. To tackle this dependency on higher-order moments, the triples in the equation above are closed using the following relation:

$$[\text{ASB}] = \kappa \frac{[\text{AS}][\text{SB}]}{[S]},$$

where $A, B \in \{S, I\}$. Common choices for κ are $(n-1)/n$ and 1. In Kiss et al. (2022), it was shown that both these closures are exact in the limit of large networks when the contact distribution is binomial and Poisson, respectively. We use the former as the average degree appears explicitly and is subject to inference. Applying $\kappa = \frac{n-1}{n}$ leads to

$$[\dot{S}] = -\tau[\text{SI}], \tag{3}$$

$$[\dot{I}] = \tau[\text{SI}] - \gamma[I], \tag{4}$$

$$[\dot{SI}] = -(\tau + \gamma)[\text{SI}] + \tau \frac{n-1}{n} \frac{[\text{SI}]([\text{SS}] - [\text{SI}])}{[S]}, \tag{5}$$

$$[\dot{SS}] = -2\tau \frac{n-1}{n} \frac{[\text{SS}][\text{SI}]}{[S]}, \tag{6}$$

which is now a self-contained system.

The leading eigenvalue, resulting from the linear stability analysis around the disease-free steady state, $([S], [I], [SS], [SI]) = (N, 0, nN, 0)$, can be easily computed from Eq. (3)-(6) as

$$\lambda = \tau(n-2) - \gamma. \tag{7}$$

An implicit equation for the final number of recovered and susceptible nodes can be derived as it is shown in Section 4.3.4 in Kiss et al. (2017), see also below

$$N(\tau + \gamma)(S_\infty)^{\frac{2}{n}} = N\gamma S_0^{\frac{1}{n}}(S_\infty)^{\frac{1}{n}} + \tau S_\infty S_0^{\frac{2}{n}}. \tag{8}$$

Equation (8) there yields the final number of susceptible nodes, $S_\infty = N - R_\infty$. Let us assume again, for sake of simplicity, that $S_0 = N$, that is, initially there are very few infected and recovered nodes. Then introducing $s_\infty = S_\infty/N$ in Eq. (8) leads to

$$\tau\left(s_\infty - s_\infty^{2/n}\right) + \gamma\left(s_\infty^{1/n} - s_\infty^{2/n}\right) = 0.$$

Thus the system relating the measured characteristic quantities λ and s_∞ to the parameters, τ, γ and n takes the form

$$\tau(n-2) - \gamma = \lambda, \tag{9}$$

$$\tau\left(s_\infty - s_\infty^{2/n}\right) + \gamma\left(s_\infty^{1/n} - s_\infty^{2/n}\right) = 0. \tag{10}$$

This system is linear in τ and γ, and hence apart from exceptional cases it has a unique solution for τ and γ if n is known and the characteristic quantities of the epidemic, λ and R_∞, are measured. That is, knowing/measuring the leading eigenvalue and final epidemic size, it is possible to uniquely determine τ and γ.

Let us turn now to the parameters τ and n. Now γ is considered to be given, and the characteristic quantities of the epidemic, λ and s_∞ are measured. We can express τ from the equations above yielding

$$\tau = \frac{\lambda + \gamma}{n - 2}, \tag{11}$$

$$\tau = \gamma\frac{s_\infty^{1/n} - s_\infty^{2/n}}{s_\infty^{2/n} - s_\infty}. \tag{12}$$

In order to show unidentifiability visually, let us plot the curves given by the above equations in the (τ, n) plane. We can see in Fig. 2 (bottom panel) that the two curves are practically indistinguishable. In fact, they have a single intersection point, i.e. the system has a unique solution, but any value of τ yields a value of n on the hyperbola-like curve, that is an approximate solution with high accuracy.

In fact the experiment that we setup here, and in some of the cases that follow, is that we start with a known set of parameters, often referred to as master set of values. These generate a particular numerical value for the lead eigenvalue, final epidemic size and time evolution of the prevalence or daily new cases. We then ask the questions: are there any other parameter combination (τ, n) that give rise to daily new cases in time that are similar to that obtained by using the master values? The top panel in Fig. 2 shows the Euclidean distance between the master daily cases vector and those resulting from (τ, n) pairs chosen between the bounds seen in the figure.

There are several important features to note about the surface showing the distances. First, there is a clear hyperbola-like valley of minimum points, where any choice of (τ, n) seems to be close enough to the output based on the master values. Several minima are observed which indicate that any kind of optimiser may struggle to find
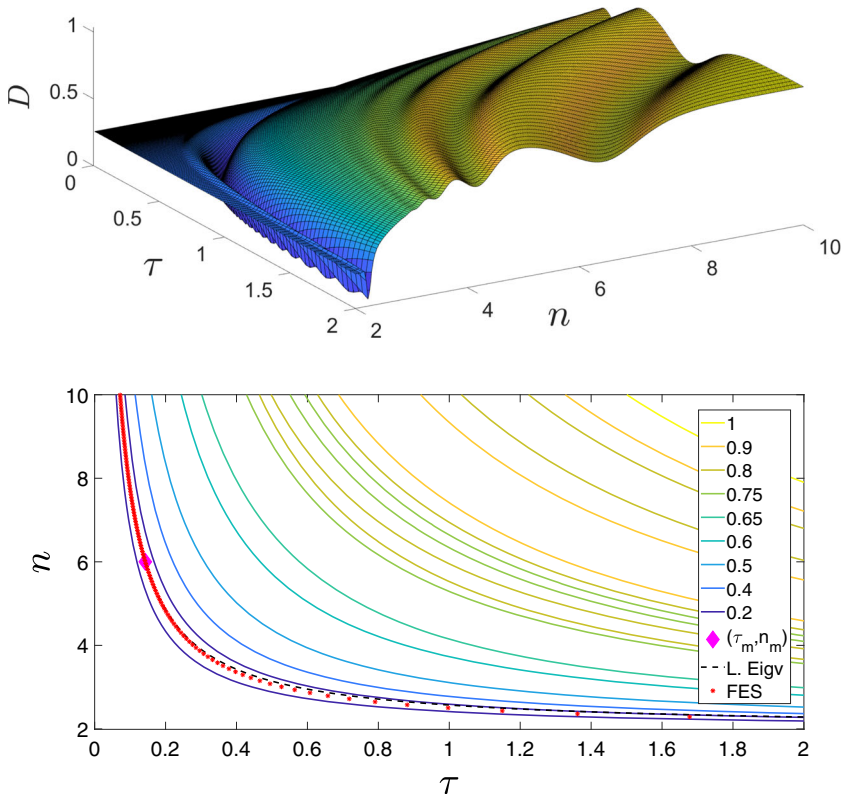
Fig. 2 (Color Figure Online) **Top panel:** illustration of the distance profile D between the daily new infections in time for a fixed set of values $(\tau_m, n_m) = (\gamma R_0/((n-1) - R_0) = 0.1429, 6)$ (magenta diamond), with $\gamma = 1/7$ and $R_0 = 2.5$, compared to daily new cases for different choices for the values of (τ, n) pair. Distance measured using an Euclidian norm scaled by the population size $N = 10000$. **Bottom panel:** the same as above as contour plot with two additional curves given by the equations for the lead eigenvalue (denoted as L. Eigv in the legend) and final epidemic size (denoted as FES in the legend) Eqs. (11) and (12), respectively, where the lead eigenvalue λ and s_∞ are calculated with (τ_m, n_m) as given above

the global optimum. Of course in this thought experiment, there is a unique (τ, n) pair that makes $D = 0$. However, given noisy observations, it is easy to see that any values along the hyperbola-like valley may return an acceptable fit, such as the one in Fig. 2.

The empirical experiment and observations above can be made more substantial by considering the bottom panel in Fig. 2. The contour plot is based on the same data as in the surface plot above but with the addition of two curves: that of the leading eigenvalue and final epidemic size, which have unique numerical values determined by the master values and fixed γ. It is clear that these two curves are indeed close to each other and that they capture the hyperbola-like valley of small values in distance.

Beyond this visualisation of unidentifiability, we formally prove it in terms of the definition given in Sect. 2. First, we reduce system (11)–(12) to a single equation as follows:

Fig. 3 (Color Figure Online)
Plots of function $f(n)$. For
different values of s_∞
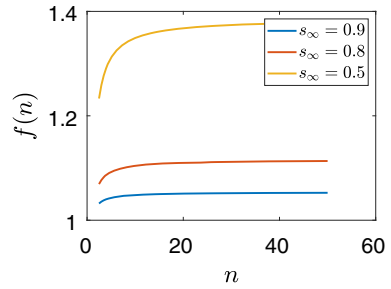
$$\lambda + \gamma = \gamma f(n),$$

where

$$f(n) = \frac{s_\infty^{1/n} - s_\infty^{2/n}}{s_\infty^{2/n} - s_\infty}(n - 2).$$

We can assume without loss of generality that the two curves have a common point, i.e. there is a value n^* of n satisfying $\lambda + \gamma = \gamma f(n^*)$. Otherwise, the measurement was so inaccurate that no values of τ and n could lead to the measured value of λ and s_∞. Thus the single equation to be solved for the unknown n takes the form

$$f(n) = f(n^*).$$

We will prove that this equation does not identify the value of n in the practical sense. In order to do so, we determine the characteristic properties of function f. These properties can be easily visualised by plotting the graph of the function for $n > 2$, see Fig. 3. It turns out that the function is very close to a constant and its value changes only slightly from $n = 2$ to infinity. For example, in the case $s_\infty = 0.9$, the functions grow from 1.027 (at $n = 2$) to 1.054 as n tends to infinity, so the function is constant with accuracy 0.027.

Simple application of L'Hospital's rule yields that the limits of f as n tends to 2 or to infinity exist and their values are

$$\lim_{n \to 2} f(n) = 2\frac{s_\infty - \sqrt{s_\infty}}{s_\infty \ln s_\infty} := f_2$$

$$\lim_{n \to \infty} f(n) = \frac{\ln s_\infty}{s_\infty - 1} := f_\infty$$

The next proposition expresses the fact that the measure of the range of this function is small.

Proposition 1 *There exists a number $0 < \bar{a} < 1$ such that $s_\infty > \bar{a}$ implies that f is increasing and $f_2 < f(n) < f_\infty$ for all $n > 2$. That is, the range of f is the interval (f_2, f_∞).*

Proof Introducing $a = s_\infty$, $x = 1/n$ and the function

$$g(x) = \frac{a^{2x} - a^x}{a - a^{2x}} \left(\frac{1}{x} - 2 \right),$$

we have $f(n) = g(1/n)$, leading to $f'(n) = -g'(1/n) \frac{1}{n^2}$. Hence it is enough to prove that $g'(x) < 0$ for all $x \in (0, 1/2)$.

Simple differentiation shows that $g'(x) < 0$ is equivalent to

$$\left(\frac{1}{x} - 2 \right) \left[(2a^{2x} - a^x)(a - a^{2x}) + 2a^{2x}(a^{2x} - a^x) \right] \ln a < \frac{1}{x^2}(a^{2x} - a^x)(a - a^{2x}),$$

that can be rearranged to (by multiplying by x^2)

$$(1 - 2x) \left[2a^{2x+1} - a^{x+1} - a^{3x} \right] \ln a^x < (a^{2x} - a^x)(a - a^{2x}).$$

Introducing the new variable $b = a^x$ and returning to n instead of x, the desired inequality takes the form (after dividing by b^3)

$$0 < n(1 - b)(1 - b^{n-2}) + (n - 2)(1 + b^{n-2} - 2b^{n-1}) \ln b := h(b).$$

This newly defined function satisfies $h(1) = 0$, and elementary differentiation shows that $h'(1) = 0 = h''(1)$. Moreover, the inequality $h'''(1) < 0$ holds. Based on this inequality, it is easy to check that h is positive in a left neighbourhood of 1, that is, there exists a number $\bar{b} < 1$, such that $h(b) > 0$ holds when $\bar{b} < b < 1$.

Let us define the desired number $\bar{a}$ as $\bar{a} = \bar{b}^2$. Then $a > \bar{a}$ is equivalent to $b^n > \bar{b}^2$. On the other hand, $n > 2$ and $b < 1$ imply that $b^2 > b^n$, hence $b^2 > b^n > \bar{b}^2$, yielding $b > \bar{b}$ leading to $h(b) > 0$. This is equivalent to $g'(x) < 0$ that we wanted to prove.

$\square$

We note that numerical evidence shows that the number $\bar{a}$ given by the proposition is relatively small, e.g. $\bar{a} < 0.1$. That is, for reasonable values of s_∞ the assertions of the proposition hold.

The proposition yields practical unidentifiability as follows. The value of γ is considered to be given, and the characteristic quantities of the epidemic, λ and s_∞ are measured. These determine the unique intersection point (n^*, τ^*) of the curves given by (11)–(12). In other words, n^* is the trivial solution of the reduced single equation $f(n) = f(n^*)$. An approximate solution n satisfies $|f(n) - f(n^*)| < \varepsilon$ with a given positive value of ε. The proposition implies that $|f(n) - f(n^*)| < \varepsilon$ holds for any $n > 2$ if $\varepsilon > f_\infty - f_2$, which is a small number. An even smaller ε is achieved if the measured data λ and s_∞ yield a value of n^* which is larger, i.e. $f(n^*)$ is closer to f_∞. Then the value of ε can be chosen as $\varepsilon = f_\infty - f(n^*)$ and then $|f(n) - f(n^*)| < \varepsilon$ holds for n values in a half-line, i.e. in a set of measure infinity. This was defined as practical unidentifiability.
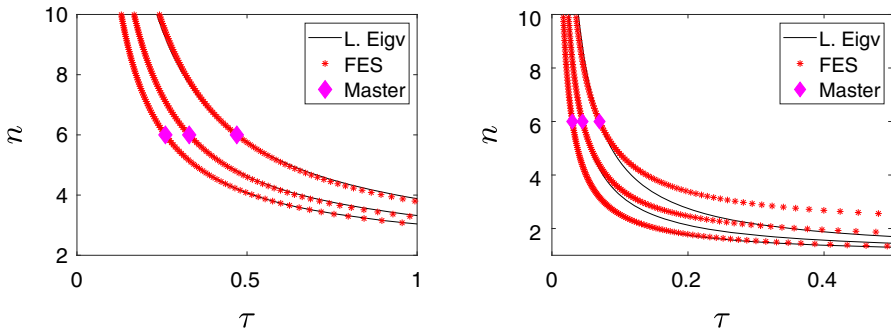
Fig. 4 (Color Figure Online) **Left panel:** From left to right curves correspond to solving Eq. (11) and (12) with the leading eigenvalue and the final epidemic size being set to values obtained by using $\tau = 0.26, 0.33, 0.47$, $\gamma = 1$ and $n = 6$. **Right panel:** Curves given by Eqs. (21) and (22) for values of the transmission rate $\tau = 0.03, 0.045, 0.07$ (from left to right). Other parameters are $\gamma = 1/7$ and $n = 6$. For both plots, the black curve represent (τ, n) pairs where the leading value is that determined by the master values shown as a diamond magenta. Similarly, the red star represent (τ, n) pairs where the final epidemic size is equal to that given by the master values

In Fig. 4, we explore the dependency of the practical unidentifiability in the pairwise model on the precise parameters used in the model. The left panel of this figure shows that this feature seems to hold for different parameter combinations and that we can find infinitely many (τ, n) pairs that lead to a desired eigenvalue and final epidemic size. Moreover, we emphasise again that the two curves do overlap to a great extent and over a large range of parameters.

Before investigating the same problem in a different model, we note that the same calculations for the leading eigenvalue and final epidemic size can be done when the pairwise model is closed with $\kappa = 1$. These calculations lead to

$$\tau = \frac{\lambda_L + \gamma}{n - 1}, \tag{13}$$

$$\tau = \frac{\gamma S_\infty (\ln(S_\infty) - \ln([S](0))}{\frac{[SS](0)}{([S](0))^2} (S_\infty)^2 - S_\infty (\ln(S_\infty) - \ln([S](0)) - \left(\frac{[SI](0)}{[S](0)} + \frac{[SS](0)}{[S](0)} \right) S_\infty}. \tag{14}$$

By using the disease-free initial condition, $[S](0) = N$, $[SS](0) = nN$, $[SI](0) = 0$ and using that $s_\infty = S_\infty/N$, the equations above lead to

$$\tau = \frac{\lambda_L + \gamma}{n - 1}, \tag{15}$$

$$\tau = \frac{\gamma \ln(s_\infty)}{n s_\infty - \ln(s_\infty) - n}. \tag{16}$$

It turns out that the formulas above are identical to those that we obtain later on for the edge-based compartmental model.

5 Identifiability in the Edge-Based Compartmental Model

The edge-based compartmental model is given by

$$\dot{\theta} = -\tau\theta + \tau\phi_S(0)\frac{\psi'(\theta)}{\psi'(1)} + \gamma(1-\theta) + \tau\phi_R(0) = f(\theta), \tag{17}$$

where θ denotes the probability that a random neighbour v of a random, initially susceptible test node u has not yet passed infection to u. Furthermore, $\phi_S(0)$ and $\phi_R(0)$ are the probabilities that, at $t = 0$, the random neighbour v of a random, initially susceptible test node u is susceptible and recovered, respectively. The disease-free steady state is given by $\theta(0) = 1$, $\phi_R(0) = 0$, $\theta(0) = 1$ and $\phi_S(0) = 1$. However, in order to generate an epidemic curve, when the system is above the epidemic threshold, one can perturb the steady state above by setting $\phi_S(0) = 1 - \varepsilon$.

We now consider the case of $\psi(x) = \exp(n(x-1))$, that is, a network with Poisson degree distribution with mean n. Linearising around $\theta = 1$, we obtain

$$f'(\theta)|_{\theta=1} = \tau\phi_S(0)\frac{\psi''(1)}{\psi'(1)} - \tau - \gamma = \tau\frac{n^2}{n} - \tau - \gamma = \tau(n-1) - \gamma = \lambda, \tag{18}$$

The final epidemic size can also be worked out by finding $\lim_{t\to\infty} \theta(t) = \theta_\infty$ and using that the final proportion of susceptible left in the population is $s_\infty = \psi(\theta_\infty)$. Setting the right-hand side of Eq. (17) to zero, an implicit equation for θ_∞ follows:

$$(\tau + \gamma)\theta_\infty - \gamma - \tau\psi_S(0)e^{n(\theta_\infty-1)} = 0. \tag{19}$$

Since $s_\infty = \exp(n(\theta_\infty - 1))$, Eq. (19) can be recast in terms of s_∞ and yields

$$\tau n\psi_S(0)s_\infty - (\tau + \gamma)\ln(s_\infty) - \tau n = 0. \tag{20}$$

We are now in a position to write down a system of equations based on (18) and (20)

$$\tau = \frac{\lambda + \gamma}{n - 1}, \tag{21}$$

$$\tau = \frac{\gamma \ln(s_\infty)}{n\psi_S(0)s_\infty - \ln(s_\infty) - n} \tag{22}$$

These curves are shown in the right panel of Fig. 4. It can be seen that the two curves are close to each other. The coincidence is more emphasised when s_∞ is larger, i.e. the final epidemic size is smaller.

Beyond this visualisation of unidentifiability, we formally prove that in terms of the definition given in Sect. 2. First, we reduce the above system to a single equation as follows:

$$\lambda + \gamma = \gamma q f(n),$$

where

$$f(n) = \frac{n-1}{n-q}, \quad \text{and} \quad q = \frac{\ln s_\infty}{s_\infty - 1} > 1.$$

We can assume without loss of generality that the two curves have a common point, i.e. there is a value n^* of n satisfying $\lambda + \gamma = \gamma q f(n^*)$. Otherwise, the measurement was so inaccurate that no values of τ and n could lead to the measured value of λ and s_∞. Thus the single equation to be solved for the unknown n takes the form

$$f(n) = f(n^*).$$

This equation does not identify the value of n in the practical sense. By plotting the graph of f, it turns out that the function is very close to a constant, its value changes only slightly from large values of n to infinity. For example, in the case $s_\infty = 0.9$, the functions change from 1.006 (at $n = 10$) to 1 as n tends to infinity, so the function is constant with accuracy 0.006 in the infinite half-line $n > 10$. In general, one can directly see that f is decreasing and its limit is 1 as n tends to infinity. Similarly to the case of the pairwise model, practical unidentifiability follows from the fact that the function f is to a constant.

6 Discussion

In this paper, we study the identifiability of parameters in network-based epidemic models. We find that network density and the transmission rate cannot be disentangled. More formally this means that when considering these parameters, the model is structurally not identifiable. Preliminary analysis suggests that combinations of n and τ and other parameters are better behaved, for example when packaged into the expression for R_0; this is in line with how to deal with identifiability problems (Villaverde et al. 2016).

In an ideal situation, the leading eigenvalue and final epidemic size can be measured to any desired accuracy. Assuming that this is the case, an exhaustive search in the parameter space, again to arbitrary precision, would be able to identify the precise parameters which generated the data. However, real-life observations are noisy and even a small measurement error can lead to a significant shift in the values of the inferred parameters. This leads to practical unidentifiability.

Contact patterns and the transmission of the disease across a link are strongly related and often are difficult to disentangle. Intuitively, it is known that dense networks with low transmission rate and spare networks with high transmission rate can produce similar epidemics. In fact, our hyperbolas trace out and connect these regimes. Of course, in this case a Bayesian approach may alleviate the problem in the sense that good informative priors are likely to reduce the dimensionality of the parameter space or at least the range of parameters. With more and more mobility data becoming available as well as data from contact surveys, contact networks can be characterised sufficiently in order to produce meaningful estimates from complex models.

In terms of future work, we believe that there is value in carrying out a systematic search over the parameter space to identify areas, both in terms of parameter subsets and ranges in parameter values, where the unidentifiability is the most significant. Our preliminary analysis shows that this is both model and parameter dependent. We also note that unidentifiability seems to be more marked for less severe epidemics. For larger epidemics, the overlap between the two hyperbolas decreases, meaning that parameters are easier to identify. Furthermore, similar analysis can be extended to different disease dynamics such the susceptible-exposed-infected-recovered (SEIR) model or alternative network-based mean-field models.

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