Recovering the time-dependent transmission rate from epidemiological data

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The transmissibility of many infectious diseases varies significantly in time, but has been thought impossible to measure directly. We devise a mathematical algorithm to recover the time-dependent transmission rate from epidemiological data. We apply our algorithm to historic UK measles data and observe that for most cities the main spectral peak of the transmission rate has a two-year period. All previous models assumed that the transmission rate has one-year period. Our construction also illustrates the danger of overfitting an epidemic transmission model with a variable transmission rate function.

I. INTRODUCTION

The SIR epidemic model was proposed by Kermack and McKendrik \cite{1} and was extensively developed by Anderson and May \cite{2}. One of the key parameters is the transmission rate, which is the product of the number of contacts a susceptible individual has with infected individuals per unit time and the probability of transmission during each contact. In Section 3.4.9 of Anderson and May \cite{2}, the authors stated that “... the direct measurement of the transmission rate is essentially impossible for most infections. But if we wish to predict the changes wrought by public health programmes, we need to know the transmission rate ... .”

The transmission rate of many infectious diseases varies significantly in time \cite{3}. For instance, one is more likely to contact the flu during winters than during summers, and childhood viral diseases (pre-vaccine) are strongly related to the school terms. For this reason, a number of epidemic models use a time-dependent transmission rate, that is almost always assumed to be a simple trigonometric \cite{5} or Haar \cite{16} function.

We consider the standard SIR epidemic model and allow the transmission rate to be a time-

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dependent function, i.e., there is a positive function $\beta(t)$ such that

\[
\frac{dS}{dt} = -\beta(t)SI, \\
\frac{dI}{dt} = \beta(t)SI - \nu I, \\
\frac{dR}{dt} = \nu I.
\]

Here $S(t), I(t),$ and $R(t)$ are the proportions of susceptible, infected, and removed individuals of time $t$. We begin by asking the mathematical question: given a smooth epidemiological data set, can one choose a transmission rate function $\beta(t)$ and removal rate $\nu$ such that the SIR epidemic model always perfectly fits the data? Mathematicians call this an inverse problem. And if this is possible, what does it imply about the infectious disease? We prove that this is always possible, and we provide an explicit formula for $\beta(t)$. The simple construction clearly illustrates the danger of overfitting an epidemic model where one can choose the time-dependent transmission rate.

To make the question more realistic, suppose in addition that the removal rate $\nu$ is prescribed. Can one always choose a transmission rate function $\beta(t)$ such that the SIR epidemic model always perfectly fits the smooth data with the given $\nu$? We prove that this is always possible subject to a mild restriction on the epidemiological data and $\nu$.

However, in practice, epidemiological data are always discrete, not continuous. We show that one can robustly estimate $\beta(t)$ by smoothly interpolating the data with a spline or rational function and then applying the formula to smooth data.

We extend our recovery algorithm to the SEIR epidemic model with vital rates, and we apply the extended algorithm to UK measles data during 1948-1958. Our recovered transmission rate $\beta(t)$ has minima during August, during the summer school vacation. We show that for most cities the main spectral peak of the Fourier transform of the transmission rate has a two-year period. All previous models assumed that the transmission rate has one-year period. For the few English cities (e.g., Newcastle and Liverpool) with one-year measles cycles, we show that the main spectral peak for the transmission rate also has a one-year period.

**II. RECOVERY ALGORITHM**

Our recovery algorithm is based on a mathematical derivation. The methods are expanded in Appendix A. To recover the transmission rate function $\beta(t)$ from an epidemiological data set, our recovery algorithm has four steps together with two conditions.
Step 1. Smoothly interpolate the epidemiological data with spline or rational functions to generate a smooth \( f(t) \). Check condition 1: \( \frac{f'(t)}{f(t)} > -\nu \), where \( \nu \) is the removal rate.

Step 2. Compute the function \( p(t) = \frac{f''(t)f(t) - f'(t)^2}{f(t)(f'(t) + \nu f(t))} \). Condition 1 prevents a zero denominator in \( p(t) \).

Step 3. Choose \( \beta(0) \) and compute the integral \( P(t) = \int_0^t p(\tau)d\tau \). Check condition 2: \( \beta(0) < \frac{1}{\int_0^T e^{P(s)}f(s)ds} \), where \( T \) is the time length of the epidemiological data. Alternatively, choose \( \beta(0) \) sufficiently small to satisfy condition 2. Note that there are infinitely many choices of \( \beta \).

Step 4. Apply the formula \( \beta(t) = \frac{1}{\left[ e^{-P(t)/\beta(0)} - e^{-P(t)} \int_0^t e^{P(s)}f(s)ds \right]} \) to compute \( \beta(t) \) on the given interval \([0, T]\).

For extensions of the standard SIR epidemic model, this recovery algorithm needs to be modified accordingly (see Appendix B).

III. RECOVERING THE TRANSMISSION RATE FROM SIMULATED DATA

We first illustrate the recovery algorithm on two simulated data sets. The “simulation year” is the unit for \( t \), and the functions \( f(t) \) and \( g(t) \) are the fractions of the infected population for two characteristic “types” of infectious diseases. The values of the transmission rate \( \beta(t) \) in these simulation examples are uncomparable to realistic transmission rates.

The first data set simulates an infectious disease with periodic outbreaks, as observed in measles (before mass vaccination) and cholera [6, 12]. We choose the periodic function \( f(t) = 0.25[1.4 + \cos(1.5t)] \) as the epidemiological data, and Figure 1(a) contains plots of both \( f(t) \) (solid) and its associated transmission rate function \( \beta(t) \) (dotted).

The second data set simulates an infectious disease with periodic outbreaks that decays in time, as observed in influenza [14]. We choose the function \( g(t) = 0.5[1.1 + \sin(t)] \exp(-0.1t) \) as the epidemiological data, and Figure 2(a) contains plots of both \( g(t) \) (solid) and its associated transmission rate function \( \beta(t) \) (dotted).

We extract discrete data from functions \( f(t) \) and \( g(t) \) by sampling them at equi-spaced intervals (see the small black squares in Figure 1(a) and Figure 2(a)). To each discrete time series, we apply three well-known interpolation algorithms (trigonometric approximation, sixth order spline approximation, tenth order rational approximation) [10, 15]. Figure 1(b) and Figure 2(b) contain
plots of $\beta(t)$ obtained from the three smooth interpolations together with the recovery algorithm. All three interpolations provide similar approximations of $\beta(t)$ in both examples.

Simple simulations show that the recovery algorithm is robust with respect to white noise up to 10\% of the data mean, as well as the number of sample points.

The peaks of $\beta(t)$ in Figure 1 are slightly increasing over time. This is, in part, a manifestation of the choice of $\beta(0)$ and $\nu$. Different values of $\beta(0)$ and $\nu$ may lead to the peaks increasing, decreasing, or non-monotone over time. We will see in Section IV that for historic UK measles, some important global characteristics of $\beta(t)$ are essentially independent of $\beta(0)$.

IV. RECOVERING THE TRANSMISSION RATE FROM UK MEASLES DATA

Previous studies [4, 9] employed the SEIR model with vital rates to explore epidemic and endemic behaviors of measles infections. To be consistent and comparable to these studies, we derive the modified recovery algorithm for the SEIR model in the presence of vital rates with a further assumption that population birth and death rates are identical (see Appendix B 5).

We now apply the modified recovery algorithm to aggregated weekly measles data from England and Wales (1948-1958) [13]. Infected individuals for different weeks of each month are partly overlapped, from which we obtain our monthly data (see Figure 3(a)). The aggregation of weekly data to monthly data is a filtering process to reduce noise. We smoothly interpolate monthly data and then compute $\beta(t)$ using the modified recovery algorithm. Eventually, we convert all units to be yearly based so that our results are comparable to previous studies.

In this recovering process of the transmission rate, we estimate parameters for measles from Anderson and May [2]: $\nu = 52$/year = 52/12/month, $a = 52$/year = 52/12/month, $\delta = 1/70$/year = 1/70/12/month, where $1/\nu$ is the removal period, $1/a$ is the latent period, $\delta$ is the birth (or death) rate.

It is already difficult to estimate the transmission rate at any single time, which can serve as $\beta(0)$ in the algorithm. Thus, it is important that the recovery algorithm is robust with respect to variation of $\beta(0)$. The authors Earn et al. [4], Keeling and Rohani [9] proposed a school term-based step function for the transmission rate, which attains the values 846/year during January 1-6 and 1408/year during January 7-31. We choose the mean value of their transmission rate function in January, $\beta(0) = 1299$, as the minimum value of $\beta(0)$, since transmission rates in old days (1948-1858) are larger than nowadays when health care has been improved. We estimate 2500/year as the maximum value of $\beta(0)$. Also, we choose an additional value of $\beta(0)$, 2000/year, between the
minimum and the maximum.

In Figure 3(b) we plot the annual transmission rate \( \beta(t) \) recovered from the 10-year data set with the three values of \( \beta(0) \). Notice that the three curves have roughly the same shape. In particular, all minima occur in August, which is the last month of summer vacation, and all maxima occur between September and the following February. This agrees with intuition and the assumptions of other modelers.

In Figure 4(a) we plot the spectrogram (Fourier transform) of the monthly data set of the number of infected individuals. Observe that the main peak occurs at 0.5/year, with period 2 years. The second largest peak occurs at 1/year with period 1 year.

To compare the transmission rates quantitatively, we compute the spectrogram of the three recovered functions for different \( \beta(0) \) and compare their spectral peaks. We see in Figure 4 that in each case the dominant spectral peak is 0.5/year, with period 2 years. This spectral peak coincides with the dominant spectral peak of the monthly infection data. In particular, this shows that the dominant spectral peak of \( \beta(t) \) is robust with respect to the choice of \( \beta(0) \).

Observe that the second largest spectral peak for \( \beta(t) \) can be 1/year (i.e., period 1 year) or 3/year (i.e., period 4 months). This is less robust with respect to the choice of \( \beta(0) \). However, all measles models with time dependent transmission rate assume that \( \beta(t) \) has period of 1 year, which is only, some times, the second most dominant frequency. We believe that determining \( \beta(t) \) for more examples of diseases and locations would be helpful, since these preliminary estimates suggest that more flexibility in choosing the periodicity in modeling diseases might lead to more accurate predictions.

In Figure 5, we compare our recovered transmission rate function \( \beta(t) \) with the school term-based step transmission rate function introduced by Earn et al. [4], Keeling and Rohani [9]. Their step function is adapted to the school term and is higher when school is in session and lower during school vacations. We chose our \( \beta(0) \) to be their average January transmission rate. We choose the monthly average instead of the value on January 1, because our data set of fractions of infectives is monthly. It is evident from the graphs that the two transmission rate functions are quite different. The mean value of our recovered \( \beta(t) \) is smaller than that of the term-based step function. The period of the term-based step function is one year, but as we have observed, the dominant frequency of our \( \beta(t) \) is 0.5/year. Our \( \beta(t) \) is decaying over time, which may be due to improvements in health care.

In Figure 6 we plot the weekly number of individuals infected with measles in seven major English cities. They appear synchronized, but the dominant periods do not all coincide. Fourier
analysis yields that Liverpool and Newcastle have strong one-year measles cycles, while four other cities have two-year measles cycles and one has a cyclic period in between. There is no known explanation for this difference.

As representative examples, we plot spectrograms of Manchester and Liverpool’s infection data and their corresponding $\beta(t)$’s in Figure 7. Manchester has a strong two-year measles cycle, and the corresponding $\beta(t)$ also has a two-year cycle. Liverpool has a one-year measles cycle, and the corresponding $\beta(t)$ also has a one-year cycle. We observe that the dominant period of the transmission rate seems strongly correlated with the dominant period of the number of infectives. Thus the one-year periodicity assumption for $\beta(t)$ that other investigators have made seems only valid for cities with one year measles cycles, such as for Liverpool, but not for most English cities.

V. DISCUSSION

In this paper, we provide what believe to be the first algorithm to recover the time-dependent transmission rate from epidemiological data. The construction also illustrates the danger of overfitting an epidemic model to epidemiological data when one has the flexibility in choosing the transmission rate function. We derive a recovery algorithm for the SEIR model with vital rates, and we apply this algorithm to UK measles data. Our recovered transmission rate looks strikingly different than the one year periodic sinusoid or Haar function assumed by previous measles modelers. Our analysis suggests that only a small number of English cities had transmission rates with dominant one year periodicity, and that most had two year periodicity. Our analysis indicates that when modeling measles, the periodicity of the transmission rate should match the periodicity of the number of infectives.

Our algorithm has some limitations to its applicability. First, the number of infected individuals, $f(t)$, can not decrease too fast over the full time interval of interest. In general, one can add a sufficiently large constant to $f(t)$ to ensure that the required condition is fulfilled. But then there is no canonical way of scaling $\beta(0)$. Second, we must assume that the number of infected individuals is always positive. In practice this restriction can be overcome by replacing zero values in the time series with a very small positive value. Finally, one either needs to know the value of the transmission rate at some fixed time, or verify that the desired properties of $\beta(t)$ hold for all $\beta(0)$ in the range where it can be estimated. It may be easiest to estimate the transmission rate when it is near its minimum, such as during the summer vacation period of childhood viral diseases.
APPENDIX A: METHODS

We derive the recovery algorithm by first posing the following mathematical question: given an arbitrary smooth positive function \( f(t) \), does there exist a positive function \( \beta(t) \) and removal rate \( \nu > 0 \) such that the solution \( I(t) \) of (2) coincides with \( f(t) \) on a large time interval \([0, T]\)? We prove that this is always possible.

**Theorem A.1** Given a smooth positive function \( f(t) \), \( b > 0 \), and \( T > 0 \), there exists \( \nu_0 > 0 \) such that if \( \nu > \nu_0 \) there is a solution \( \beta(t) \) with \( \beta(0) = b \) and such that \( I(t) = f(t) \) for \( 0 \leq t \leq T \).

Theorem A.1 implies that there are infinitely many solutions \( \beta(t) \) for each sufficiently large \( \nu \).

A more realistic question is whether this is possible if \( \nu \) is prescribed. The answer is provided by Theorem A.2. The growth condition in Theorem A.2 imposes no restrictions on how \( f(t) \) increases, but requires that \( f(t) \) cannot decrease too fast, in the sense that its logarithmic derivative is always bounded below by \(-\nu\).

**Theorem A.2** Given a smooth positive function \( f(t) \), \( \nu > 0 \), and \( T > 0 \), there exists \( \beta_0 > 0 \) such that if \( \beta(0) < \beta_0 \) there is a solution \( \beta(t) \) with this initial condition such that \( I(t) = f(t) \) for \( 0 \leq t \leq T \) if and only if \( f'(t)/f(t) > -\nu \) for \( 0 \leq t \leq T \).

The proofs of both theorems are nearly identical and elementary.

It is easy to see that \( f'(t)/f(t) > -\nu \) is a necessary condition, since Equation (2) implies that \( f'(t) + \nu f(t) = \beta(t)S(t)f(t) \), which must be positive for \( 0 \leq t \leq T \). We now show this condition is also sufficient. We rewrite Equation (2) as

\[
S = \frac{f' + \nu f}{\beta f},
\]

(A1)

then compute \((d/dt)S\), and then equate with Equation (1) to obtain

\[
\frac{d}{dt} \left( \frac{f' + \nu f}{\beta f} \right) = -\beta \left( \frac{f' + \nu f}{\beta f} \right) f.
\]

(A2)

Calculating the derivative and simplifying the resulting expression yields the following Bernoulli differential equation for \( \beta \)

\[
\beta' - p\beta - f\beta^2 = 0, \quad \text{where} \quad p = \frac{f'' f - f'^2}{f(f' + \nu f)}.
\]

(A3)

The change of coordinates \( x = 1/\beta \) transforms this nonlinear ODE into the linear ODE

\[
x' - p(t)x - f(t) = 0.
\]

(A4)
The method of integrating factors provides the explicit solution

\[
\frac{1}{\beta(t)} = x(t) = x(0)e^{-P(t)} - e^{-P(t)} \int_0^t e^{P(s)} f(s)ds, \quad \text{where} \quad P(t) = \int_0^t p(\tau)d\tau. \quad (A5)
\]

The only problem that could arise with this procedure is for the denominator of \( p(t) \) to be zero. If there is no restriction on \( \nu \), this can be prevented by choosing \( \nu \) sufficiently large such that

\[
\nu \cdot \min\{f(t) : 0 \leq t \leq T\} > -\max\{f'(t) : 0 \leq t \leq T\}. \quad (A6)
\]

The initial condition \( \beta(0) \) is arbitrary.

If \( \nu \) is prescribed, a singular denominator is prevented by requiring that the denominator be always positive, i.e., \( f' + \nu f > 0 \). Having done this, to ensure that \( \beta(t) \) is positive, one must choose \( \beta(0) \) sufficiently small such that

\[
\int_0^T e^{P(s)} f(s)ds < 1/\beta(0). \quad (A7)
\]

There are clearly infinitely many choices of \( \beta(0) \) and thus infinitely many transmission functions \( \beta(t) \). This observation clearly illustrates some dangers of overfitting an epidemic transmission model and raises a question on how to choose \( \beta(0) \).

**APPENDIX B: EXTENSIONS OF THE BASIC MODEL**

Analogous results hold for all standard variations of the standard SIR model and their combinations. The proofs are very similar to the proof of Theorems (A.1) and (A.2). Here, we only present the full algorithm for the SEIR model with vital rates, since we apply this algorithm to UK measles data.

1. **SIR model with vital rates**

\[
\dot{S} = \delta - \beta(t)SI - \delta S, \quad (B1)
\]
\[
\dot{I} = \beta(t)SI - \nu I - \delta I, \quad (B2)
\]
\[
\dot{R} = \nu I - \delta R. \quad (B3)
\]

The necessary and sufficient condition for recovering \( \beta(t) \) given \( \nu \) and \( \delta \) is \( f'(t)/f(t) > -(\nu + \delta) \).
2. SIR model with waning immunity

\[ \dot{S} = mR - \beta(t)SI, \]  
\[ \dot{I} = \beta(t)SI - \nu I, \]  
\[ \dot{R} = \nu I - mR, \]

where \(1/m\) is the memory period of immunity. The necessary and sufficient condition for recovering \(\beta(t)\) given \(\nu\) is \(f'(t)/f(t) > -\nu\).

3. SIR model with time-dependent indirect transmission rate (Joh et al. [8])

\[ \dot{S} = -\omega(t)S, \]  
\[ \dot{I} = \omega(t)S - \nu I, \]  
\[ \dot{R} = \nu I, \]

where \(\omega(t)\) is the time-dependent indirect transmission rate. The necessary and sufficient condition for recovering \(\beta(t)\) given \(\nu\) is \(f'(t)/f(t) > -\nu\).

4. SEIR model

\[ \frac{dS}{dt} = -\beta(t)SI \]  
\[ \frac{dE}{dt} = \beta(t)SI - \alpha E \]  
\[ \frac{dI}{dt} = \alpha E - \nu I \]  
\[ \frac{dR}{dt} = \nu I, \]

where \(1/\alpha\) is the latent period for the disease. By simple calculations, we can show that the necessary and sufficient condition for recovering \(\beta(t)\) from epidemiological data is \(f'(t)/f(t) > -\nu\).

5. SEIR model with vital rates

\[ \frac{dS}{dt} = \delta - \beta(t)SI - \delta S, \]  
\[ \frac{dE}{dt} = \beta(t)SI - \alpha E - \delta E, \]  
\[ \frac{dI}{dt} = \alpha E - \nu I - \delta I, \]  
\[ \frac{dR}{dt} = \nu I - \delta R. \]
The necessary and sufficient conditions for recovering \( \beta(t) \) from epidemiological data are

\[
f'(t) + (\nu + \delta)f(t) > 0 \quad \text{and} \quad f''(t) + (\nu + 2\delta + a)f'(t) + (\delta + a)(\nu + \delta)f(t) > 0. \tag{B18}
\]

In this case, \( \beta(t) \) satisfies the Bernoulli equation

\[
\beta' + p(t)\beta + q(t)\beta^2 = 0, \tag{B19}
\]

where

\[
p = \frac{-af'' - a(\nu + 2\delta + a)f' - a(\delta + a)(\nu + \delta)f'f + af'' + a(\nu + 2\delta + a)f^2}{af[f'' + (\nu + 2\delta + a)f'(\delta + a)(\nu + \delta)f]},
\]

\[
q = \frac{\delta a^2 f^2 - a(\nu + 2\delta + a)f'f^2 - a(\delta + a)(\nu + \delta)f^3}{af[f'' + (\nu + 2\delta + a)f'(\delta + a)(\nu + \delta)f]).}
\]

The modified recovery algorithm has five steps together with three conditions.

**Step 1.** Smoothly interpolate the epidemiological data to generate a smooth function \( f(t) \) that has at least a continuous second derivative. Check condition 1: \( f'(t) + (\nu + \delta)f(t) > 0 \); and check condition 2: \( f''(t) + (\nu + 2\delta + a)f'(t) + (\delta + a)(\nu + \delta)f(t) > 0 \).

**Step 2.** Compute the function \( p(t) = \frac{-af'' - a(\nu + 2\delta + a)f' - a(\delta + a)(\nu + \delta)f'f + af'' + a(\nu + 2\delta + a)f^2}{af[f'' + (\nu + 2\delta + a)f'(\delta + a)(\nu + \delta)f]} \).

**Step 3.** Choose \( \beta(0) \) and compute the integral \( P(t) = \int_0^t p(\tau)d\tau \). Check condition 3: \( \frac{1}{\beta(0)} + \int_0^T e^{-P(s)}q(s)ds > 0 \).

**Step 4.** Compute the function \( q(t) = \frac{\delta a^2 f^2 - a(\nu + 2\delta + a)f'f^2 - a(\delta + a)(\nu + \delta)f^3}{af[f'' + (\nu + 2\delta + a)f'(\delta + a)(\nu + \delta)f]} \).

**Step 5.** Apply the formula \( \beta(t) = 1 \left[ e^{P(t)/\beta(0)} + e^{P(t)} \int_0^t e^{-P(s)}q(s)ds \right] \) to compute \( \beta(t) \) on the given interval \([0, T]\).

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[13] The weekly OPCS (Office of Population Censuses and Surveys) reports, the Registrar General’s Quarterly or Annual Reports, & various English census reports.


FIG. 1: (a) We extract 21 data points from the periodic function $f(t) = 0.25[1.4 + \cos(1.5t)]$; the dotted curve is $\beta(t)$ generated from the periodic function. (b) These transmission functions are obtained from three different smooth interpolations of extracted discrete data points.

FIG. 2: (a) We extract 21 data points from the oscillatory decaying function $g(t) = 0.5[1.1 + \sin(t)]\exp(-0.1t)$; the dotted curve is $\beta(t)$ generated from the oscillatory decaying function. (b) These transmission functions are obtained from three different smooth interpolations of extracted discrete data points.
FIG. 3: (a) Aggregated monthly measles data from England and Wales in 1948-1958; (b) $\beta(t)$ obtained from aggregated monthly data with different $\beta(0)$ values.

FIG. 4: We eliminate the artificial peaks at zero frequency in the Fourier transform by applying the method “zero-phase forward and reverse digital filtering” to the original data set (monthly fractions or $\beta(t)$). (a) Fourier analysis of aggregated monthly data to show dominant frequencies; (b) Fourier analysis of $\beta(t)$ with $\beta(0) = 1299$ to show dominant frequencies; (c) Fourier analysis of $\beta(t)$ with $\beta(0) = 2000$ to show dominant frequencies; (d) Fourier analysis of $\beta(t)$ with $\beta(0) = 2500$ to show dominant frequencies.
FIG. 5: Compare $\beta(t)$ from our algorithm with the term-based step function proposed by Keeling and Rohani [9]. The initial transmission rate $\beta(0) = 1299$/year, which is the averaged transmission rate in January computed from the term-based step function.

FIG. 6: Time series of weekly patient data for seven major cities in England.
FIG. 7: (a) Fourier analysis of Manchester monthly data to show dominant frequencies; (b) Fourier analysis of $\beta(t)$ of Manchester to show dominant frequencies; (c) Fourier analysis of Liverpool monthly data to show dominant frequencies; (d) Fourier analysis of $\beta(t)$ of Liverpool to show dominant frequencies.