Estimates of the reproduction numbers of Spanish influenza using morbidity data

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Background There have been several studies of the transmissibility of the 1918 (Spanish) influenza virus, which has attributed to >20 million deaths. Many of the analyses to date have involved fitting predictions from a transmission model to the observed epidemic curves from different settings.

Methods Using morbidity data from cities in Europe and America and from confined settings during the 1918 influenza pandemic, we contrast the use of several different methods based on the growth rate and final size of the epidemic, which do not rely on transmission models, to estimate the effective and basic reproduction numbers.

Results The effective reproduction number (the average number of secondary infectious cases produced by a typical infectious case in a given population) for the 1918 influenza virus was in the range 1.2–3.0 and 2.1–7.5 for community-based and confined settings, respectively.

Conclusions Assuming further that 30 and 50% of individuals were immune to Spanish influenza after the wave in April 1918 and the first subsequent wave, respectively, these findings imply that, in a totally susceptible population, an infectious case could have led to 2.4–4.3 and 2.6–10.6 cases in community-based and confined settings, respectively. These findings for community-based populations confirm the relatively low transmissibility of the 1918 (Spanish) influenza virus, which has been found by other studies using alternative data sources and methods.

Keywords Modelling, reproduction numbers, Spanish influenza

Introduction
The recent emergence of the highly pathogenic H5N1 virus among poultry and ducks and the clinical, epidemiological and laboratory indications among the human cases attributed to H5N1 to date, has led to fears of an imminent influenza pandemic similar in impact to that of the Spanish influenza pandemic,1 which is reported to have caused more deaths than the first World War.2

The impact of any pandemic and its potential for control depends greatly on the transmissibility of the causal pathogen and its ability to lead to infectious cases. This is usually described using its basic reproduction number (R₀), defined as the average number of secondary infectious cases resulting from a typical infectious case in a totally susceptible population.

There are several methods for estimating the R₀ and most of the studies to date for Spanish influenza have used similar methods, involving the development of a transmission model and fitting predictions of the epidemic curve to the available data.3–5 The conclusions from these studies have been very similar, i.e. the R₀ was approximately 3–4.

We here illustrate the application of several different methods, which do not rely on the development of transmission models, to estimate the reproduction numbers for Spanish influenza for a variety of different settings, using data from the first few weeks of the epidemic and assumptions about the serial interval.
Materials and methods

Data sources

Data were obtained after a review of the English language literature to identify suitable studies presenting daily or weekly data on the incidence of influenza during 1918–19. Four types of study settings were identified from the spring of 1918, when an increase in influenza incidence was first observed, namely: confined populations [the San Quentin prison (USA) and Australian boats], communities in Maryland, USA, where cases were ascertained actively through house-to-house surveys and several cities in Scandinavia (Copenhagen, Gothenberg and Stockholm) and the USA (Boston, Chicago and New York) where cases were ascertained passively.2,6,7 The characteristics of the populations, together with the weekly incidence of cases reported in these settings are summarized in Table 1 and Figure 1.

For the San Quentin prison, the first outbreak was reported in April 1918, with further outbreaks occurring in October and December 1918; the first influenza outbreaks in Scandinavian cities were reported in July 1918, with second waves occurring in October 1918; for settings in the US and for the Australian boats, the data relate to outbreaks occurring during October–November 1918. As shown in Table 1, the proportion of individuals reported to have experienced disease was high in community settings in Maryland (i.e. 22–59%) and on two of the boats (32% for the ‘Medic’ and 40% for the ‘Boonah’). In contrast, this proportion was low (1–3%) in Stockholm and in cities in the USA, as reflected in the correspondingly lower weekly reporting rate shown in Figure 1. This low proportion may be partly attributable to the fact that cases were reported passively in cities in Scandinavia and USA (Table 1).

Estimates of the effective and basic reproduction numbers

The effective and basic reproduction numbers were first calculated for each study setting using the growth rate in the cumulative numbers of cases during the growth phase of the outbreak8 (see below). The estimates obtained using this method are relatively insensitive to the level of under-reporting of cases, since the growth rate in the cumulative number of reported cases should be identical to that in the true cumulative number of cases in the population, unless the level of reporting changed over time. On the other hand, the estimates are sensitive to assumptions about the latent and infectious periods.9

To validate these estimates, we therefore recalculated the reproduction numbers using an approach which was independent of assumptions about the latent and infectious periods.

Table 1 Summary of the data used to estimate the basic reproduction number of Spanish influenza

<table>
<thead>
<tr>
<th>Type of population</th>
<th>Study setting</th>
<th>Observation period</th>
<th>Percentage of the population experiencing disease (number of reported cases/population size)</th>
<th>Method of data collection</th>
</tr>
</thead>
<tbody>
<tr>
<td>Confined</td>
<td>San Quentin prison</td>
<td>15/4/1918–27/5/1918</td>
<td>5.2 (99/1900)</td>
<td>Passive: inmates reported</td>
</tr>
<tr>
<td></td>
<td></td>
<td>9/11/1918–4/12/1918</td>
<td>3.7 (71/1900)</td>
<td>to the prison infirmary</td>
</tr>
<tr>
<td></td>
<td></td>
<td>11/11/1918–15/12/1918</td>
<td>3.1 (58/1900)</td>
<td>when ill</td>
</tr>
<tr>
<td></td>
<td>The ‘Devon’ sailing boat</td>
<td>14/10/1918–31/10/1918</td>
<td>7.4 (81/1096)</td>
<td>Passive and daily inspections</td>
</tr>
<tr>
<td></td>
<td>The ‘Medic’ sailing boat</td>
<td>11/11/1918–15/12/1918</td>
<td>31.5 (312/989)</td>
<td>Passive and daily inspections</td>
</tr>
<tr>
<td>Communities in Maryland</td>
<td>Baltimore</td>
<td>1/9/1918–30/11/1918</td>
<td>22.2 (7489/33776)</td>
<td>Active: house to house survey</td>
</tr>
<tr>
<td></td>
<td>Cumberland</td>
<td></td>
<td>39.8 (2085/5234)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Frederick</td>
<td></td>
<td>31.7 (768/2420)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Lonaconing</td>
<td></td>
<td>59.4 (1093/1840)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Salisbury</td>
<td></td>
<td>44.1 (765/1735)</td>
<td></td>
</tr>
<tr>
<td>Scandinavian cities</td>
<td>Copenhagen</td>
<td>30/6/1918–31/8/1918</td>
<td>4.7 (25,147/539,000)</td>
<td>Routine notification data</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1/9/1918–28/12/1918</td>
<td>13.3 (71,707/539,000)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gothenberg</td>
<td>30/6/1918–31/8/1918</td>
<td>2.3 (4657/198,948)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1/9/1918–28/12/1918</td>
<td>9.8 (19,484/198,948)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Stockholm</td>
<td>30/6/1918–31/8/1918</td>
<td>0.3 (1293/413,163)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1/9/1918–28/12/1918</td>
<td>1.0 (4217/413,163)</td>
<td></td>
</tr>
<tr>
<td>Cities in the USA</td>
<td>Boston</td>
<td>29/9/1918–2/11/1918</td>
<td>0.4 (3327/767,813)</td>
<td>Routine notification data</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3/11/1918–25/1/1919</td>
<td>1.6 (11,952/76,7813)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Chicago</td>
<td>15/9/1918–16/11/1918</td>
<td>1.5 (37,907/2,596,681)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>17/11/1918–3/4/1919</td>
<td>0.7 (18,937/2,596,681)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>New York</td>
<td>22/9/1918–23/11/1918</td>
<td>2.0 (11,845/5,872,667)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>24/11/1918–29/03/1919</td>
<td>0.5 (31,325/5,872,667)</td>
<td></td>
</tr>
</tbody>
</table>

* New inmates entered the prison but their number and time of entry was not available.
but which depended on reliable estimates of the final size of the outbreak, for settings where there was likely to be little underreporting of cases (i.e. where at least 30% of the population was reported to have experienced influenza). For simplicity, the contribution of asymptomatic individuals is not considered here, as these affect estimates of the reproduction numbers based on the growth rate of the outbreak only if the proportion of individuals who are asymptomatic changes over time, and such changes are unlikely to have been substantial.

Estimates of the reproduction numbers using the growth rate of the epidemic
The effective reproduction number for influenza \( R_n \) at the start of each wave for the data shown in Figure 1 was calculated using the expression, as provided by Wearing et al.:  
\[
R_n = \frac{L}{C} \left(\frac{L}{C} + D\right) + 1
\]

where \( L \) and \( D \) are the average durations of the latent and infectious periods, respectively and \( A \) is growth rate in the cumulative number of cases during the growth phase of the given outbreak. The above equation holds when the latent and infectious periods are assumed to follow the negative exponential distribution; in this situation, the term \( L + D \) equals the serial interval, defined as the time interval between successive cases in a chain of transmission. Equation (1) thus highlights the fact that the reproduction number increases with the size of the serial interval. The above expression for the effective reproduction number is analogous to that used to calculate the basic reproduction number using data from outbreaks for an infection which is introduced into a population for the first time, and has been applied to data for SARS and HIV.

The average growth rate (\( \Lambda \)) in the cumulative numbers of cases in a given setting was calculated as the gradient of the straight line fitted, using linear regression, to the natural

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**Figure 1** Summary of the weekly incidence of influenza cases observed in confined settings, in population-based studies in Maryland (USA), Scandinavian cities and in American cities during the period April 1918 to April 1919.
logarithm of the, daily (where available) or weekly observed, cumulative number of cases, during the stage of the epidemic when the observed number of cases increased exponentially.

According to experimental studies, individuals are first infectious (i.e. shed virus) 1–2 days after inoculation (i.e. infection) and shed virus for 3 or 4 days thereafter. We therefore assume that the average latent period is 2 days and, assuming that the infectious period follows the negative exponential distribution, the average infectious period is 2 days. The latter assumption is consistent with 61, 37, 22 and 14% of individuals still being infectious 1, 2, 3 and 4 days, respectively after onset of infectiousness. These assumptions for the latent and infectious periods imply an average serial interval of 4 days.

Given recent estimates of an average serial interval lasting 2.5 days and the possibility that some individuals may shed virus for time periods which are longer than the average, we explore the sensitivity of our reproduction number estimates to the assumption that the average serial interval was 2.5 or 6 days, using an average infectious period of 0.5 and 4 days, respectively and an average latent period of 2 days.

Estimates of the basic reproduction number for each epidemic wave were then obtained using the expression:

\[ R_n = \frac{R_0}{\text{proportion susceptible at the start of the wave}} \]

It was assumed that 100% of individuals were susceptible at the start of April 1918. The extent to which this proportion declined thereafter, as a result of the increased incidence of influenza in some settings during the spring of 1918 is unknown. We here assume that 70% and 50% were susceptible at the start of the first and second subsequent waves after April 1918, which is consistent with the level of seroconversion found as a result of the first wave of the Hong Kong influenza pandemic and the observations that, during a typical influenza A season, 20–30% of individuals experience rises in their titres of antibodies attributable to the circulating strain of influenza. Other analyses of the \( R_0 \) for Spanish influenza also used 70% as a lower bound for the proportion of the population which was susceptible at the start of outbreaks during the autumn of 1918.

The assumption that the latent and infectious periods follow the negative exponential distribution may lead to under- or over-estimates of the reproduction numbers, as calculated using equation (1). To test the sensitivity of our reproduction number estimates to this assumption, we recalculated them using the following formula provided by Wearing et al.:

\[ R_n = \frac{AD[(AL/m) + 1]^m}{[1 - [(AD/n) + 1]^{-n}]} \]

using the extreme assumptions \( m = n = 100 \). This formula is related to the above formula for the net reproduction number, but allows the distributions of the latent and infectious periods to vary according to the size of \( m \) and \( n \), respectively. The value \( m = 1 \) (or \( n = 1 \)) corresponds to the assumption that the latent (or infectious period) follows the negative exponential distribution; the value \( m = 100 \) (or \( n = 100 \)) corresponds to the assumption that the latent (or infectious) period is tightly distributed around the mean (Figure A1).

### Estimates of the reproduction numbers using the final size of the epidemic

For settings with a high level of reporting, i.e. where >30% of the population was reported to have experienced influenza [the ‘Boonah’, the ‘Medic’ and all the Maryland study sites, apart from Baltimore (Table 1)], the \( R_n \) was calculated using the final epidemic size using the approach of Becker:

\[ R_n = \frac{N - 1}{C} \sum_{i=n+1}^{N-1} 1/i \]  

where \( N \) is the population size, \( C \) is the total number of cases in the given wave and \( S_0 \) and \( S_f \) are the numbers of susceptible individuals in the population at the start and end of the given wave, respectively. The standard error in the \( R_n \) was calculated using the expression:

\[ SE(R_n) = \frac{N - 1}{C} \sqrt{\sum_{i=n+1}^{N-1} 1/i^2} \]  

where \( N \) is the population size, \( C \) is the total number of cases in the given wave and \( S_0 \) and \( S_f \) are the numbers of susceptible individuals in the population at the start and end of the given wave, respectively. The effective reproduction number and its standard error were calculated using expressions (2) and (3), substituting the term for the number of susceptible individuals at the start of the outbreak with the total population size.

### Results

Figure 2A summarizes estimates of the effective reproduction number for the settings considered here.

In general, the estimates were low for community-based settings, ranging between 1.2 and 3.0, based on the assumption that the average serial interval was 4 days. For confined settings and for the same assumption about the serial interval, the effective reproduction number ranged between 2.1 and 7.5, with the highest value estimated for ships (e.g. 3.8 for ‘The Medic’ and 7.5 for ‘The Devon’). Excepting that estimated for the San Quentin prison, the effective reproduction number associated with the second wave of the pandemic in each setting was lower than that for the first (e.g. 3.0 in Gothenberg in July 1818 vs 1.5 in October 1918), which is attributable to the correspondingly lower proportion of individuals who are susceptible to infection at the start of the second wave.

The implications of these estimates for the basic reproduction number, based on the assumption that 100, 70 and 50% of the population was susceptible at the start of April 1918 and the first and second subsequent waves, respectively, are summarized in Figure 2B. For all community-based settings, the \( R_0 \) as calculated using the growth rate of the outbreak, was between 2 and 4.3, assuming that the serial interval was either 2.5 or 4 days. For the assumption that the serial interval was 6 days, the lowest basic reproduction number (\( \approx 2.4 \)) was estimated for Baltimore, Cumberland, Frederick and for New York in October 1918 and the highest (4.3) was estimated for Gothenberg in July 1918.

For confined settings, the basic reproduction number, as calculated using the growth rate of the given wave, was lowest for the San Quentin prison in April 1918 and highest for the outbreak on ‘The Devon’, occurring in the ranges 1.9–5.6
For the assumption that the serial interval was 2.5 and 4 days, respectively. The assumption of a 6 day serial interval was associated with very high $R_0$ estimates for all outbreaks in confined settings (e.g. >15 for ‘The Devon’).

For community-based settings, estimates of the reproduction numbers calculated using the final size of the outbreak were consistent with those estimated using the growth rate of the wave (Figure 2). For the outbreaks occurring on the boats,
on the other hand, they were substantially lower than those estimated using the growth rate of the outbreak (e.g. an $R_0$ of 2.1 vs 7.0 for ‘The Boonah’, as calculated using the outbreak size and the growth rate of the outbreak, respectively assuming an average serial interval of 4 days).

As shown in Figure A2 in the appendix, estimates for the reproduction numbers were relatively insensitive to assumptions about the distribution of the latent and infectious periods, for all settings except for ‘The Devon’. In this setting, the assumption that the latent and infectious periods were tightly distributed resulted in an $R_0$ estimate of 16.7, as compared with 10.6 if it was assumed that they followed the negative exponential distribution.

Discussion

Our analyses illustrate the application of different methods for estimating the reproduction numbers of Spanish influenza, which are based on the growth rate and the final size of the epidemic. These methods are slightly simpler than those used in previous estimates of the reproduction number for Spanish influenza,\textsuperscript{3-5} which involved fitting predictions from a transmission model to the observed data; those based on the growth rate of the epidemic also had the advantage of being relatively insensitive to the level of underreporting of cases, provided that this did not change over time. Our estimates are of the same order as the estimates from those studies, confirming the conclusion that, in the general population, despite its high pathogenicity, the transmissibility of the Spanish influenza virus was relatively low, with a basic reproduction number lying in the range 2–4.

The reproduction numbers were estimated for all settings using the growth rate in the cumulative numbers of cases during the growth phase of each pandemic wave. The advantage of this method is that the estimates were relatively insensitive to the level of underreporting, since the growth rate in the cumulative number of reported cases should be identical to that in the true cumulative number of cases in the population, unless the level of underreporting changed over time. Changes in the reporting of cases are likely to have been small, at least in the city-based community studies, where cases were ascertained passively, given our finding that the reproduction numbers in these settings were similar to those in Maryland, where cases were ascertained actively through house-to-house surveys and where the level of underreporting was probably low.\textsuperscript{7}

In our analyses of the reproduction numbers based on the growth rate in the cumulative numbers of cases, the average serial interval was assumed to be 4 days. This assumption is consistent with data presented in three family-based studies during the Asian and Hong Kong influenza pandemics,\textsuperscript{28–30} for which, considering cases who had onset within 10 days of the first case in the household, the median time interval between the first and subsequent cases was approximately 4 days. Our finding, that at least for community-based studies in Maryland, where the reporting of cases was likely to have been reliable, the reproduction numbers, as calculated using the outbreak size (and independently of the serial interval), were consistent with those calculated using the growth rate of the cumulative numbers of cases (Figure 2), provides further justification for our assumed values for the serial interval. We discuss the discrepancy between the estimates obtained using the two methods for confined settings below.

In practice, the serial interval depends on many factors, e.g. the time when symptoms are their most severe and individuals isolate themselves from others and the amount of viral shedding, which appears to be correlated with the severity of the illness\textsuperscript{17,21} and varies throughout the period of viral shedding.\textsuperscript{17-22} It is also possible that the duration of infectiousness is shorter for epidemic than for pandemic influenza, given that virus replication and shedding may be limited if individuals have some protection resulting from previous exposure to a strain, which is antigenically related to that causing the current infection. This may partly explain the recent low estimates of the serial interval of 2.5 days for influenza,\textsuperscript{24} which were based on household data of epidemic influenza transmission from France in the year 2002.

Our estimates of the reproduction numbers for the boats based on the growth rate of the outbreak were much higher than those estimated for population-based settings (Figure 2). This is consistent with the crowded conditions on these boats, and hence the increased opportunity for exposure, as reflected in the high attack rates.

The reproduction numbers calculated for the boats using the growth rate of the outbreak (where the latent and infectious periods were parameters) were substantially higher than those calculated using the final outbreak size. The discrepancy could be due to genuine reductions in the (basic) reproduction number during the outbreak, which would have affected the estimates calculated using the final outbreak size more than those calculated using the growth rate in the cumulative numbers of cases. Such reductions could have occurred because of reduced contact, once individuals became aware of the outbreak, or control measures. For example, daily ‘thermometer parades’ were carried out on each of the boats, and any individuals with signs of fever or reporting sick were removed for observation or immediately isolated.\textsuperscript{2}

Overall, the analyses presented here support the findings from other studies, which were based on alternative data sources and methods, that the $R_0$ for Spanish influenza was relatively low when the virus first appeared in the general population, ranging between 2 and 4.3. Many factors have changed since 1918, e.g. household sizes have probably decreased over time, although the spread of the influenza virus may now be rapid because of the increased connectivity of individuals. Control measures which are now available are, in theory, more effective than those available in 1918, which consisted of shutting down music halls and theatres and staggering the opening times of offices and shops to reduce aggregation of individuals.\textsuperscript{2} It is hoped that good planning, basic infection control measures and the availability of antivirals will help to ensure that any future influenza pandemic has a smaller impact than that of the Spanish influenza pandemic.

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Conflict of interest: None declared.
**KEY MESSAGES**

- This study uses morbidity data from cities in Europe and America and from confined settings, and several different methods based on the growth rate and final size of the epidemic, to estimate the effective and basic reproduction numbers for the 1918 (Spanish) influenza virus.

- The effective reproduction number (the average number of secondary infectious cases produced by a typical infectious case in a given population) for the 1918 influenza virus was in the range 1.2–3.0 and 2.1–7.5 for community-based and confined settings, respectively.

- The basic reproduction number (the average number of secondary infectious cases resulting from a typical infectious case in a totally susceptible population) was in the range 2.4–4.3 and 2.6–10.6 cases in community-based and confined settings, respectively.

- These findings for community-based populations confirm the relatively low transmissibility of the 1918 (Spanish) influenza virus, which has been found by other studies using alternative data sources and methods.

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**References**

Appendix

Figure A1 Comparison between the distributions of the latent period obtained assuming that the values for \( m = 1 \) and 100 and the average latent period is 2 days. The formula for this distribution is
\[
(\frac{m}{L})^m e^{-m/L} e^{(-m/L)}/(m - 1).
\]

(A) Effective reproduction number

Figure A2 Comparison between the effective and basic reproduction numbers as calculated using the growth rate of the epidemic wave, assuming that the latent and infectious periods either followed the negative exponential distribution or were tightly distributed around the mean value \((m = n = 100)\). The lower and upper limits for the estimates reflect reproduction numbers obtained assuming a serial interval of 2.5 and 6 days, respectively.
(B) Basic reproduction number

Confined settings  Maryland community studies  Scandinavian cities  American cities

San Quentin prison April 1918  San Quentin prison Oct 1918  San Quentin prison Dec 1918
San Quentin prison April 1918  San Quentin prison Oct 1918  San Quentin prison Dec 1918
The Boonah Nov 1918  The Devon Oct 1918  The Medlic Nov 1918
Cumberland Sept 1918  Frederick Sept 1918  Salisbury Sept 1918
Frederick Sept 1918  Salisbury Sept 1918  Copenhagen July 1918
Frederick Sept 1918  Salisbury Sept 1918  Copenhagen July 1918
Frederick Sept 1918  Salisbury Sept 1918  Copenhagen July 1918
Frederick Sept 1918  Salisbury Sept 1918  Copenhagen July 1918

Study setting

Figure A2  Continued.