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Estimating Incidence Curves of Several Infections Using Symptom Surveillance Data

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Abstract
We introduce a method for estimating incidence curves of several co-circulating infectious pathogens, where each infection has its own probabilities of particular symptom profiles. Our deconvolution method utilizes weekly surveillance data on symptoms from a defined population as well as additional data on symptoms from a sample of virologically confirmed infectious episodes. We illustrate this method by numerical simulations and by using data from a survey conducted on the University of Michigan campus. Last, we describe the data needs to make such estimates accurate.


Introduction
Timely and accurate estimates of influenza virus infection incidence rates in a population are difficult to obtain because most infectious episodes are unaccounted for, while influenza-like illness can have a variety of etiologies other than influenza virus infection. Many countries use sentinel surveillance systems to ascertain rates of infectious episodes. We illustrate this method by numerical simulations and by using data from a survey conducted on the University of Michigan campus.

Methods

We introduce a method for estimating incidence curves of several co-circulating infectious pathogens, where each infection has its own probabilities of particular symptom profiles. Our deconvolution method utilizes weekly surveillance data on symptoms from a defined population as well as additional data on symptoms from a sample of virologically confirmed infectious episodes. We illustrate this method by numerical simulations and by using data from a survey conducted on the University of Michigan campus. Last, we describe the data needs to make such estimates accurate.


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advantageous.

profile, so more parsimonious sets of symptom profiles may be

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infections occur). Let

Pop

number of persons with symptom profile

number of asymptomatic persons and

Pop

the population on week

population for which symptom data is gathered.

various circulating pathogens does not change in time for the

group of people assumed to be homogeneous in the sense than the

population. Throughout this paper by "population" we denote a

identifiability of different infections we assume that the matrix

can be reduced to a vector

on their symptoms during the preceding week. The weekly data

selected person becomes symptomatic with infection

becomes infected for all infections in the population

1. Multinomial model

Suppose there are

m

different pathogens causing infection in a

population. Throughout this paper by "population" we denote a

group of people assumed to be homogeneous in the sense than the

population. Throughout this paper by "population" we denote a

Wrinkle in paper: seems to be a partial page of a document, but not enough context is provided to understand the full content. The text appears to be discussing the estimation of incidence using symptom data, with a focus on multinomial models and symptom profile distributions. It mentions the use of symptom surveillance data and the need for additional data on symptom profiles for various infections. The text includes mathematical notation and statistical concepts, but without a complete view of the page, it is challenging to provide a comprehensive interpretation.
The distribution of symptom profiles reported by cases with ARI not associated with influenza may be quite specific to the location and the circulating respiratory viruses. One may be able to use symptom surveillance data itself during a period when one knows that the percent of flu among symptomatic individuals is very low to suggest that almost all symptoms are attributable to non-flu causes. Thus overall counts of symptom profiles reported by all symptomatic individuals during that period give an estimate of the non-flu symptom profile distribution. In this case that period should also be removed from subsequent inference of influenza incidence.

3. Inference process

3.1 EM iterations. Estimation of the parameters \((p_i)\) and \((d_j)\) can be done with the aid of the Expectation Maximization (EM) algorithm [6,7,13] which iterates in the space of parameters \((p_i)\) and \((d_j)\) increasing the likelihood of observations \((Q^i, O^j)\) with each iteration. Specifically let \((p'/(n))\) and \((d'/(n))\) be the values of the parameters after \(n\) EM iterations. To understand the iterative process, denote for any parameters \((p,d)\) the expectation of the variable \(X^n\) conditional on the observations \(Q^n\) [13]:

\[
E(X^n|Q^n,p,d) = Q^n \frac{p^n d^n}{\sum_k p^n_k d^n_k} \tag{3}
\]

The parameter values after the next EM iteration are given by

\[
p'(n+1) = \frac{1}{Q^n} \sum_j E(X^n_j|Q^n,p(n),d(n)) \tag{4}
\]

and

\[
d'(n+1) = \frac{\sum_t \sum_k E(X^n|Q^n,p(n),d(n)) + O^t}{\sum_t \sum_k E(X^n|Q^n,p(n),d(n)) + N_t} \tag{5}
\]

3.2 Inference Method 1. Several inference methods for the model’s parameters are possible, and their robustness for a given data set can be tested by the SEM algorithm [14], as well as by bootstrapping. Similarly our inference process involves a choice of certain symptom profiles for symptomatic individuals – e.g. the one given by equation (2a) or (2b). Assessing the robustness of each estimation method should also aid in the model selection for the inference process.

Method 1 essentially assumes that the distribution of symptoms is known. This deconvolution method based on equations (3) and (4) was introduced in the optics literature [13,16] and subsequently used in the epidemiological literature [13,17,18]:

Fix the initial estimate of the symptom profile distribution

\[
d'_0 = \frac{O^t}{N_t}
\]

Using this estimate, iterate in the parameters \((p_i)\) using equation (4) (keeping the parameters \((d_j)\) constant). Such iterates will converge to the unique maximum likelihood estimate \((p^*)\) for the incidence parameters conditional on the parameters \((d^j)\) [see section S1] regardless of the initial choice of non-zero initial conditions.

3.3 Inference Method 2. Other inference methods involve iterations in all of the model’s parameters \((p_i)\) and \((d_j)\)- the latter is generally known as “blind deconvolution” in the optics literature [19]. The advantage of those methods over Method 1 is that they allow to update the symptom profile distributions from the initial, data-derived estimate \((d^j)\) by increasing the likelihood of all observations \((Q^i, O^j)\). However given the lack of identifiability of the parameters using observations \((Q^i)\) alone as specified by equation (1), iterations in the symptom profile distribution parameters might move them further away from their true value and worsen the incidence curve estimates if the counts \((N_t)\) are too small.

Several inference methods involving EM iterations in all the parameters are possible, such as starting from an estimate in Method 1 and using both equations (4) and (5) for subsequent iterations. We have found that the classical EM scheme is fairly robust for sufficiently large data sets:

Iterate all the parameters simultaneously using both equations (4) and (5) in each step until convergence. An initial condition used in this paper corresponded to expected weekly incidence 1 for each infection in the survey sample \((Q^i.p^t(0) = 1)\).

4. Testing the deconvolution process by numerical simulations

To test the deconvolution process we generated synthetic weekly incidence curves both for influenza and non-influenza symptomatic cases over a 22-week period. The influenza incidence curve corresponds to an epidemic with basic reproductive number 1.35 and the serial interval distribution with mean 2.6 days [20] truncated at 7 days in a homogeneous population of 3,000,000.

We assumed that each week the number of individuals filling out the symptom survey is random, Poisson distributed with mean 5000. For our simulations, we used both choices of the symptom profiles described by equations (2a) and (2b), with their distribution for symptomatic flu cases estimated from the data in [12]. Similarly, for illustration purposes we have generated the non-flu symptom profile distribution for our simulations using the data from [21] (see section 5 of the methods).

We used weekly synthetic incidence and distribution of symptom profiles for flu and non-flu cases as described above to perform the following independent 3-step simulations:

1. Generate the (weekly) symptom count curves using the given incidence curves, symptom profile distributions and the weekly number of survey respondents.

2. Assume that the estimate of the symptom profile distribution \(d_{nu}\) is obtained from data on 500 symptomatic flu cases. Re-estimate the influenza symptom profile distribution by multinomial binning of size 500 with the initial distribution \(d_{nu}\). For non-flu symptoms, use the simulated symptom data from the first 3 weeks and the last 3 weeks (weeks 20–22) of the epidemic for an estimate the non-flu symptom profile distribution. During that period there are 2055 expected symptomatic cases given the incidence curves used in simulations and 99.6% of them are non-flu cases.

3. Using the symptom data in step 1 for weeks 4–19 and the re-estimates of the symptom profile distributions from step 2, apply the deconvolution scheme from the corresponding method; the output of the deconvolution process is an estimate of incidence between weeks 4–19.

We wish to point out that the accuracy of the deconvolution process depends not just on the number of individuals of survey but also on the level of circulation of influenza as well as other symptom causing pathogens in the community. Generally,
accuracy would be higher if the counts for symptom profiles specific to influenza (primarily fever) in the survey are significantly larger than the magnitude of the noise in the corresponding counts for non-influenza symptomatic cases in the survey. In section S3 we perform various sensitivity analyses for the accuracy of the deconvolution process (Figures S1, S2 and S4).

5. University of Michigan outbreak
We have used symptom surveillance data from a randomized controlled trial of non-pharmaceutical interventions for preventing transmission of influenza collected in February–March 2008 on the University of Michigan campus [21]. With 1,000 individuals initially recruited, the weekly number of survey respondents ranged from 830 to 902. The eight weeks in the symptom surveillance data represent a period after an apparent peak of a seasonal influenza outbreak on the wider campus, as can be seen from data on influenza positive tests and ILI consultations on the campus medical facilities. The latter data suggest that flu circulation during the last two of the eight weeks was particularly low (figure S6 in section S5); surveillance data for those last two weeks in the survey was used to assess the non-flu symptom profile distribution. This symptom profile data from the last two weeks, available for 642 symptomatic individuals was combined with symptom data for the 118 RT-PCR positive household contacts of flu cases, as specified in section 2 of the methods to assess the influenza outbreak during weeks 1–6 in the survey period.

Weekly symptom profile counts attributable to influenza cases in the survey were estimated to be quite low, of the same magnitude as the noise (departure from expected values) in the symptom profile counts attributable to non-flu cases. As result, weekly estimates of flu incidence for such a small sample size in addition to having wide confidence bounds are also generally upwardly biased because they cannot go below 0. Consequently we have combined all the surveillance data and were only able to estimate the cumulative flu attack rate during the surveillance period, which the bootstrap simulations have shown to be unbiased.

Results

1. Symptom profile distributions
Figure 1A plots the distribution of symptom profiles (as defined in equation (2a) in the Methods) for flu cases taken from [12], as described in section 3.1 of the methods. For our simulations we use the symptom profile distribution for non-flu cases obtained from the data in [21] (Figure 1B) – see also figure S5 in section S4.

Figure 1 suggests that fever is much more common for flu vs. non-flu cases, and one non-fever symptom only (cough, runny nose, or sore throat) is much more common for non-flu vs. flu cases.

2. Synthetic incidence and symptom data deconvolution

2.1 Synthetic incidence curves. We have generated synthetic incidence curves for flu and non-flu symptomatic cases as described in the Methods; those curves are plotted in Figure 2.

2.2 Symptom profiles (2a). We have performed 600 3-step simulations as specified in section 4 of the methods, both for Method 1 and Method 2. Figure 3 plots two samples of 5 deconvolved influenza symptomatic incidence curves against the original one (black) between weeks 4–19. One sample is for Method 1 and another is for Method 2.

The cumulative number of symptomatic influenza cases between weeks 4 and 19 was 993,693. For Method 1, for the sample of 600 deconvolved symptomatic influenza incidence curves, their cumulative incidences have mean 978,266, with 95% of them falling between 762,556 and 1,197,579. For Method 2, the mean is 1,004,402, with the 95% range between 823,519 and 1,185,116. We see that Method 2 gives a somewhat sharper estimate than Method 1 in this scenario.

2.3 Symptom profiles (2b). Figure 4 plots a sample of 5 deconvolved influenza symptomatic incidence curves against the original one (black) between weeks 4–19, where symptom profiles (2b) and deconvolution Method 2 were used.

The cumulative number of symptomatic influenza cases between weeks 4 and 19 was 993,693. For the sample of 600 deconvolved symptomatic influenza incidence curves, their cumulative incidences have mean 1,011,040, with 95% of them falling between 793,340 and 1,209,297. We see that the estimates are somewhat better using symptom profiles (2a) than (2b) in this scenario.

3. University of Michigan outbreak
Figure 5 plots the weekly percentage of cases with fever among the symptomatic cases during weeks 1–8 in the survey data from [21]. This percentage declined towards the end of the survey period,
Figure 2. Synthetic weekly symptomatic incidence curves (as described in section 4 of the Methods) used to test the robustness of the deconvolution process: flu (black), non-flu (red).
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Figure 3. Two samples of 5 deconvolved influenza symptomatic incidence curves (as described in section 4 of the Methods) against the original one (black). (A) Method 1 deconvolution. (B) Method 2 deconvolution.
doi:10.1371/journal.pone.0023380.g003
reflecting the decline in the flu outbreak. The latter decline is statistically significant: for example during the first 3 weeks, 221/1555 (14.21%) of symptomatic individuals in the survey had fever; during the next 3 weeks, 108/1004 (10.76%) of symptomatic individuals had fever (OR 1.37, p-value 0.011 for the Fisher exact test).

The cumulative symptomatic attack rate of influenza during the first 6 weeks was estimated to be 15.3%; however the 95% confidence bounds were wide (2.2%, 28.6%), suggesting that a larger survey sample size is needed for an accurate estimate.

Discussion

Timely estimates of the progression of an influenza epidemic are difficult to obtain. Currently available surveillance methods render a limited assessment of the epidemic’s growth patterns while serological surveillance is not commonly employed. Here we propose an alternative method to estimate incidence based on syndromic surveillance from population samples on regular times intervals. Such surveillance (e.g. [22]), combined with estimates of

Figure 4. A sample of 5 deconvolved influenza symptomatic incidence curves (as described in section 4 of the Methods) against the original one (black) for symptom profiles (2b), deconvolution method 2.

doi:10.1371/journal.pone.0023380.g004

Figure 5. Weekly percent of cases with fever among the symptomatic cases in the survey from [21].

doi:10.1371/journal.pone.0023380.g005
the distribution of symptom profiles for symptomatic influenza cases may, in principle, render an accurate estimate of the influenza incidence curve via the deconvolution process. We have proposed a collection of symptom profiles to be used in the deconvolution process, suggested how the corresponding symptom profile distributions can be estimated from data and tested the robustness of our method by numerical simulations. We wish to point out that while we restricted our methodology to influenza-like symptoms, it could in principle be adapted to estimation of incidence of other types of diseases (e.g., enteric infections), particularly if the infection of interest has a profile of symptoms which largely sets it apart from other related infections (similarly to the presence of fever, which is much more common for flu than for other respiratory infections).

The key potential limitation of our method is the ability to accurately estimate the distribution of symptom profiles for influenza and non-influenza cases. Estimate of the flu incidence is particularly sensitive to an estimate of the non-flu symptom profile distribution because there are many more symptomatic non-flu cases compared to the number of symptomatic flu cases in a survey, so a misattribution of a certain percentage of non-flu cases to flu is magnified relative to the flu data. Since the distribution of symptom profiles for non-flu cases may be specific to the given population, we propose to consider a time period in the surveillance data when very little influenza circulation is known to have taken place and use the symptom surveillance data for that period for an estimate of the symptom profile distribution for non-influenza cases. In this way, large sample size for the surveillance data would also ensure a more accurate estimate of the non-flu symptom profile distribution. Additionally, larger samples increase the size of the symptomatic counts attributable to influenza both in absolute terms and also relative to the noise in such counts attributable to non-flu cases, further improving the accuracy of the deconvolution process.

An additional potential issue with the symptom profile distribution for non-flu symptomatic cases is that it might change in time. The latter might occur due to an outbreak of a particular respiratory agent, such as human rhinovirus, coronavirus, or respiratory syncytial virus. The symptom profile distribution of these infections might be different from the overall distribution for symptomatic non-flu cases. One way to deal with this is to include this agent into the list of infections whose incidence is estimated through the deconvolution process. Alternatively, one may stick with flu and symptomatic non-flu cases as the two infectious profiles and use the excess fever approach (symptom profiles given by equation (2b)). The latter might still be robust because fever is much more common for flu than for non-flu cases and excess fever attributable to flu when flu circulation is sufficiently high should be larger than excess fever attributable to the potential difference in the probability of fever given non-flu symptoms during different time periods. This issue is examined through simulations in section S3, where a large non-flu outbreak with “atypical” symptoms is added as an unobserved component (Figure S3).

For the influenza symptom profile distribution, the most accurate estimates should be obtained using data for each specific (evolving) influenza season. Here for illustration purposes we have used data from [12] on RT-PCR positive household contacts recruited when a household index influenza case sought medical care. It is known that the accuracy of the PCR test is correlated with symptom presentation [23]. While three RT-PCR tests were administered on each household contact in [12], it is possible that some infected household contacts have tested negative, and this group is correlated with a weaker presentation of symptoms. Due to a relatively small sample size in [12] we did not attempt to derive age-stratified estimates of the symptom profile distribution. Some difference in symptom profile distribution for seasonal influenza A and B cases is possible (see section S2), though no statistically significant difference could be detected for the small sample of cases where sub-typing was performed. We believe that larger studies involving serology may render more accurate, age-stratified assessment of the syndrome distribution for seasonal influenza.

We have employed the above method for the data from a seasonal influenza outbreak on the University of Michigan campus. Those estimates have several potential limitations. The survey was not initially designed for our estimation method, with its size being too small for accurate estimates of influenza incidence. Data on symptom profiles for influenza used in the deconvolution process for the University of Michigan campus is obtained from a different population in [12]. Our assumption, based on the campus medical facilities data, that the influenza outbreak has waned towards the end of the study period may not be representative of the whole University of Michigan campus. Therefore our estimates for the University of Michigan outbreak are mostly given for illustrative purposes. A careful study design should be used to avoid some of those issues. Such design should perhaps involve the recruitment of a large number of individuals (larger than what is needed for a weekly survey) with a commitment from them to complete a certain number of surveys when prompted during the study period. The latter should decrease the correlation between the weekly symptom reports and increase the percent of weekly recruits who fill out a report, taking away from the recruitment bias when participation might be correlated with symptom presentation. Finally, serologic data if available could validate the syndrome-based estimation of infection attack rates.

**Supporting Information**

**Section S1** Convexity of the log likelihood function. (DOC)

**Section S2** Influenza A and B symptom profiles. (DOC)

**Section S3** Numerical simulations for the deconvolution process. (DOC)

**Section S4** Symptom profile distribution for PCR-negative, symptomatic household contacts. (DOC)

**Section S5** Influenza incidence proxy on the University of Michigan campus. (DOC)

Figure S1 Two samples of 5 deconvolved influenza symptomatic incidence curves (as described in section S3) against the original one (black). (A) Method 1 deconvolution. (B) Method 2 deconvolution. (TIF)

Figure S2 A sample of 5 deconvolved influenza symptomatic incidence curves (as described in section S3) against the original one (black). Symptom profiles (2b), Method 2. (TIF)

Figure S3 Adding an “unobserved” non-flu outbreak with atypical symptoms (as described in section S3). Symptomatic influenza incidence (black), “regular” non-flu incidence (red) and “outbreak” non-flu incidence (dashed red). (TIF)
Figure S4 The effect of an “unobserved” non-flu outbreak with atypical symptoms (as described in section S3) on the deconvolution process. A sample of 5 deconvolved influenza symptomatic incidence curves against the original one (black). Symptom profiles (2b), Method 2. Flu and non-flu incidence curves given by Figure S3.

Figure S5 Symptom profile distribution for PCR negative, symptomatic household contacts from [12] (A). Non-flu symptom profile distribution from the main body of the text (B).

References