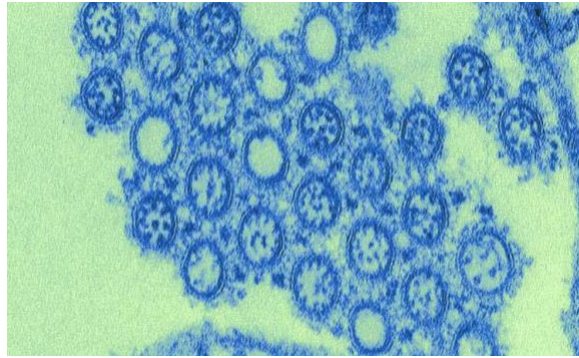


## Outbreak analysis practical: estimating the reproduction number

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2009 H1N1 influenza virus (source: CDC)

### Background

Pandemics arise when a new virus capable of human-to-human transmission emerges that is sufficiently distinct from circulating viruses so that the level of population immunity is low or nil. New strains emerge by transfer from a zoonotic reservoir. Exactly how new viruses emerge is not clear and may differ for different pandemics. Possibilities include genetic re-assortment or recombination between human and avian viral strains, possibly via intermediary species (e.g. pigs, poultry or other animals), or by gradual accumulation of adaptive mutations.

The potential for pandemic viruses to cause significant mortality is illustrated not only by SARS-CoV-2, the causative agent of COVID-19, but also the 1918-20 H1N1 'Spanish flu' which is estimated to have killed at least 20,000,000 people worldwide. Note however that the much lower mortality caused by the 1957 H2N2 'Asian flu', the 1966 H3N1 'Hong Kong flu' or the 2009 H1N1 pandemics shows that devastation is not an inevitable result of a pandemic but depends on the biology of each new strain as well as the impact of interventions.

Preparedness is greatly helped by knowledge of the epidemiological determinants of virus spread, such as the basic reproduction number  $R_0$  and the duration of infectiousness. The aim of this practical is to estimate some of these quantities.

### Objectives

From a methodological perspective, the practical will introduce you to some of the methods and issues surrounding parameter estimation in epidemic models. More specifically, we are going to use *2 different methods* to estimate the reproduction number from epidemic data. In part 1 of the practical, we will use the tree reconstruction method called EpiEstim, and in part 2 we will estimate the reproduction number by fitting a compartmental SIR model to the epidemic curve.

We are going to consider data from a school outbreak of H1N1 pandemic influenza virus which occurred in Pennsylvania in 2009 (data from Cauchemez et al, PNAS, 2011; paper attached to practical).

## Part 1

### Using tree reconstruction methods to estimate the reproduction number

Fitting a transmission model to data imposes making a range of assumptions for example about the population size or the initial proportion of susceptibles in the population. Rather than making such assumptions, we are now going to use tree reconstruction methods described in the lecture to estimate the instantaneous reproduction number  $R_t$  in the school.

For this, we only need the epidemic curve and the distribution of the generation time. In this section we talk about serial interval as a synonymous with generation time. We will use the same incidence dataset as in section 1.

- Open the influenza.txt file to see the incidence data
- Open the Excel file EpiEstim.xls

There are several sheets in it: Readme, Data, Output1 serial interval, Output2 R estimates and Figures. Readme will provide you with information on how to use the document, which is summarized in the following.

Data is the only sheet you have to modify; only light coloured cells have to be modified.

1. **Fill in the Incidence section** as shown in Snapshot 1; this will be done only once as we will only look at one dataset. Take 1 and 32 as the Min and Max times to match the data.

#### Snapshot 1:

	A	B	C	D
1	Incidence			
2				
3	Min Time (when first case appears)	Time	Incidence	
4				
5	Max Time			
6				
7				

**Incidence:**  
•Specify the first and last time steps in A4 and A6  
•Paste the incidence time series in B4-B...

2. **Specify your assumptions about the serial interval distributions** (see snapshot 2).

#### Snapshot 2:

Serial interval (SI)	
Account for uncertainty? (Y/N)	
<i>if uncertainty, specify:</i>	<i>If no uncertainty, specify:</i>
Mean Mean(SI)	Parametric? (Y/N)
Standard deviation (std) of Mean(SI)	<i>if parametric, specify:</i>
Min Mean(SI)	Mean SI (must be >=1 time step)
Max Mean(SI)	Standard deviation of SI
Mean Std(SI)	<i>If not parametric, specify the discrete distribution (starting from t=0)</i>
Std of Std(SI)	Time
Min Std(SI)	Discrete SI distribution
Max Std(SI)	
No. of SI distributions sampled	
Posterior sample size for each SI distribution	

**Serial interval (SI):**

- Specify in F4 whether you want to account for uncertainty in the SI distribution (Y) or not (N)
- First option (N):** not accounting for uncertainty  
Specify the SI distribution either in a parametric or non parametric way (H8)  
→If parametric, provide mean and sd for the SI (H12 and H14)  
→If non parametric, provide (in I20-I...) the whole distribution of the SI (time step given by data, starting at t=0)
- Second option (Y):** accounting for uncertainty  
Provide Mean, Sd, Min and Max for the mean SI (F8, F11, F13, F15)  
for the sd of the SI (F17, F19, F21, F23)  
Provide in F25 the number of SI distributions to explore (50 by default, the bigger the longer the estimation)  
Provide in F28 the number of R values to be drawn for each SI distribution explored (50 by default, the bigger the longer the estimation)

In a first analysis, we will use a FIXED parametric serial interval with mean 1.18 day and sd 0.96 day. Fill in the cells shown in red and yellow in Snapshot 2 accordingly.

3. **Specify the time windows** you want to use (see snapshot 3). Keep the posterior coefficient of variation to its default value of 0.3

**Snapshot 3:**

Time step choice	
Aimed posterior CV	
Custom time steps? (Y/N)	
<i>Is not custom, specify</i>	<i>If custom, specify time steps</i>
Length of time steps (e.g. =7 for estimates at the end of 7 day periods)	Start (Must be after the first case appearance)
No. of steps at which estimation is performed (e.g. =1 for performing estimation every day)	End

**Time windows: Note that time windows can overlap!**

- Specify in K4 the aimed posterior coefficient of variation (default 0.3, the smaller the more precise the R estimates but the longer the time windows need to be to get this precision)
- Specify in K7 whether you want custom time windows (Y) or not (N).
- First option (N):** custom time windows  
Give start times in M14-M... and end times in N14-N...
- Second option (Y):** non custom time windows  
Give the windows length in K13 (eg 7 if daily data and weekly widows)  
Give, in K18, the number of time windows at which estimation is performed (1 suggested to get estimates on sliding windows ending on each time step with data)

In a first analysis, we will explore the temporal variations of the reproduction number. For this, choose non-custom weekly sliding windows with a one-day lag between two successive windows (yellow and blue cells).

4. **Specify the prior mean and standard deviation** (see snapshot 4). Keep the default values of 5 and 5.

#### Snapshot 4:

P	<b>Prior distribution:</b>
<b>Prior distribution</b>	Specify the prior mean and standard deviation in P4 and P6.
Mean	Those reflect your knowledge on the value of R prior to observing those data.
5	A wide prior such as the default one (Mean = Sd = 5) is recommended.
Std	
5	

#### 5. Enable Macros

Click the File Menu and select Options from the left sidebar. In options, select Trust Center from the left sidebar and click Trust Center Settings button on the main window.

Now in Trust Center Settings dialog window, select Macro Settings from the left sidebar, choose Enable All Macros option and hit OK.

#### 6. Run the estimation!

#### Snapshot 5:

Click here to run!

Estimate R

WARNINGS:

This will delete all results in Output sheets and all figures in the Figure sheet

The estimation can take a few minutes

7. **Results** are presented as tables in sheets “Output1 serial interval” and “Output2 R estimates” and as figures in sheet “Figures”.

What is your estimate of the initial R? How does it compare with the estimate of Cauchemez et al.? See highlight in Cauchemez et al, page 5.

When does your mean R estimate fall below the threshold 1?

What happens at the end of the epidemic (look at the third figure)? What is a possible explanation?

### **Impact of school holidays**

The school closed during time interval day 18-day 24. Repeat the analysis using the following custom time windows (Change the yellow and green cells in Snapshot 3):

Day 1 to 17

Day 18 to 24

Day 25 to 31

What are your estimates for R before, during and after the holidays?

What is the estimated reduction in the reproduction number during school closure compared to before school closure? How does that compare to the one obtained by Cauchemez et al (see highlight, page 4)?

Is the effect statistically significant? How does that compare to Cauchemez et al.?

How do you think underreporting would affect R estimates? Would underreporting have an effect if the level of reporting was constant over time?

## Part 2

### Estimating the reproduction number by fitting a dynamical transmission model

In part 2 of the practical we are going to learn how to estimate the reproduction number using a compartmental model fitted to time series data.

#### Fitting a model and estimating parameters

For this analysis, we are going to make the following simplifying assumptions: 1) the outbreak in the school was closed (i.e. there were no importations and exportations of cases); 2) there was homogeneous mixing in the school; 3) there is no latent period and cases are infectious for the entire time they are infected; 4) we ignore issues of missing data and censoring in the data (see Cauchemez et al, PNAS, 2011 for an analysis of the data dealing with these problems).

Here, we will consider a simple SIR model:



$$N = S + I + R$$

Differential equations:

$$\frac{dS}{dt} = -\beta \cdot \frac{I}{N} \cdot S$$

$$\frac{dI}{dt} = \beta \cdot \frac{I}{N} \cdot S - \gamma \cdot I$$

$$\frac{dR}{dt} = \gamma \cdot I$$

Other helpful equations and how they can be rearranged:

$$R_0 = \beta / \gamma \quad \text{OR} \quad \beta = R_0 / D \quad \text{OR} \quad R_0 = \beta * D$$

$$D = 1 / \gamma \quad \text{OR} \quad \gamma = 1 / D$$

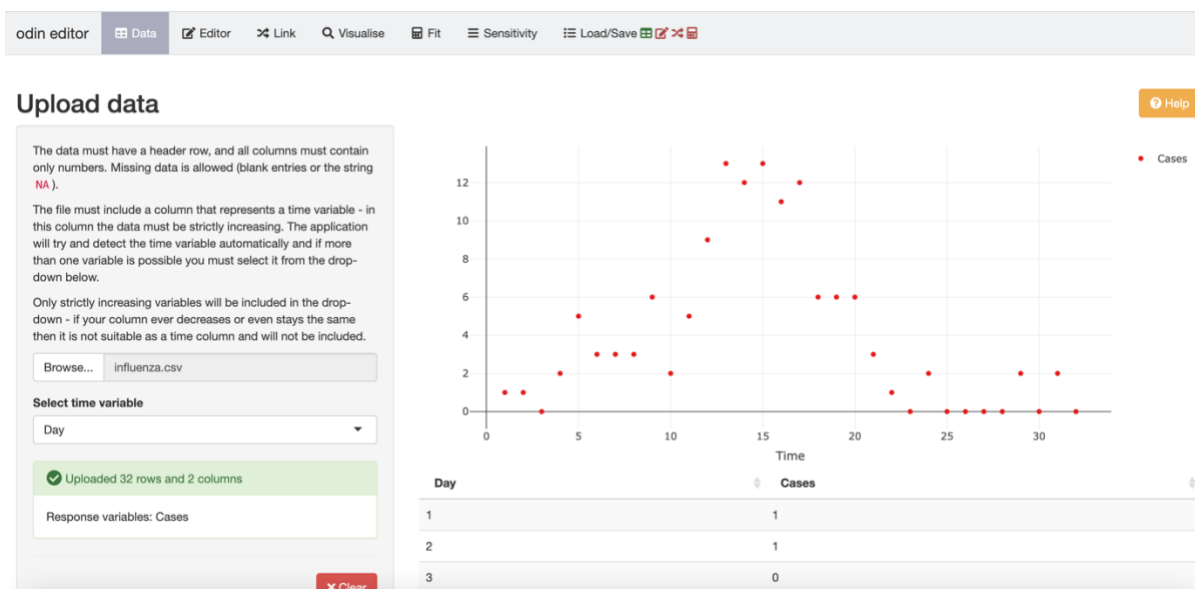
## Download the data and models

Access the odin app by following the link in the supporting files, or using the following link: <https://shiny.dide.imperial.ac.uk/infectiousdiseasemodels-lusaka-2022/>

In the Wednesday section, click the link “Influenza data” which will download “influenza\_data.csv”. Save this file in a convenient place.

## Run the model and link to the data

- Open the app “1. Basic SIR” and move to the “Data” tab if not there automatically.
- Click “Browse” and select “influenza.csv” in the location you saved it.
- The data should appear as a graph and table.



“Cases” gives the daily number of children of the school with symptoms onset.

→ Move to the “Editor” tab.

→ The Editor tab should now look like the screen below:

# Editor

Upload model file

Browse... SIR editor code.R

```
1 # initial conditions
2 initial(S) <- N - I_0
3 initial(I) <- I_0
4 initial(R) <- 0
5
6 # equations
7 deriv(S) <- -beta * S * (I / N)
8 deriv(I) <- beta * (I / N) * S - gamma * I
9 deriv(R) <- gamma * I
10
11 # parameter values
12 R_0 <- user(1.5)
13 D <- user(1)
14 I_0 <- 1 # default value
15 N <- 370
16
17 # convert parameters
18 beta <- R_0 / D
19 gamma <- 1 / D
20
```

Initially all 370 children are susceptible, apart from a single imported case

Define your transmission rate parameters

Compile Validate Reset Save

Auto validate

Look at how the SIR model is coded. What are the parameters  $D$  and  $I_0$ ? (NB the model begins at Day 0 with the onset of the first case within the school”).

Click “compile” to compile the model.

Now select the “Link” tab. Ensure there are tick marks to confirm the data has been successfully uploaded and model code has successfully been compiled.

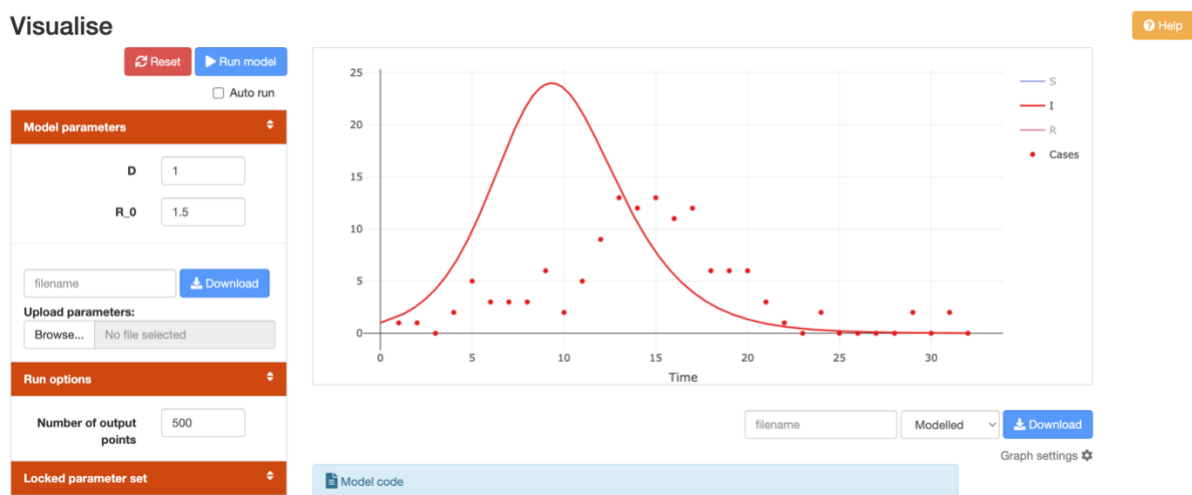


In the “Link” section we link the model to the data by specifying the variable in the model that is appropriate to fit to the data (i.e. “Cases”). Which variable is this?

Now move to the “Visualise” tab. Guess a value for D and R\_0 (all positive!) and click “Run model”.

### Manual fit

You should now see a chart of the dynamics of the variables of the model over time for your chosen set of parameter values, alongside the case data. How does your choice of parameter values match to the data? (NB it will help to visualise if you deselect all but the relevant). The picture below gives one example (of a poor fit!).



Vary the two parameters, how does each one affect the model output? Once you have a set of parameters which gives you a fit you’re happy with (NB don’t spend ages on this – if you haven’t got a set you’re happy with within, say, 5-10 minutes then just note down the set you think fits best of those you’ve explored so far).

$R_0$  =  
D = days

Move to the “sensitivity” tab and enter your best fitting set of parameters. Under “vary parameter” select each parameter in turn and select “range”, specify a reasonably wide range of values for each parameter and 10 runs. Click “Run model”. Can you describe the effect each parameter has on your output? Understanding this may help you to find a set of parameters you are happy with...

### Automated fit

Now we will assess the extent to which we are as skilled as the computer in finding a good fit to the data. In the “Fit” tab enter the set of parameter values you think gives you the best fit. This will replot the data, in the tab alongside a number called “sum of squares” – this is a weighted sum of the square of the differences between each data point and the variable you are fitting (i.e. if they were exactly the same the sum of the squares would be zero indicating a perfect fit).

If there are more than one set of parameters you think give an equally good fit (or you had a different set before and after you visited the ‘sensitivity’ tab) compare the sum of squares and set the values to those that give you the smallest number (as this is the one closest to going through all of the data points). Now make sure  $R_0$  and  $D$  are all ticked (to include them in the fitting process) and click ‘Fit model’. Note down the fitted sum of squares.

Sum of squares =

Auto fit parameters:

$R_0$  =

$D$  = days

### The relationship between the epidemic growth rate $r$ , the basic reproduction number $R_0$ and the generation time $T_g$ .

The generation time  $T_g$  is the time it takes between infection of one individual and subsequent infection of others by that individual.

If the epidemic growth rate  $r$  and the generation time  $T_g$  are known, it is possible to derive  $R_0$  from the following equation:

$$R_0 = \frac{1}{\int_0^{\infty} \exp(-r.t) g(t) dt} \quad (2)$$

where  $g(t)$  is the generation time distribution (i.e., the probability that the generation time is equal to  $t$ ).

For an SIR model, if the growth rate ( $r$ ) and  $D$  are known, the equation for  $R_0$  can be simplified as follows:

$$R_0 = 1 + rD$$

If  $R_0$  and  $D$  are known, this can be rearranged to estimate  $r$ :

$$r = (R_0 - 1) / D$$

And if  $r$  and  $R_0$  are known, the generation time ( $T_g$ ) can be estimated:

$$T_g = (R_0 - 1) / r$$

Based on this knowledge, what is the generation time,  $T_g$ , of the best-fitting model?

Why does the generation time in the school appear to be shorter than the generation time in the household? See highlight in Cauchemez et al, page 2.

How do your estimates of  $R$  and the generation time compare with those of Cauchemez et al? See highlight in Cauchemez et al, page 5. How does it compare with your estimate from EpiEstim?

### **Impact of school holidays**

The school closed during time interval day 18-day 24. We are going to try to estimate the impact of school closure.

→ Head back to the Wednesday section and now open the app “2. School holidays” app. This should then display code that has been modified so that the reproduction number is different when the school is open ( $R_0$ ) and when the school is closed ( $R_{0\_closure}$ ).

**Hit compile! Then link the model and data in the “link” tab**

The “Visualise” and “Fit” tab should reflect the new model with the additional parameter. If not retrace your steps from the “**Run the model and link to the data**” section previously.

Play around with this model to your hearts delight then redo the auto-fitting process, making sure you now tick three parameters (D, R\_0, and R\_0\_closure). Repeat this a couple of time with different initial guesses to check the computer has identified a good solution (if different values, again use the one with lowest sum of squares):

Sum of squares =  
R\_0 =  
R\_0\_closure =  
D = days

What is the estimated reduction in the reproduction number during school closure? How does that compare to the one obtained by Cauchemez et al (see highlight, page 4)?

Is the effect statistically significant?

What are the aspects of the outbreak investigation that you haven't accounted and that may lead to bias estimates?

### **Summary and discussion**

After trying out these 2 methods of estimating R (EpiEstim vs model fitting), can you think of pros and cons of the different methods? What are the key sensitivities?