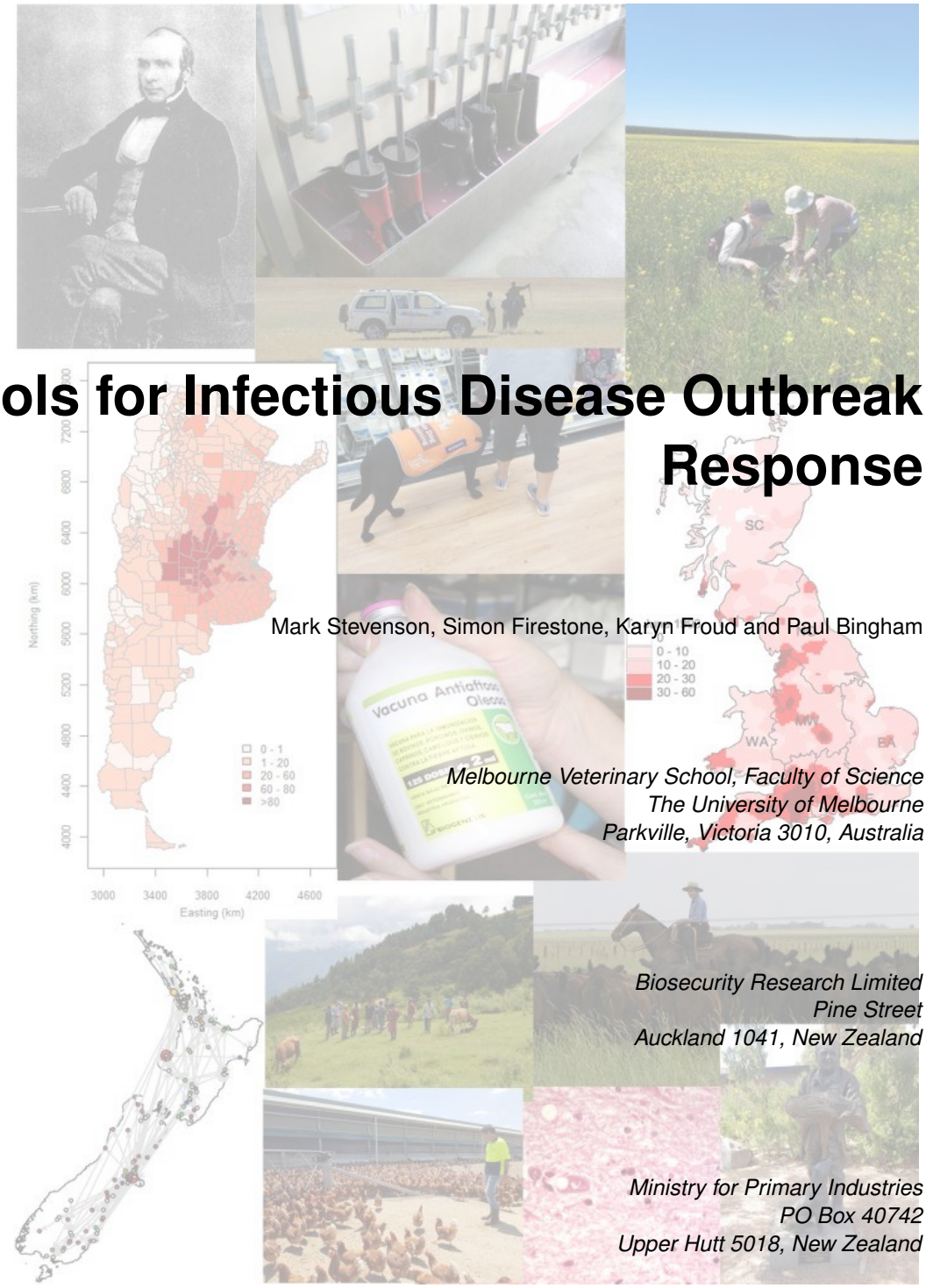

Tools for Infectious Disease Outbreak Response

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Contents

1 Time

1.1 Epidemic curve

Description

Plots an epidemic curve, that is, a frequency histogram of the count of incident events (e.g., disease cases) as a function of calendar time or number of days since outbreak start.

Usage

Upload a two-column CSV file listing:

Variable	Details
oid	Event identifier (integer, min 0, max ∞).
edate	Event date (date, format dd/mm/yyyy).

Function settings are as follows:

Variable	Details
CSV file	The name of the CSV file listing event identifiers and event date (character string).
Days between horizontal axis ticks	The number of days between horizontal axis tick marks (integer, default 7).
Bin width	Days represented by each bar of the frequency histogram (integer, default 1).
Maximum value for primary vertical axis	Upper limit of vertical axis of the plot (integer, default 40).
DPI for PNG	Dots per inch for the plot PNG file (integer, default 2400).

Details

The temporal pattern of an epidemic can be described by drawing a histogram in which the number of cases of disease are plotted as a function of calendar date or time. This graph, called an epidemic curve, provides a visual representation of an outbreak's magnitude over time. Through review of the incident case pattern(s) evident in an epidemic curve, it is possible to hypothesise:

- How an epidemic spread throughout a population.
- At what point you are in an epidemic.
- The likely date of exposure of the primary case.

Common source epidemics

In a common source epidemic subjects are exposed to a common noxious influence. A common point source epidemic is an epidemic in which a group of individuals are exposed to an infectious agent or a toxin from the same (point, i.e., single) source. An epidemic curve for a common point source epidemic is typically comprised of a rapid rise in case numbers over a single incubation period (in the case of an infectious disease) and a fall

in case numbers as either the number of susceptible individuals becomes exhausted or the level of infectious agent or toxin in the population becomes depleted. A common intermittent source epidemic is an epidemic in which exposure to an infectious agent or toxin occurs over an extended period of time in episodes. An epidemic curve for a common intermittent source epidemic in a large population is comprised of a series of waves of elevated case numbers corresponding to the (intermittent) periods of exposure.

A common continuous source epidemic is an epidemic in which exposure to an infectious agent or toxin occurs over an extended period of time (over more than one incubation period in the case of infectious agents). An epidemic curve for a common continuous source epidemic is typically comprised of a rise in case numbers over a single incubation period (a rise that is typically more gradual than a common point source epidemic) and a decrease in case numbers as the number of susceptible individuals in the population decreases. Compared with common point source epidemics the decrease in case numbers as a function of time tends to be more gradual because exposure continues to occur in a smaller susceptible population.

Propagated epidemics

A propagated epidemic occurs when a case of disease serves as a source of infection for subsequent cases and those subsequent cases, in turn, serve as sources for later cases. In this situation the epidemic curve is characterised by waves (peaks in case numbers) that are separated by a period roughly equivalent to the incubation period. Because of this local transmission effect, incident case numbers per day typically don't tend to be as high as with common point source, common intermittent source epidemics or common continuous source epidemics (but this will depend on the pathogen involved).

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Stephens, N., Sault, C., Firestone, S., Lightfoot, D., and Bell, C. (2007). Large outbreaks of *Salmonella Typhimurium* phage type 135 infections associated with the consumption of products containing raw egg in Tasmania. *Communicable Disease Intelligence Quarterly Report*, 31:118 – 124.

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Wilesmith, J., Stevenson, M., King, C., and Morris, R. (2003). Spatio-temporal epidemiology of foot-and-mouth disease in two counties of Great Britain in 2001. *Preventive Veterinary Medicine*, 61:157 – 170.

1.2 Growth phase of an outbreak

Description

Plots an epidemic curve, that is, a frequency histogram of the count of incident events (e.g., disease cases) as a function of calendar time or number of days since outbreak start with a superimposed line indicating the growth phase of the epidemic.

Usage

Upload a two-column CSV file listing:

Variable	Details
oid	Event identifier (integer, min 0, max ∞).
edate	Event date (date, format dd/mm/yyyy).

Function settings:

Variable	Details
CSV file	The name of the CSV file listing event identifiers and event date (character string).
Start of growth phase of epidemic	Integer representing the day on which the outbreak started to grow (integer, default 1).
End of growth phase of epidemic	Integer representing the day on which the outbreak stopped growing (integer, default 22).
Days between horizontal axis ticks	The number of days between horizontal axis tick marks (integer, default 7).
Bin width	Days represented by each bar of the frequency histogram (integer, default 1).
Maximum value for primary vertical axis	Upper limit of vertical axis of the plot (integer, default 40).
DPI for PNG	Dots per inch for the plot PNG file (integer, default 2400).

Details

This function returns predictions for the growth phase of an outbreak, using incident case counts. A log linear regression model is used for this purpose with the model taking the form:

$$log(y) = \beta_0 + \beta_1 t \tag{1}$$

Where y is the predicted number of incident cases of disease per day, t is the number of days from the start of the outbreak and β_1 the outbreak growth rate.

The function superimposes predictions from the model as a line over the number of detected cases per day, plotted as a frequency histogram. Uncertainty in model predictions are shown by the lower and upper 95% confidence interval, shown on the plot as dashed lines. The vertical dashed lines indicate the start of the outbreak and the end of the growth phase of the outbreak.

References

de Oliveira Otto, M., Brito, F., Tark, J., Bakota, E., Yamal, J., Marko, D., Sharma, S., Brown, M., Appana, S.,

Rector, A., Linder, S., Kiger, J., Tseng, K., Morrison, A., and Boerwinkle, E. (2022). Case growth analysis to inform local response to COVID-19 epidemic in a diverse U.S community. *Scientific Reports*, 12:16217.

1.3 Estimated dissemination ratio

Description

Plots an epidemic curve, that is, a frequency histogram of the count of incident events (e.g., disease cases) as a function of calendar time or number of days since outbreak start with a superimposed line indicating the estimated dissemination ratio.

Usage

Upload a two-column CSV file listing:

Variable	Details
oid	Event identifier (integer, min 0, max 8).
edate	Event date (date, format dd/mm/yyyy).

Function settings:

Variable	Details
CSV file	The name of the CSV file listing event identifiers and event date (character string).
EDR interval (days)	The estimated dissemination ratio interval, in days (integer, default 4).
Span for loess smooth	Amount of loess smoothing to apply to the computed EDR (numeric, min 0, max 1).
Include confidence intervals for EDR	Include confidence interval for EDR? (binary, yes or no).
Confidence interval for EDR	Magnitude of confidence interval for EDR plot (min 0, max = 1, default 0.95).
Days between horizontal axis ticks	The number of days between horizontal axis tick marks (integer, default 7).
Bin width	Days represented by each bar of the frequency histogram (integer, default 1).
Maximum value for primary vertical axis	Upper limit of vertical axis of the plot (integer, default 40).
DPI for PNG	Dots per inch for the plot PNG file (integer, default 2400).

Details

In infectious disease outbreaks the *n*-day estimated dissemination ratio (EDR) at day *n* equals the total number of incident disease cases between day *n* and day *[i - (n - 1)]* (inclusive) divided by the total number of incident disease cases between day *(i - n)* and day *(i - 2n) + 1* (inclusive). EDR values are often calculated for each day of an outbreak and presented as a time series analysis. If the EDR is consistently less than one, the epidemic is said to be 'under control'.

A simulation approach is used to calculate confidence intervals for each daily EDR estimate. The numerator and denominator of the EDR estimate for each day is taken in turn and a random number drawn from a Poisson distribution, using the calculated numerator and denominator value as the mean. EDR is then calculated for these simulated values and the process repeated 99 times. Confidence intervals are then derived from the vector of simulated values for each day.

Advantages

- An EDR plot provides the same information as an effective reproduction number plot using event counts only.

- During an ongoing outbreak EDR estimates are unbiased up until the last day of analysis.

Disadvantages

- EDR estimates can only be calculated when you're *2n* days into an outbreak.

This function uses the `epi.edr` function in the contributed `epiR` package (Stevenson et al., 2025) in R (R Development Core Team 2025).

References

Miller, W. (1976). A state-transition model of epidemic foot-and-mouth disease. pages 56 – 72. Estimated dissemination ratio.

Morris, R., Sanson, R., Stern, M., Stevenson, M., and Wilesmith, J. (2002). Decision-support tools for foot and mouth disease control. *Revue Scientifique et Technique de lOffice International des Epizooties*, 21:557 – 567.

Pérez-Reche, F. J., Taylor, N., McGuigan, C., Conaglen, P., Forbes, K., Strachan, N., and Honhold, N. (2021). Estimated Dissemination Ratio — A practical alternative to the reproduction number for infectious diseases. *Frontiers in Public Health*, 9.

Stevenson, M., Sargeant, E., Nunes, T., Heuer, C., Marshall, J., Sanchez, J., Thornton, R., Reiczigel, J., Robison-Cox, J., Sebastiani, P., Solymos, P., Yoshida, K., Jones, G., Pirikahu, S., Firestone, S., Kyle, R., Popp, J., and Mathew, J. (2025). epiR: Tools for the Analysis of Epidemiological Data.

R Core Team (2025). R: A language and environment for statistical computing. Technical report.

1.4 Effective reproduction numbers

Description

Plots an epidemic curve, that is, a frequency histogram of the count of incident events (e.g., disease cases) as a function of calendar time or number of days since outbreak start with a superimposed error bar plot showing effective reproductive numbers per unit of time.

Usage

Upload a two-column CSV file listing:

Variable	Details
oid	Event identifier (integer, min 0, max ∞).
edate	Event date (date, format dd/mm/yyyy).

Function settings:

Variable	Details
CSV file	The name of the CSV file listing event identifiers and event date (character string).
Mean serial interval (days)	Mean serial interval in days (integer, min 1, max 100, default 5.77).
SD serial interval (days)	Standard deviation of serial interval in days (integer, min 1, max 100, default 1.27).
Days between horizontal axis ticks	The number of days between horizontal axis tick marks (integer, default 7).
Bin width	Days represented by each bar of the frequency histogram (integer, default 1).
Maximum value for primary vertical axis	Upper limit of vertical axis of the plot (integer, default 40).
DPI for PNG	Dots per inch for the plot PNG file (integer, default 2400).

Details

This function provides estimates of the case reproduction number over time for an epidemic, for a disease with a specified serial interval defined as the period of time between the clinical signs onset times of the infector and infectee in a direct transmission pair. The methodology used follows that of Wallinga and Teunis (2004). Confidence intervals for case reproductive number are obtained by simulation.

For foot and mouth disease Hugh-Jones and Tinline (1976) report a median farm serial interval of 6 days (minimum 3 days, maximum 9 days). Assuming the farm level serial interval for FMD follows a gamma distribution, the corresponding shape and scale parameters for these data (calculated using quantile matching) are 20.7 and 0.278, respectively. The mean and standard deviation (set as default inputs for this function) are 5.77 and 1.27, respectively.

Advantages

- During an outbreak response unbiased effective reproduction number plots can be developed before estimated dissemination ratio plots.
- The concept of effective reproduction number tends to be better understood than estimated dissemination ratio by the general public.

Disadvantages

- Collecting data during an outbreak to calculate serial intervals can be challenging. In addition, it is likely that serial intervals will vary dependent on disease and the characteristics of the population at risk.
- During an ongoing outbreak effective reproduction number estimates are underestimated for the 7 to 10 days prior to the end of analysis period.

This function uses the `wallinga_teunis` function in the contributed `EpiEstim` package (Cori et al., 2021) in R (R Development Core Team 2025).

References

Aghaali, M., Kolifarhood, G., Nikbakht, R., Saadati, H., and Hashemi Nazari, S. (2020). Estimation of the serial interval and basic reproduction number of COVID-19 in Qom, Iran, and three other countries: A data-driven analysis in the early phase of the outbreak. *Transboundary and Emerging Diseases*, 67:2860 – 2868.

Cori, A., Ferguson, N., Fraser, C., and Cauchemez, S. (2013). A new framework and software to estimate time-varying reproduction numbers during epidemics. *American Journal of Epidemiology*, 178:1505 – 1512.

Cori, A., Cauchemez, S., Ferguson, N., Fraser, C., Dahlqwist, E., Demarsh, A., Jombart, T., Kamvar, Z., Lessler, J., Li, S., Polonsky, J., Stockwin, J., Thompson, R., and van Gaalen, R. (2021). EpiEstim: Estimate Time Varying Reproduction Numbers from Epidemic Curves.

Hugh-Jones, M. and Tinline, R. (1976). Studies on the 1967–68 foot and mouth disease epidemic: incubation period and herd serial interval. *Journal of Hygiene*, 77:141 – 153.

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Stockdale, J., Susvitasari, K., Tupper, P., Sobkowiak, B., Mulberry, N., Goncalves da Silva, A., Watt, A., Sherry, N., Minko, C., Howden, B., Lane, C., and Colijn, C. (2023). Genomic epidemiology offers high resolution estimates of serial intervals for COVID-19. *Nature Communications*, 14:4830.

Susvitasari, K., Tupper, P., Stockdale, J., and Colijn, C. (2023). A method to estimate the serial interval distribution under partially-sampled data. *Epidemics*, 45:100733.

Wallinga, J. and Teunis, P. (2004). Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. *American Journal of Epidemiology*, 160:509 – 516.

1.5 Tracing windows

Description

This function calculates start and end date of backward and forward trace windows given mode, minimum and maximum incubation periods, date of holding examination, age of lesions at the time of examination, examination date to end of cleaning and disinfection interval and length of back trace buffer period.

Usage

Variable	Details
Minimum incubation period	Minimum incubation period in days (integer, min 0, max 100, default 1).
Mode incubation period	Mode incubation period in days (integer, min 0, max 100, default 4).
Maximum incubation period	Maximum incubation period in days (integer, min 0, max 100, default 16).
Incubation period length	Incubation period length method (min and max values entered or confidence interval).
Date of examination	Date of on which animals on holding examined (date, default TODAY).
Lesion age at time of examination	Age of lesions at time of examination (integer, min 0, max 100, default 7).
Exam date to end of cleaning and disinfection	Exam date to end of cleaning and disinfection (integer, min 0, max 100, default 7).
Length of back trace buffer	Length of back trace buffer (integer, min 0, max 100, default 14).
Level of confidence	Magnitude of confidence interval (integer, min 0, max 1, default 0.95).

Details

Given an examination date, the back trace start date is:

$$\text{BT}_{start} = \text{Exam date} - \text{Lesion age} - \text{Incubation}_{max} - \text{Buffer} \tag{2}$$

The back trace end date is:

$$\text{BT}_{end} = \text{Exam date} - \text{Lesion age} - \text{Incubation}_{min} \tag{3}$$

The forward trace start date is:

$$\text{FT}_{start} = \text{Exam date} - \text{Lesion age} - \text{Incubation}_{max} - \text{Buffer} \tag{4}$$

The forward trace end date is:

$$\text{FT}_{end} = \text{Exam date} + \text{Clean disinfection interval} \tag{5}$$

Mode, minimum and maximum incubation periods for several infectious diseases of livestock are shown in the table below.

References

Arzt, J., Pacheco, J., and Rodriguez, L. (2010). The early pathogenesis of foot-and-mouth disease in cattle after aerosol inoculation. Identification of the nasopharynx as the primary site of infection. *Veterinary Pathology*, 47:1048 – 1063.

Disease	Incubation period (days)			References
	Min	Mode	Max	
African swine fever	3	5 to 7	21	Sanchez-Cordon et al. (2018)
Avian influenza	1	2 to 5	14	WOAH (2025)
Classical swine fever	2	4 to 7	14	Blome et al. (2017)
Foot and mouth disease	2	3 to 5	14 to 21	Arzt et al. (2010)

Blome, S., Staubach, C., Henke, J., Carlson, J., and Beer, M. (2017). Classical swine fever — an updated review. *Viruses*, 9.

Sanchez-Cordon, P., Montoya, M., Reis, A., and Dixon, L. (2018). African swine fever: A re-emerging viral disease threatening the global pig industry. *The Veterinary Journal*, 233:41 – 48.

WOAH (2025). Terrestrial Animal Health Code. World Organisation for Animal Health, Paris.

2 Space

2.1 Geocode a single address

Description

Returns the longitude and latitude (in decimal degrees) of a single address entered by the user as a text string. This function uses the Google geocoding API.

Details

References

Anonymous. Google Maps. Google Corporation, Mountain View, California. Accessed: 15 Apr 2025.

2.2 Geocode multiple addresses

Description

Returns the longitude and latitude (in decimal degrees) of addresses listed in a CSV file uploaded by the user. This function uses the Google geocoding API and is limited to geocoding 100 addresses per day.

Usage

Upload a two-column CSV file listing:

Variable	Details
id	Location identifier (integer, min 0, max ∞).
address	Location address (character string).

Details

References

Anonymous. Google Maps. Google Corporation, Mountain View, California. Accessed: 15 Apr 2025.

3 Space and time

3.1 Space time KML file

Description

Returns a space-time KML file using event date, longitude and latitude details listed in a CSV file uploaded by the user.

Usage

Upload a four-column CSV file listing:

Variable	Details
oid	Event identifier (integer, min 0, max 8).
edate	Event date (date, format dd/mm/yyyy).
lon	Longitude of event location (decimal degrees).
lat	Latitude of event location (decimal degrees).

A three-column CSV file (without `edate`) will return a space KML file (instead of a space-time KML file).

Details

Early versions of this function used the `plotKML` package in R. Since removal of `plotKML` from CRAN the function has been re-written, eliminating dependence on third party packages.

References

Hengl, T., Roudier, P., Beaudette, D., and Pebesma, E. (2015). plotKML: Scientific Visualization of Spatio-Temporal Data. *Journal of Statistical Software*, 63.

R Core Team (2025). R: A language and environment for statistical computing. Technical report.

4 About

Outbreak management tools is a collection of functions useful for outbreak response (e.g., the tracing window calculator) and outbreak response monitoring (e.g., the estimated dissemination ratio plot).

These functions were designed and developed by the Veterinary Epidemiology group (Mark Stevenson, Simon Firestone, Anke Wiethoelter, Caitlin Pfeiffer and Sandra Steele) at the University of Melbourne with inputs and suggestions from Karyn Froud (Biosecurity Research New Zealand) and Paul Bingham (Ministry for Primary Industries, New Zealand).

Many of the back end calculations are based on those implemented in the contributed epiR package in R also developed by the Veterinary Epidemiology group at the University of Melbourne.

References

Stevenson, M., Sargeant, E., Nunes, T., Heuer, C., Marshall, J., Sanchez, J., Thornton, R., Reiczigel, J., Robison-Cox, J., Sebastiani, P., Solymos, P., Yoshida, K., Jones, G., Pirikahu, S., Firestone, S., Kyle, R., Popp, J., and Mathew, J. (2025). epiR: Tools for the Analysis of Epidemiological Data.

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[3] Arzt, J., Pacheco, J., and Rodriguez, L. (2010). The early pathogenesis of foot-and-mouth disease in cattle after aerosol inoculation. Identification of the nasopharynx as the primary site of infection. *Veterinary Pathology*, 47:1048 – 1063.

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[5] Cori, A., Cauchemez, S., Ferguson, N., Fraser, C., Dahlqwist, E., Demarsh, A., Jombart, T., Kamvar, Z., Lessler, J., Li, S., Polonsky, J., Stockwin, J., Thompson, R., and van Gaalen, R. (2021). EpiEstim: Estimate Time Varying Reproduction Numbers from Epidemic Curves.

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[15] Stephens, N., Sault, C., Firestone, S., Lightfoot, D., and Bell, C. (2007). Large outbreaks of *Salmonella Typhimurium* phage type 135 infections associated with the consumption of products containing raw egg in Tasmania. *Communicable Disease Intelligence Quarterly Report*, 31:118 – 124.

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