

Package ‘EpiEstim’

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Title EpiEstim: a package to estimate time varying reproduction numbers from epidemic curves.

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Description This package provides tools to quantify transmissibility throughout an epidemic from the analysis of time series of incidence.

License GPL (>= 2)

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R topics documented:

EpiEstim-package	2
DiscrSI	3
EstimateR	4
Flu1918	8
Flu2009	9
Measles1861	10
OverallInfectivity	11
SARS2003	12
Smallpox1972	13
WT	14
Index	17

Description

Quantifying transmissibility during epidemics is essential to calibrate and adjust public health responses. Transmissibility at a certain time step can be measured by the instantaneous reproduction number R , the ratio of the number of new infections in this time step to the current infectivity due to previously infected cases. In this package, we propose a ready-to-use tool for estimating R from the incidence time-series. This tool uses novel analytical estimates of R , and also incorporates uncertainty on the serial interval distribution.

We also propose an implementation of the method proposed by Wallinga and Teunis (AJE, 2004) to estimate a related, though different, quantity, the case reproduction number (see Fraser, PLoS One, 2007 for the difference between the two).

The functions implemented in this package are:

- [DiscrSI](#), which computes the discrete distribution of the serial interval with a given mean and standard deviation;
- [OverallInfectivity](#), which calculates, at each time step, the overall infectivity due to previously infected individuals;
- [EstimateR](#), which estimates, for each time step, the instantaneous reproduction number, given the incidence time series and the serial interval distribution.
- [WT](#), which estimates, for each time step, the case reproduction number, given the incidence time series and the serial interval distribution.

Together with the package a few datasets are provided that contain time series of incidence and serial interval distribution for the following epidemics:

- [Measles1861](#): 1861 measles epidemic in Hagelloch, Germany;
- [Flu1918](#): 1918 H1N1 influenza pandemic in Baltimore;
- [Smallpox1972](#): 1972 smallpox epidemic in Kosovo;
- [SARS2003](#): 2003 severe acute respiratory syndrome (SARS) epidemic in Hong Kong;
- [Flu2009](#): 2009 H1N1 influenza pandemic in a school in Pennsylvania.

Details

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Author(s)

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with contributions from Simon Cauchemez, Neil Ferguson, Christophe Fraser and Thibaut Jombart.

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics. (submitted) Fraser, C. (2007) Estimating individual and household reproduction numbers in an emerging epidemic. PLoS One 2(1): e758. Wallinga, J. and P. Teunis (2004). Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. Am J Epidemiol 160(6): 509-516.

DiscrSI	<i>Discretized Generation Time Distribution Assuming A Shifted Gamma Distribution</i>
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Description

DiscrSI computes the discrete distribution of the serial interval, assuming that the serial interval is shifted Gamma distributed, with shift 1.

Usage

DiscrSI(k, mu, sigma)

Arguments

k	positive integer for which the discrete distribution is desired.
mu	a positive real giving the mean of the Gamma distribution.
sigma	a non-negative real giving the standard deviation of the Gamma distribution.

Details

Assuming that the serial interval is shifted Gamma distributed with mean μ , standard deviation σ and shift 1, the discrete probability w_k that the serial interval is equal to k is:

$$w_k = kF_{\{\mu-1, \sigma\}}(k) + (k-2)F_{\{\mu-1, \sigma\}}(k-2) - 2(k-1)F_{\{\mu-1, \sigma\}}(k-1) + (\mu-1)(2F_{\{\mu-1+\frac{\sigma^2}{\mu-1}, \sigma\sqrt{1+\frac{\sigma^2}{\mu-1}}\}}(k-1) - F_{\{\mu-1+\frac{\sigma^2}{\mu-1}, \sigma\sqrt{1+\frac{\sigma^2}{\mu-1}}\}}(k-2) - F_{\{\mu-1+\frac{\sigma^2}{\mu-1}, \sigma\sqrt{1+\frac{\sigma^2}{\mu-1}}\}}(k))$$

where $F_{\{\mu, \sigma\}}$ is the cumulative density function of a Gamma distribution with mean μ and standard deviation σ .

Value

DiscrSI(k, mu, sigma) gives the discrete probability w_k that the serial interval is equal to k .

Author(s)

Anne Cori <a.corii@imperial.ac.uk>

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics. (submitted)

See Also

[OverallInfectivity](#), [EstimateR](#), [WT](#)

Examples

```
## Computing the discrete serial interval of influenza
MeanFluSI <- 2.6
SdFluSI <- 1.5
DiscreteSIDistr <- vector()
for(i in 0:20)
{
  DiscreteSIDistr[i+1] <- DiscrSI(i, MeanFluSI, SdFluSI)
}
plot(0:20, DiscreteSIDistr, type="h", lwd=10, lend=1, xlab="time (days)", ylab="frequency")
title(main="Discrete distribution of the serial interval of influenza")
```

EstimateR

Estimation of the instantaneous reproduction number

Description

EstimateR estimates the instantaneous reproduction number of an epidemic, given the incidence time series and the serial interval distribution.

Usage

```
EstimateR(I, T.Start, T.End,
  method=c("NonParametricSI", "ParametricSI", "UncertainSI"),
  n1=NULL, n2=NULL, Mean.SI=NULL, Std.SI=NULL,
  Std.Mean.SI=NULL, Min.Mean.SI=NULL, Max.Mean.SI=NULL,
  Std.Std.SI=NULL, Min.Std.SI=NULL, Max.Std.SI=NULL,
  SI.Distr=NULL, Mean.Prior=5, Std.Prior=5, CV.Posterior=0.3,
  plot=FALSE, leg.pos="topright")
```

Arguments

I	vector of non-negative integers containing the incidence time series.
T.Start, T.End	vectors of positive integers giving the starting end ending times of each window over which the reproduction number will be estimated. These must be in ascending order, and so that for all i, T.Start[i] ≤ T.End[i]. T.Start[1] should be strictly after the first day with non null incidence.
method	one of "NonParametricSI", "ParametricSI" or "UncertainSI" (see details).

n1	for method "UncertainSI" ; positive integer giving the size of the sample of pairs (Mean SI (serial interval), Std SI) to be drawn (see details).
n2	for method "UncertainSI" ; positive integer giving the size of the sample drawn from each posterior distribution conditional to a pair (Mean SI, Std SI) (see details).
Mean.SI	for method "ParametricSI" and "UncertainSI" ; positive real giving the mean serial interval (method "ParametricSI") or the average mean serial interval (method "UncertainSI", see details).
Std.SI	for method "ParametricSI" and "UncertainSI" ; non negative real giving the standard deviation of the serial interval (method "ParametricSI") or the average standard deviation of the serial interval (method "UncertainSI", see details).
Std.Mean.SI	for method "UncertainSI" ; standard deviation of the distribution from which mean serial intervals are drawn (see details).
Min.Mean.SI	for method "UncertainSI" ; lower bound of the distribution from which mean serial intervals are drawn (see details).
Max.Mean.SI	for method "UncertainSI" ; upper bound of the distribution from which mean serial intervals are drawn (see details).
Std.Std.SI	for method "UncertainSI" ; standard deviation of the distribution from which standard deviations of the serial interval are drawn (see details).
Min.Std.SI	for method "UncertainSI" ; lower bound of the distribution from which standard deviations of the serial interval are drawn (see details).
Max.Std.SI	for method "UncertainSI" ; upper bound of the distribution from which standard deviations of the serial interval are drawn (see details).
SI.Distr	for method "NonParametricSI" ; vector of probabilities giving the discrete distribution of the serial interval, starting with SI.Distr[1] (probability that the serial interval is zero), which should be zero.
Mean.Prior	a positive number giving the mean of the common prior distribution for all reproduction numbers (see details).
Std.Prior	a positive number giving the standard deviation of the common prior distribution for all reproduction numbers (see details).
CV.Posterior	a positive number giving the aimed posterior coefficient of variation (see details).
plot	logical. If TRUE (default is FALSE), output is plotted (see value).
leg.pos	one of "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", "center" or <code>xy.coords(x, y)</code> , with x and y real numbers. This specifies the position of the legend in the plot. Alternatively, <code>locator(1)</code> can be used ; the user will then need to click where the legend needs to be written.

Details

Analytical estimates of the instantaneous reproduction number for an epidemic over predefined time windows can be obtained within a Bayesian framework, for a given discrete distribution of the serial interval (see references).

The more incident cases are observed over a time window, the smallest the posterior coefficient of variation (CV, ratio of standard deviation over mean) of the reproduction number. An aimed CV can be specified in the argument `CV.Posterior` (default is 0.3), and a warning will be produced if the incidence within one of the time windows considered is too low to get this CV.

The methods vary in the way the serial interval distribution is specified. The plots are also different according to the method used.

————— method "NonParametricSI" —————

The discrete distribution of the serial interval is directly specified in the argument `SI.Distr`.

If `plot` is TRUE, 3 plots are produced. The first one shows the epidemic curve. The second one shows the posterior median and 95% credible interval of the reproduction number. The estimate for a time window is plotted at the end of the time window. The position of the legend on that graph can be monitored by the argument `leg.pos` (default is "topright"). The third plot shows the discrete distribution of the serial interval.

————— method "ParametricSI" —————

The mean and standard deviation of the continuous distribution of the serial interval are given in the arguments `Mean.SI` and `Std.SI`. The discrete distribution of the serial interval is derived automatically using `DiscrSI`.

If `plot` is TRUE, 3 plots are produced, which are identical to the ones for method "NonParametricSI".

————— method "UncertainSI" —————

Method "UncertainSI" allows accounting for uncertainty on the serial interval distribution (see references). We allow the mean μ and standard deviation σ of the serial interval to vary according to truncated normal distributions. We sample n_1 pairs of mean and standard deviations, $(\mu^{(1)}, \sigma^{(1)}), \dots, (\mu^{(n_1)}, \sigma^{(n_1)})$, by first sampling the mean $\mu^{(k)}$ from its truncated normal distribution (with mean `Mean.SI`, standard deviation `Std.Mean.SI`, minimum `Min.Mean.SI` and maximum `Max.Mean.SI`), and then sampling the standard deviation $\sigma^{(k)}$ from its truncated normal distribution (with mean `Std.SI`, standard deviation `Std.Std.SI`, minimum `Min.Std.SI` and maximum `Max.Std.SI`), but imposing that $\sigma^{(k)} < \mu^{(k)}$. This constraint ensures that the Gamma probability density function of the serial interval is null at $t = 0$. Warnings are produced when the truncated normal distributions are not symmetric around the mean. For each pair $(\mu^{(k)}, \sigma^{(k)})$, we then draw a sample of size n_2 in the posterior distribution of the reproduction number over each time window, conditionally on this serial interval distribution. After pooling, a sample of size $n_1 \times n_2$ of the joint posterior distribution of the reproduction number over each time window is obtained. The posterior mean, standard deviation, and 0.025, 0.05, 0.25, 0.5, 0.75, 0.95, 0.975 quantiles of the reproduction number for each time window are obtained from this sample.

If `plot` is TRUE, 4 plots are produced. The first one shows the epidemic curve. The second one shows the posterior median and 95% credible interval of the reproduction number. The estimate for a time window is plotted at the end of the time window. The position of the legend on that graph can be monitored by the argument `leg.pos` (default is "topright"). The third and fourth plots show histograms of the sampled means and standard deviations of the serial interval.

Value

a list with components:

R	a dataframe containing: the times of start and end of each time window considered ; the posterior mean, std, and 0.025, 0.05, 0.25, 0.5, 0.75, 0.95, 0.975 quantiles of the reproduction number for each time window.
SIDistr	a dataframe containing: for method "NonParametricSI", the mean and standard deviation of the discrete serial interval distribution; for method "ParametricSI", the discrete serial interval distribution; for method "UncertainSI", the means and standard deviations of the serial interval sampled to account for uncertainty on the serial interval distribution (see details).

Author(s)

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References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics. (submitted)

See Also

[OverallInfectivity](#), [DiscrSI](#), [WT](#)

Examples

```
## load data on pandemic flu in a school in 2009
data("Flu2009")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="NonParametricSI",
  SI.Distr=Flu2009$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,3))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.

## estimate the instantaneous reproduction number (method "ParametricSI")
EstimateR(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="ParametricSI",
  Mean.SI=2.6, Std.SI=1.5, plot=TRUE)
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.

## estimate the instantaneous reproduction number (method "UncertainSI")
EstimateR(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="UncertainSI",
  Mean.SI=2.6, Std.Mean.SI=1, Min.Mean.SI=1, Max.Mean.SI=4.2,
  Std.SI=1.5, Std.Std.SI=0.5, Min.Std.SI=0.5, Max.Std.SI=2.5,
  n1=100, n2=100, plot=TRUE)
# the bottom left plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

Flu1918

Data on the 1918 H1N1 influenza pandemic in Baltimore

Description

This data set gives

1/ the daily incidence of onset of disease in Baltimore during the 1918 H1N1 influenza pandemic (see source and references),

2/ the discrete daily distribution of the serial interval for influenza, assuming a shifted Gamma distribution with mean 2.6 days, standard deviation 1.5 days and shift 1 day (see references).

Usage

Flu1918

Format

A list of two elements:

1/ "Incidence": a vector containing 92 days of observation,

2/ "SI.Distr": a vector containing a set of 12 probabilities.

Source

Frost W. and E. Sydenstricker (1919) Influenza in Maryland: preliminary statistics of certain localities. Public Health Rep.(34): 491-504.

References

Cauchemez S. et al. (2011) Role of social networks in shaping disease transmission during a community outbreak of 2009 H1N1 pandemic influenza. Proc Natl Acad Sci U S A 108(7), 2825-2830.

Ferguson N.M. et al. (2005) Strategies for containing an emerging influenza pandemic in Southeast Asia. Nature 437(7056), 209-214.

Fraser C. et al. (2011) Influenza Transmission in Households During the 1918 Pandemic. Am J Epidemiol 174(5): 505-514.

Frost W. and E. Sydenstricker (1919) Influenza in Maryland: preliminary statistics of certain localities. Public Health Rep.(34): 491-504.

Vynnycky E. et al. (2007) Estimates of the reproduction numbers of Spanish influenza using morbidity data. Int J Epidemiol 36(4): 881-889.

White L.F. and M. Pagano (2008) Transmissibility of the influenza virus in the 1918 pandemic. PLoS One 3(1): e1498.

Examples

```
## load data on pandemic flu in Baltimore in 1918
data("Flu1918")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(Flu1918$Incidence, T.Start=2:86, T.End=8:92, method="NonParametricSI",
SI.Distr=Flu1918$SI.Distr, plot=TRUE, leg.pos=xy.coords(60,2.5))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

Flu2009	<i>Data on the 2009 H1N1 influenza pandemic in a school in Pennsylvania</i>
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Description

This data set gives

1/ the daily incidence of onset of acute respiratory illness (ARI, defined as at least two symptoms among fever, cough, sore throat, and runny nose) amongst children in a school in Pennsylvania during the 2009 H1N1 influenza pandemic (see source and references),

2/ the discrete daily distribution of the serial interval for influenza, assuming a shifted Gamma distribution with mean 2.6 days, standard deviation 1.5 days and shift 1 day (see references).

Usage

```
Flu2009
```

Format

A list of two elements:

1/ "Incidence": a vector containing 32 days of observation,

2/ "SI.Distr": a vector containing a set of 12 probabilities.

Source

Cauchemez S. et al. (2011) Role of social networks in shaping disease transmission during a community outbreak of 2009 H1N1 pandemic influenza. *Proc Natl Acad Sci U S A* 108(7), 2825-2830.

References

Cauchemez S. et al. (2011) Role of social networks in shaping disease transmission during a community outbreak of 2009 H1N1 pandemic influenza. *Proc Natl Acad Sci U S A* 108(7), 2825-2830.

Ferguson N.M. et al. (2005) Strategies for containing an emerging influenza pandemic in Southeast Asia. *Nature* 437(7056), 209-214.

Examples

```
## load data on pandemic flu in a school in 2009
data("Flu2009")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="NonParametricSI",
SI.Distr=Flu2009$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,3))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

Measles1861

Data on the 1861 measles epidemic in Haggeloch, Germany

Description

This data set gives

1/ the daily incidence of onset of symptoms in Hallegoch (Germany) during the 1861 measles epidemic (see source and references),

2/ the discrete daily distribution of the serial interval for measles, assuming a shifted Gamma distribution with mean 14.9 days, standard deviation 3.9 days and shift 1 day (see references).

Usage

```
Measles1861
```

Format

A list of two elements:

1/ "Incidence": a vector containing 48 days of observation,

2/ "SI.Distr": a vector containing a set of 38 probabilities.

Source

Groendyke C. et al. (2011) Bayesian Inference for Contact Networks Given Epidemic Data. Scandinavian Journal of Statistics 38(3): 600-616.

References

Groendyke C. et al. (2011) Bayesian Inference for Contact Networks Given Epidemic Data. Scandinavian Journal of Statistics 38(3): 600-616.

Examples

```
## load data on measles in Hallegoch in 1861
data("Measles1861")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(Measles1861$Incidence, T.Start=17:42, T.End=23:48, method="NonParametricSI",
SI.Distr=Measles1861$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,7))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

OverallInfectivity *Overall Infectivity Due To Previously Infected Individuals*

Description

OverallInfectivity computes the overall infectivity due to previously infected individuals.

Usage

```
OverallInfectivity(I, SI.Distr)
```

Arguments

I vector of non-negative integers containing an incidence time series.
SI.Distr vector of probabilities giving the discrete distribution of the serial interval.

Details

The overall infectivity λ_t at time step t is equal to the sum of the previously infected individuals (given by the incidence vector I), weighed by their infectivity at time t (given by the discrete serial interval distribution w_k).

In mathematical terms:

$$\lambda_t = \sum_{k=1}^{t-1} I_{t-k} w_k$$

Value

OverallInfectivity(I, SI.Distr) returns a vector which contains the overall infectivity λ_t at each time step t .

Author(s)

Anne Cori <a.corii@imperial.ac.uk>

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics. (submitted)

See Also

[DiscrSI](#), [EstimateR](#)

Examples

```
## load data on pandemic flu in a school in 2009
data("Flu2009")

## compute overall infectivity
lambda <- OverallInfectivity(Flu2009$Incidence, Flu2009$SI.Distr)
par(mfrow=c(2,1))
plot(Flu2009$Incidence, type="s", xlab="time (days)", ylab="Incidence")
title(main="Epidemic curve")
plot(lambda, type="s", xlab="time (days)", ylab="Infectivity")
title(main="Overall infectivity")
```

SARS2003

Data on the 2003 SARS epidemic in Hong Kong

Description

This data set gives

1/ the daily incidence of onset of symptoms in Hong Kong during the 2003 severe acute respiratory syndrome (SARS) epidemic (see source and references),

2/ the discrete daily distribution of the serial interval for SARS, assuming a shifted Gamma distribution with mean 8.4 days, standard deviation 3.8 days and shift 1 day (see references).

Usage

```
SARS2003
```

Format

A list of two elements:

1/ "Incidence": a vector containing 107 days of observation,

2/ "SI.Distr": a vector containing a set of 25 probabilities.

Source

Cori A. et al. (2009) Temporal variability and social heterogeneity in disease transmission: the case of SARS in Hong Kong. *PLoS Comput Biol* 5(8): e1000471.

References

Cori A. et al. (2009) Temporal variability and social heterogeneity in disease transmission: the case of SARS in Hong Kong. *PLoS Comput Biol* 5(8): e1000471.

Lipsitch M. et al. (2003) Transmission dynamics and control of severe acute respiratory syndrome. *Science* 300(5627): 1966-1970.

Examples

```
## load data on SARS in Hong Kong in 2003
data("SARS2003")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(SARS2003$Incidence, T.Start=14:101, T.End=20:107, method="NonParametricSI",
SI.Distr=SARS2003$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,7))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

Smallpox1972

Data on the 1972 smallpox epidemic in Kosovo

Description

This data set gives

1/ the daily incidence of onset of symptoms in Kosovo during the 1972 smallpox epidemic (see source and references),

2/ the discrete daily distribution of the serial interval for smallpox, assuming a shifted Gamma distribution with mean 22.4 days, standard deviation 6.1 days and shift 1 day (see references).

Usage

```
Smallpox1972
```

Format

A list of two elements:

1/ "Incidence": a vector containing 57 days of observation,

2/ "SI.Distr": a vector containing a set of 46 probabilities.

Source

Fenner F. et al. (1988) *Smallpox and its Eradication*. Geneva, World Health Organization.

References

- Fenner F. et al. (1988) Smallpox and its Eradication. Geneva, World Health Organization.
- Gani R. and S. Leach (2001) Transmission potential of smallpox in contemporary populations. *Nature* 414(6865): 748-751.
- Riley S. and N. M. Ferguson (2006) Smallpox transmission and control: spatial dynamics in Great Britain. *Proc Natl Acad Sci U S A* 103(33): 12637-12642.

Examples

```
## load data on smallpox in Kosovo in 1972
data("Smallpox1972")

## estimate the instantaneous reproduction number (method "NonParametricSI")
EstimateR(Smallpox1972$Incidence, T.Start=27:51, T.End=33:57, method="NonParametricSI",
SI.Distr=Smallpox1972$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,15))
# the second plot produced shows, at each each day,
# the estimate of the instantaneous reproduction number over the 7-day window finishing on that day.
```

WT	<i>Estimation of the case reproduction number using the Wallinga and Teunis method</i>
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Description

WT estimates the case reproduction number of an epidemic, given the incidence time series and the serial interval distribution.

Usage

```
WT(I, T.Start, T.End,
method=c("NonParametricSI", "ParametricSI"),
Mean.SI=NULL, Std.SI=NULL,
SI.Distr=NULL, nSim=10,
plot=FALSE, leg.pos="topright")
```

Arguments

- | | |
|----------------|---|
| I | vector of non-negative integers containing the incidence time series. |
| T.Start, T.End | vectors of positive integers giving the starting end ending times of each window over which the reproduction number will be estimated. These must be in ascending order, and so that for all i, T.Start[i] ≤ T.End[i]. T.Start[1] should be strictly after the first day with non null incidence. |
| method | one of "NonParametricSI" or "ParametricSI" (see details). |
| Mean.SI | for method "ParametricSI" ; positive real giving the mean serial interval. |

Std.SI	for method "ParametricSI" ; non negative real giving the standard deviation of the serial interval.
SI.Distr	for method "NonParametricSI" ; vector of probabilities giving the discrete distribution of the serial interval, starting with SI.Distr[1] (probability that the serial interval is zero), which should be zero.
nSim	a positive integer giving the number of simulated epidemic trees used for computation of the confidence intervals of the case reproduction number (see details).
plot	logical. If TRUE (default is FALSE), output is plotted (see value).
leg.pos	one of "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right", "center" or <code>xy.coords(x, y)</code> , with x and y real numbers. This specifies the position of the legend in the plot. Alternatively, <code>locator(1)</code> can be used ; the user will then need to click where the legend needs to be written.

Details

Estimates of the case reproduction number for an epidemic over predefined time windows can be obtained, for a given discrete distribution of the serial interval, as proposed by Wallinga and Teunis (AJE, 2004). Confidence intervals are obtained by simulating a number (nSim) of possible transmission trees.

The methods vary in the way the serial interval distribution is specified.

————— method "NonParametricSI" —————

The discrete distribution of the serial interval is directly specified in the argument `SI.Distr`.

If `plot` is TRUE, 3 plots are produced. The first one shows the epidemic curve. The second one shows the posterior median and 95% credible interval of the reproduction number. The estimate for a time window is plotted at the end of the time window. The position of the legend on that graph can be monitored by the argument `leg.pos` (default is "topright"). The third plot shows the discrete distribution of the serial interval.

————— method "ParametricSI" —————

The mean and standard deviation of the continuous distribution of the serial interval are given in the arguments `Mean.SI` and `Std.SI`. The discrete distribution of the serial interval is derived automatically using [DiscrSI](#).

If `plot` is TRUE, 3 plots are produced, which are identical to the ones for method "NonParametricSI"

.

Value

a list with components:

R	a dataframe containing: the times of start and end of each time window considered ; the estimated mean, std, and 0.025 and 0.975 quantiles of the reproduction number for each time window.
SIDistr	a dataframe containing: for method "NonParametricSI", the mean and standard deviation of the discrete serial interval distribution; for method "ParametricSI", the discrete serial interval distribution.

Author(s)

Anne Cori <a.cor@imperial.ac.uk>

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics. (submitted) Wallinga, J. and P. Teunis (2004). Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. *Am J Epidemiol* 160(6): 509-516.

See Also

[DiscrSI](#), [EstimateR](#)

Examples

```
## load data on pandemic flu in a school in 2009
data("Flu2009")

## estimate the case reproduction number (method "NonParametricSI")
WT(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="NonParametricSI",
  SI.Distr=Flu2009$SI.Distr, plot=TRUE, leg.pos=xy.coords(1,1.75), nSim=100)
# the second plot produced shows, at each each day,
# the estimate of the cqse reproduction number over the 7-day window finishing on that day.

## estimate the case reproduction number (method "ParametricSI")
WT(Flu2009$Incidence, T.Start=2:26, T.End=8:32, method="ParametricSI",
  Mean.SI=2.6, Std.SI=1.5, plot=TRUE, nSim=100)
# the second plot produced shows, at each each day,
# the estimate of the cqse reproduction number over the 7-day window finishing on that day.
```


Index

*Topic **datasets**

Flu1918, [8](#)

Flu2009, [9](#)

Measles1861, [10](#)

SARS2003, [12](#)

Smallpox1972, [13](#)

*Topic **distribution**

DiscrSI, [3](#)

EstimateR, [4](#)

WT, [14](#)

DiscrSI, [2](#), [3](#), [6](#), [7](#), [12](#), [15](#), [16](#)

EpiEstim (EpiEstim-package), [2](#)

EpiEstim-package, [2](#)

EstimateR, [2](#), [4](#), [4](#), [12](#), [16](#)

Flu1918, [2](#), [8](#)

Flu2009, [2](#), [9](#)

Measles1861, [2](#), [10](#)

OverallInfectivity, [2](#), [4](#), [7](#), [11](#)

SARS2003, [2](#), [12](#)

Smallpox1972, [2](#), [13](#)

WT, [2](#), [4](#), [7](#), [14](#)

xy.coords, [5](#), [15](#)