Package: EpiEstim (via r-universe)

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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.

Depends R (>= 2.10)

Imports coarseDataTools, stats, graphics, reshape2, ggplot2, plyr, grid, gridExtra, plotly, fitdistrplus, coda, incidence, scales, grDevices, knitr

Remotes reconhub/incidence, nickreich/coarseDataTools@hackout3

Suggests testthat, compare, utils

License GPL (>=2)

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`check_cdt_samples_convergence` *Checking convergence of an MCMC chain by using the Gelman-Rubin algorithm*

Description

`check_cdt_samples_convergence` Checking convergence of an MCMC chain by using the Gelman-Rubin algorithm

Usage

```
check_cdt_samples_convergence(cdt_samples)
```

Arguments

`cdt_samples`	the `@sample` slot of a `cd.fit.mcmc` S4 object (see package `coarseDataTools`)

Details

This function splits an MCMC chain in two halfs and uses the Gelman-Rubin algorithm to assess convergence of the chain by comparing its two halves.

Value

TRUE if the Gelman Rubin test for convergence was successful, FALSE otherwise

Author(s)

Anne Cori

See Also

estimate_R

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## estimate the serial interval from data
SI_fit <- coarseDataTools::dic.fit.mcmc(dat = MockRotavirus$si_data,
                    dist="G",
                    init_pars=init_mcmc_params(MockRotavirus$si_data, "G"),
                    burnin = 1000,
                    n.samples = 5000)

## use check_cdt_samples_convergence to check convergence
converg_diag <- check_cdt_samples_convergence(SI_fit@samples)
converg_diag


## End(Not run)
```

---

coarse2estim *Link coarseDataTools and EpiEstim*

Description

coarse2estim Transforms outputs of coarseDataTools::dic.fit.mcmc to right format for input into estimate_R

Usage

```
coarse2estim(x = NULL, dist = x@dist, samples = x@samples, thin = 10)
```

Arguments

x	An object generated by function coarseDataTools::dic.fit.mcmc, containing posterior estimates of the serial interval distribution.
dist	The parametric distribution used when estimating the serial interval. #' Should be one of "G" (Gamma), "W" (Weibull), "L" (Lognormal), "off1G" (Gamma shifted by 1), "off1W" (Weibull shifted by 1), or "off1L" (Lognormal shifted by 1). If not present, computed automatically from x.
samples	A dataframe containing the posterior samples of serial interval parameters corresponding to the parametric choice specified in dist. If not present, computed automatically from x.
thin	A positive integer corresponding to thinning parameter; of the posterior sample of serial interval distributions in x, only 1 in thin will be kept, the rest will be discarded.

Value

A list with two elements:

- si_sample: a matrix where each column gives one distribution of the serial interval to be explored, obtained from x by thinning the MCMC chain.
- si_parametric_distr: the parametric distribution used when estimating the serial interval stored in x.

Author(s)

The Hackout3 Parameter Estimation team.

See Also

estimate_R

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## estimate the serial interval from data
SI.fit <- coarseDataTools::dic.fit.mcmc(dat = MockRotavirus$si_data,
                    dist = "G",
                    init.pars = init_mcmc_params(MockRotavirus$si_data, "G"),
                    burnin = 1000,
                    n.samples = 5000)

## use coarse2estim to turn this in the right format for estimate_R
```

```
si_sample <- coarse2estim(SI.fit, thin = 10)$si_sample

## use estimate_R to estimate the reproduction number
## based on these estimates of the serial interval
R_si_from_sample <- estimate_R(MockRotavirus$incidence,
                           method="si_from_sample",
                           si_sample=si_sample,
                           config = make_config(list(n2 = 50)))
plot(R_si_from_sample)

## End(Not run)
```

`discr_si` *Discretized Generation Time Distribution Assuming A Shifted Gamma Distribution*

Description

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

Usage

```
discr_si(k, mu, sigma)
```

Arguments

`k`	Positive integer, or vector of positive ingerers 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:

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

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

Value

Gives the discrete probability w_k that the serial interval is equal to k.

Author(s)

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

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics (AJE 2013).

See Also

overall_infectivity, estimate_R

Examples

```
## Computing the discrete serial interval of influenza
mean_flu_si <- 2.6
sd_flu_si <- 1.5
dicrete_si_distr <- discr_si(seq(0, 20), mean_flu_si, sd_flu_si)
plot(seq(0, 20), dicrete_si_distr, type = "h",
          lwd = 10, lend = 1, xlab = "time (days)", ylab = "frequency")
title(main = "Discrete distribution of the serial interval of influenza")
```

DiscrSI *Function to ensure compatibility with EpiEstim versions <2.0*

Description

Please only use for compatibility; Prefer the new discr_si function instead

Usage

```
DiscrSI(k, mu, sigma)
```

Arguments

k	see k in discr_si
mu	see mu in discr_si
sigma	see sigma in discr_si

estimate_R *Estimated Instantaneous Reproduction Number*

Description

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

Usage

```
estimate_R(incid, method = c("non_parametric_si", "parametric_si",
  "uncertain_si", "si_from_data", "si_from_sample"), si_data = NULL,
  si_sample = NULL, config = make_config(incid = incid, method = method))
```

Arguments

incid	One of the following • A vector (or a dataframe with a single column) of non-negative integers containing the incidence time series • A dataframe of non-negative integers with either i) incid$I containing the total incidence, or ii) two columns, so that incid$local contains the incidence of cases due to local transmission and incid$imported contains the incidence of imported cases (with incid$local + incid$imported the total incidence). If the dataframe contains a column incid$dates, this is used for plotting. incid$dates must contains only dates in a row. • An object of class incidence Note that the cases from the first time step are always all assumed to be imported cases.
method	One of "non_parametric_si", "parametric_si", "uncertain_si", "si_from_data" or "si_from_sample" (see details).
si_data	For method "si_from_data" ; the data on dates of symptoms of pairs of infector/infected individuals to be used to estimate the serial interval distribution (see details).
si_sample	For method "si_from_sample" ; a matrix where each column gives one distribution of the serial interval to be explored (see details).
config	An object of class estimate_R_config, as returned by function make_config.

Details

Analytical estimates of the 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).

Several methods are available to specify the serial interval distribution.

In short there are five methods to specify the serial interval distribution (see help for function `make_config` for more detail on each method). In the first two methods, a unique serial interval distribution is considered, whereas in the last three, a range of serial interval distributions are integrated over:

- In method "non_parametric_si" the user specifies the discrete distribution of the serial interval
- In method "parametric_si" the user specifies the mean and sd of the serial interval
- In method "uncertain_si" the mean and sd of the serial interval are each drawn from truncated normal distributions, with parameters specified by the user
- In method "si_from_data", the serial interval distribution is directly estimated, using MCMC, from interval censored exposure data, with data provided by the user together with a choice of parametric distribution for the serial interval
- In method "si_from_sample", the user directly provides the sample of serial interval distribution to use for estimation of R. This can be a useful alternative to the previous method, where the MCMC estimation of the serial interval distribution could be run once, and the same estimated SI distribution then used in estimate_R in different contexts, e.g. with different time windows, hence avoiding to rerun the MCMC everytime estimate_R is called.

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.
- method: the method used to estimate R, one of "non_parametric_si", "parametric_si", "uncertain_si", "si_from_data" or "si_from_sample"
- si_distr: a vector or dataframe (depending on the method) containing the discrete serial interval distribution(s) used for estimation
- SI.Moments: a vector or dataframe (depending on the method) containing the mean and std of the discrete serial interval distribution(s) used for estimation
- I: the time series of total incidence
- I_local: the time series of incidence of local cases (so that `I_local + I_imported = I`)
- I_imported: the time series of incidence of imported cases (so that `I_local + I_imported = I`)
- dates: a vector of dates corresponding to the incidence time series
- MCMC_converged (only for method `si_from_data`): a boolean showing whether the Gelman-Rubin MCMC convergence diagnostic was successful (`TRUE`) or not (`FALSE`)

Author(s)

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

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics (AJE 2013). Wallinga, J. and P. Teunis. Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures (AJE 2004). Reich, N.G. et al. Estimating incubation period distributions with coarse data (Statis. Med. 2009)

See Also

discr_si make_config

Examples

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

## estimate the reproduction number (method "non_parametric_si")
## when not specifying t_start and t_end in config, they are set to estimate
## the reproduction number on sliding weekly windows
res <- estimate_R(incid = Flu2009$incidence,
                  method = "non_parametric_si",
                  config = make_config(list(si_distr = Flu2009$si_distr)))
plot(res)

## the second plot produced shows, at each each day,
## the estimate of the reproduction number over the 7-day window
## finishing on that day.

## to specify t_start and t_end in config, e.g. to have biweekly sliding
## windows
t_start <- seq(2, nrow(Flu2009$incidence)-13)
t_end <- t_start + 13
res <- estimate_R(incid = Flu2009$incidence,
                  method = "non_parametric_si",
                  config = make_config(list(
                      si_distr = Flu2009$si_distr,
                      t_start = t_start,
                      t_end = t_end)))
plot(res)

## the second plot produced shows, at each each day,
## the estimate of the reproduction number over the 14-day window
## finishing on that day.

## example with an incidence object

## create fake data
library(incidence)
data <- c(0,1,1,2,1,3,4,5,5,5,5,4,4,26,6,7,9)
location <- sample(c("local","imported"), length(data), replace=TRUE)
location[1] <- "imported" # forcing the first case to be imported

## get incidence per group (location)
```

```
incid <- incidence(data, groups = location)

## Estimate R with assumptions on serial interval
res <- estimate_R(incid, method = "parametric_si",
                  config = make_config(list(
                  mean_si = 2.6, std_si = 1.5)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number over the 7-day window
## finishing on that day.

## estimate the reproduction number (method "parametric_si")
res <- estimate_R(Flu2009$incidence, method = "parametric_si",
                  config = make_config(list(mean_si = 2.6, std_si = 1.5)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number over the 7-day window
## finishing on that day.

## estimate the reproduction number (method "uncertain_si")
res <- estimate_R(Flu2009$incidence, method = "uncertain_si",
                  config = make_config(list(
                  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(res)
## the bottom left plot produced shows, at each each day,
## the estimate of the reproduction number over the 7-day window
## finishing on that day.

## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## estimate the reproduction number (method "si_from_data")
MCMC_seed <- 1
overall_seed <- 2
R_si_from_data <- estimate_R(MockRotavirus$incidence,
                             method = "si_from_data",
                             si_data = MockRotavirus$si_data,
                             config = make_config(list(si_parametric_distr = "G",
                                     mcmc_control = make_mcmc_control(list(burnin = 1000,
                                         thin = 10, seed = MCMC_seed),
                                         n1 = 500, n2 = 50,
                                         seed = overall_seed))))

## compare with version with no uncertainty
```

```
R_Parametric <- estimate_R(MockRotavirus$incidence,
                           method = "parametric_si",
                           config = make_config(list(
                           mean_si = mean(R_si_from_data$SI.Moments$Mean),
                              std_si = mean(R_si_from_data$SI.Moments$Std))))
## generate plots
p_uncertainty <- plot(R_si_from_data, "R", options_R=list(ylim=c(0, 1.5)))
p_no_uncertainty <- plot(R_Parametric, "R", options_R=list(ylim=c(0, 1.5)))
gridExtra::grid.arrange(p_uncertainty, p_no_uncertainty,ncol=2)

## the left hand side graph is with uncertainty in the SI distribution, the
## right hand side without.
## The credible intervals are wider when accounting for uncertainty in the SI
## distribution.

## estimate the reproduction number (method "si_from_sample")
MCMC_seed <- 1
overall_seed <- 2
SI.fit <- coarseDataTools::dic.fit.mcmc(dat = MockRotavirus$si_data,
                 dist = "G",
                 init.pars = init_mcmc_params(MockRotavirus$si_data, "G"),
                 burnin = 1000,
                 n.samples = 5000,
                 seed = MCMC_seed)
si_sample <- coarse2estim(SI.fit, thin = 10)$si_sample
R_si_from_sample <- estimate_R(MockRotavirus$incidence,
                               method = "si_from_sample",
                               si_sample = si_sample,
                               config = make_config(list(n2 = 50,
                               seed = overall_seed)))
plot(R_si_from_sample)

## check that R_si_from_sample is the same as R_si_from_data
## since they were generated using the same MCMC algorithm to generate the SI
## sample (either internally to EpiEstim or externally)
all(R_si_from_sample$R$`Mean(R)` == R_si_from_data$R$`Mean(R)`)

## End(Not run)
```

`EstimateR` *Function to ensure compatibility with EpiEstim versions <2.0*

Description

Please only use for compatibility; Prefer the new estimate_R function instead

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	see incid in estimate_R
T.Start	see config$t_start in estimate_R
T.End	see config$t_end in estimate_R
method	see method in estimate_R (but EstimateR uses CamelCase where estimate_R uses snake_case for the method names)
n1	see n1 in estimate_R
n2	see n2 in estimate_R
Mean.SI	see config$mean_si in estimate_R
Std.SI	see config$std_si in estimate_R
Std.Mean.SI	see config$std_mean_si in estimate_R
Min.Mean.SI	see config$min_mean_si in estimate_R
Max.Mean.SI	see config$max_mean_si in estimate_R
Std.Std.SI	see config$std_std_si in estimate_R
Min.Std.SI	see config$min_std_si in estimate_R
Max.Std.SI	see config$max_std_si in estimate_R
SI.Distr	see config$si_distr in estimate_R
Mean.Prior	see config$mean_prior in estimate_R
Std.Prior	see config$std_prior in estimate_R
CV.Posterior	see config$cv_posterior in estimate_R
plot	Not used anymore, only there for compatibility
leg.pos	Not used anymore, only there for compatibility

---

flu_2009_NYC_school *Data on the 2009 H1N1 influenza pandemic in a school in New York city*

Description

This data set gives: 1/ the daily incidence of self-reported and laboratory-confirmed cases of influenza amongst children in a school in New York city during the 2009 H1N1 influenza pandemic (see source and references), 2/ interval-censored serial interval data from the 2009 outbreak of H1N1 influenza in a New York city school (see references).

Format

A list of two elements:

incidence a dataframe with 14 lines containing dates in first column, and daily incidence in second column ,

si_data a dataframe containing data on the generation time for 16 pairs of infector/infected individuals (see references and see argument `si_data` of function `estimate_R` for details on columns)

Source

Lessler J. et al. (2009) Outbreak of 2009 pandemic influenza A (H1N1) at a New York City school. New Eng J Med 361: 2628-2636.

References

Lessler J. et al. (2009) Outbreak of 2009 pandemic influenza A (H1N1) at a New York City school. New Eng J Med 361: 2628-2636.

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on pandemic flu in a New York school in 2009
data("flu_2009_NYC_school")

## estimate the reproduction number (method "si_from_data")
res <- estimate_R(flu_2009_NYC_school$incidence, method="si_from_data",
         si_data = flu_2009_NYC_school$si_data,
          config = make_config(list(
                      t_start = seq(2, 8),
                      t_end = seq(8, 14),
                      si_parametric_distr = "G",
                      mcmc_control = make_mcmc_control(list(burnin = 1000,
                                  thin = 10, seed = 1)),
                      n1 = 1000, n2 = 50))
          )
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.

## End(Not run)
```

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).

Format

A list of two elements:

incidence a vector containing 92 days of observation,

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 reproduction number (method "non_parametric_si")
res <- estimate_R(Flu1918$incidence,
          method = "non_parametric_si",
          config = make_config(list(si_distr = Flu1918$si_distr)))
```

```
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.
```

`Flu2009` *Data on the 2009 H1N1 influenza pandemic in a school in Pennsylvania.*

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). 3/ interval-censored serial interval data from the 2009 outbreak of H1N1 influenza in San Antonio, Texas, USA (see references).

Format

A list of three elements:

incidence a dataframe with 32 lines containing dates in first column, and daily incidence in second column (Cauchemez et al., 2011),

si_distr a vector containing a set of 12 probabilities (Ferguson et al, 2005),

si_data a dataframe with 16 lines giving serial interval patient data collected in a household study in San Antonio, Texas throughout the 2009 H1N1 outbreak (Morgan et al., 2010).

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.

Morgan O.W. et al. (2010) Household transmission of pandemic (H1N1) 2009, San Antonio, Texas, USA, April-May 2009. Emerg Infect Dis 16: 631-637.

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 reproduction number (method "non_parametric_si")
res <- estimate_R(Flu2009$incidence, method="non_parametric_si",
          config = make_config(list(si_distr = Flu2009$si_distr)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.

## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## estimate the reproduction number (method "si_from_data")
res <- estimate_R(Flu2009$incidence, method="si_from_data",
          si_data = Flu2009$si_data,
          config = make_config(list(mcmc_control = make_mcmc_control(list(
                                burnin = 1000,
                                thin = 10, seed = 1)),
                      n1 = 1000, n2 = 50,
                      si_parametric_distr = "G")))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.

## End(Not run)
```

`init_mcmc_params` *init_mcmc_params Finds clever starting points for the MCMC to be used to estimate the serial interval, e.g. when using option* `si_from_data` *in* `estimate_R`

Description

`init_mcmc_params` Finds values of the serial interval distribution parameters, used to initalise the MCMC estimation of the serial interval distribution. Initial values are computed based on the observed mean and standard deviation of the sample from which the parameters are to be estiamted.

Usage

```
init_mcmc_params(si_data, dist = c("G", "W", "L", "off1G", "off1W", "off1L"))
```

Arguments

si_data	the data on dates of symptoms of pairs of infector/infected individuals to be used to estimate the serial interval distribution. This should be a dataframe with 5 columns: • EL: the lower bound of the symptom onset date of the infector (given as an integer) • ER: the upper bound of the symptom onset date of the infector (given as an integer). Should be such that ER>=EL • SL: the lower bound of the symptom onset date of the infected indivdiual (given as an integer) • SR: the upper bound of the symptom onset date of the infected indivdiual (given as an integer). Should be such that SR>=SL • type (optional): can have entries 0, 1, or 2, corresponding to doubly interval-censored, single interval-censored or exact observations, respectively, see Reich et al. Statist. Med. 2009. If not specified, this will be automatically computed from the dates
dist	the parametric distribution to use for the serial interval. Should be one of "G" (Gamma), "W" (Weibull), "L" (Lognormal), "off1G" (Gamma shifted by 1), "off1W" (Weibull shifted by 1), or "off1L" (Lognormal shifted by 1).

Value

A vector containing the initial values for the two parameters of the distribution of the serial interval. These are the shape and scale for all but the lognormal distribution, for which it is the meanlog and sdlog.

Author(s)

Anne Cori

See Also

estimate_R

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## get clever initial values for shape and scale of a Gamma distribution
## fitted to the the data MockRotavirus$si_data
clever_init_param <- init_mcmc_params(MockRotavirus$si_data, "G")

## estimate the serial interval from data using a clever starting point for
```

```
## the MCMC chain
SI_fit_clever <- coarseDataTools::dic.fit.mcmc(dat = MockRotavirus$si_data,
                              dist = "G",
                              init.pars = clever_init_param,
                              burnin = 1000,
                              n.samples = 5000)

## estimate the serial interval from data using a random starting point for
## the MCMC chain
SI_fit_naive <- coarseDataTools::dic.fit.mcmc(dat = MockRotavirus$si_data,
                              dist = "G",
                              burnin = 1000,
                              n.samples = 5000)


## use check_cdt_samples_convergence to check convergence in both situations
converg_diag_clever <- check_cdt_samples_convergence(SI_fit_clever@samples)
converg_diag_naive <- check_cdt_samples_convergence(SI_fit_naive@samples)
converg_diag_clever
converg_diag_naive


## End(Not run)
```

`make_config` *Set and check parameter settings of estimate_R*

Description

This function defines settings for estimate_R It takes a list of named items as input, set defaults where arguments are missing, and return a list of settings.

Usage

```
make_config(..., incid = NULL, method = c("non_parametric_si",
  "parametric_si", "uncertain_si", "si_from_data", "si_from_sample"))
```

Arguments

`...` Acceptables arguments for ... are:

t_start Vector of positive integers giving the starting 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.

t_end Vector of positive integers giving the 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]`.

n1 For method "uncertain_si" and "si_from_data"; positive integer giving the size of the sample of SI distributions to be drawn (see details).

n2 For methods "uncertain_si", "si_from_data" and "si_from_sample"; positive integer giving the size of the sample drawn from the posterior distribution of R for each serial interval distribution considered (see details).

mean_si For method "parametric_si" and "uncertain_si" ; positive real giving the mean serial interval (method "parametric_si") or the average mean serial interval (method "uncertain_si", see details).

std_si For method "parametric_si" and "uncertain_si" ; non negative real giving the stadard deviation of the serial interval (method "parametric_si") or the average standard deviation of the serial interval (method "uncertain_si", see details).

std_mean_si For method "uncertain_si" ; standard deviation of the distribution from which mean serial intervals are drawn (see details).

min_mean_si For method "uncertain_si" ; lower bound of the distribution from which mean serial intervals are drawn (see details).

max_mean_si For method "uncertain_si" ; upper bound of the distribution from which mean serial intervals are drawn (see details).

std_std_si For method "uncertain_si" ; standard deviation of the distribution from which standard deviations of the serial interval are drawn (see details).

min_std_si For method "uncertain_si" ; lower bound of the distribution from which standard deviations of the serial interval are drawn (see details).

max_std_si For method "uncertain_si" ; upper bound of the distribution from which standard deviations of the serial interval are drawn (see details).

si_distr For method "non_parametric_si" ; 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.

si_parametric_distr For method "si_from_data" ; the parametric distribution to use when estimating the serial interval from data on dates of symptoms of pairs of infector/infected individuals (see details). Should be one of "G" (Gamma), "W" (Weibull), "L" (Lognormal), "off1G" (Gamma shifted by 1), "off1W" (Weibull shifted by 1), or "off1L" (Lognormal shifted by 1).

mcmc_control An object of class `estimate_R_mcmc_control`, as returned by function `make_mcmc_control`.

seed An optional integer used as the seed for the random number generator at the start of the function (then potentially reset within the MCMC for method `si_from_data`); useful to get reproducible results.

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).

`incid` As in function`estimate_R`.

`method` As in function`estimate_R`.

Details

Analytical estimates of the reproduction number for an epidemic over predefined time windows can be obtained using function `estimate_R`, for a given discrete distribution of the serial interval. `make_config` allows to generate a configuration specifying the way the estimation will be performed.

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.

In short there are five methods to specify the serial interval distribution (see below for details on each method). In the first two methods, a unique serial interval distribution is considered, whereas in the last three, a range of serial interval distributions are integrated over:

- In method "non_parametric_si" the user specifies the discrete distribution of the serial interval
- In method "parametric_si" the user specifies the mean and sd of the serial interval
- In method "uncertain_si" the mean and sd of the serial interval are each drawn from truncated normal distributions, with parameters specified by the user
- In method "si_from_data", the serial interval distribution is directly estimated, using MCMC, from interval censored exposure data, with data provided by the user together with a choice of parametric distribution for the serial interval
- In method "si_from_sample", the user directly provides the sample of serial interval distribution to use for estimation of R. This can be a useful alternative to the previous method, where the MCMC estimation of the serial interval distribution could be run once, and the same estimated SI distribution then used in estimate_R in different contexts, e.g. with different time windows, hence avoiding to rerun the MCMC everytime estimate_R is called.

——————— `method "non_parametric_si"` ———————-

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

——————— `method "parametric_si"` ———————

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 `discr_si`.

——————— `method "uncertain_si"` ———————

`Method "uncertain_si"` allows accounting for uncertainty on the serial interval distribution as described in Cori et al. AJE 2013. We allow the mean μ and standard deviation σ of the serial interval to vary according to truncated normal distributions. We sample `n1` pairs of mean and standard deviations, $(\mu^{(1)}, \sigma^{(1)}), ..., (\mu^{(n_2)}, \sigma^{(n_2)})$, 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 `n2` in the posterior distribution of the reproduction number over each time

window, conditionnally on this serial interval distribution. After pooling, a sample of size n1 × n2 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.

——————— method "si_from_data" ———————

Method "si_from_data" allows accounting for uncertainty on the serial interval distribution. Unlike method "uncertain_si", where we arbitrarily vary the mean and std of the SI in truncated normal distributions, here, the scope of serial interval distributions considered is directly informed by data on the (potentially censored) dates of symptoms of pairs of infector/infected individuals. This data, specified in argument si_data, should be a dataframe with 5 columns:

- EL: the lower bound of the symptom onset date of the infector (given as an integer)
- ER: the upper bound of the symptom onset date of the infector (given as an integer). Should be such that ER>=EL
- SL: the lower bound of the symptom onset date of the infected indivdiual (given as an integer)
- SR: the upper bound of the symptom onset date of the infected indivdiual (given as an integer). Should be such that SR>=SL
- type (optional): can have entries 0, 1, or 2, corresponding to doubly interval-censored, single interval-censored or exact observations, respectively, see Reich et al. Statist. Med. 2009. If not specified, this will be automatically computed from the dates

Assuming a given parametric distribution for the serial interval distribution (specified in si_parametric_distr), the posterior distribution of the serial interval is estimated directly fom these data using MCMC methods implemented in the package coarsedatatools. The argument mcmc_control is a list of characteristics which control the MCMC. The MCMC is run for a total number of iterations of mcmc_control$burnin + n1*mcmc_control$thin; but the output is only recorded after the burnin, and only 1 in every mcmc_control$thin iterations, so that the posterior sample size is n1. For each element in the posterior sample of serial interval distribution, we then draw a sample of size n2 in the posterior distribution of the reproduction number over each time window, conditionnally on this serial interval distribution. After pooling, a sample of size n1 × n2 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.

——————— method "si_from_sample" ———————-

Method "si_from_sample" also allows accounting for uncertainty on the serial interval distribution. Unlike methods "uncertain_si" and "si_from_data", the user directly provides (in argument si_sample) a sample of serial interval distribution to be explored.

Value

An object of class estimate_R_config with components t_start, t_end, n1, n2, mean_si, std_si, std_mean_si, min_mean_si, max_mean_si, std_std_si, min_std_si, max_std_si, si_distr, si_parametric_distr, mcmc_control, seed, mean_prior, std_prior, cv_posterior, which can be used as an argument of function estimate_R.

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## estimate the reproduction number (method "si_from_data")
## we are not specifying the time windows, so by defaults this will estimate
## R on sliding weekly windows
incid <- MockRotavirus$incidence
method <- "si_from_data"
config <- make_config(incid = incid,
                      method = method,
                      list(si_parametric_distr = "G",
                      mcmc_control = make_mcmc_control(burnin = 1000,
                      thin = 10, seed = 1),
                      n1 = 500,
                      n2 = 50,
                      seed = 2))

R_si_from_data <- estimate_R(incid,
                             method = method,
                             si_data = MockRotavirus$si_data,
                             config = config)
plot(R_si_from_data)

## you can also create the config straight within the estimate_R call,
## in that case incid and method are automatically used from the estimate_R
## arguments:
R_si_from_data <- estimate_R(incid,
                             method = method,
                             si_data = MockRotavirus$si_data,
                             config = make_config(
                      list(si_parametric_distr = "G",
                      mcmc_control = make_mcmc_control(burnin = 1000,
                      thin = 10, seed = 1),
                      n1 = 500,
                      n2 = 50,
                      seed = 2)))
plot(R_si_from_data)

## End(Not run)
```

make_mcmc_control *make_mcmc_control Creates a list of mcmc control parameters to be used in* config$mcmc_control*, where* config *is an argument of the* estimate_R *function. This is used to configure the MCMC chain used to estimate the serial interval within* estimate_R *(with method "si_from_data").*

Description

make_mcmc_control Creates a list of mcmc control parameters to be used in config$mcmc_control, where config is an argument of the estimate_R function. This is used to configure the MCMC chain used to estimate the serial interval within estimate_R (with method "si_from_data").

Usage

```
make_mcmc_control(burnin = 3000, thin = 10, seed = as.integer(Sys.time()),
  init_pars = NULL)
```

Arguments

burnin	A positive integer giving the burnin used in the MCMC when estimating the serial interval distribution.
thin	A positive integer corresponding to thinning parameter; the MCMC will be run for burnin+n1*thin iterations; 1 in thin iterations will be recorded, after the burnin phase, so the posterior sample size is n1.
seed	An integer used as the seed for the random number generator at the start of the MCMC estimation; useful to get reproducible results.
init_pars	vector of size 2 corresponding to the initial values of parameters to use for the SI distribution. This is the shape and scale for all but the lognormal distribution, for which it is the meanlog and sdlog.

Details

The argument si_data, should be a dataframe with 5 columns:

- EL: the lower bound of the symptom onset date of the infector (given as an integer)
- ER: the upper bound of the symptom onset date of the infector (given as an integer). Should be such that ER>=EL
- SL: the lower bound of the symptom onset date of the infected indivdiual (given as an integer)
- SR: the upper bound of the symptom onset date of the infected indivdiual (given as an integer). Should be such that SR>=SL
- type (optional): can have entries 0, 1, or 2, corresponding to doubly interval-censored, single interval-censored or exact observations, respectively, see Reich et al. Statist. Med. 2009. If not specified, this will be automatically computed from the dates

Assuming a given parametric distribution for the serial interval distribution (specified in si_parametric_distr), the posterior distribution of the serial interval is estimated directly fom these data using MCMC methods implemented in the package

Value

An object of class `estimate_R_mcmc_control` with components burnin, thin, seed, init_pars. This can be used as an argument of function `make_config`.

Examples

```
## Not run:
## Note the following examples use an MCMC routine
## to estimate the serial interval distribution from data,
## so they may take a few minutes to run

## load data on rotavirus
data("MockRotavirus")

## estimate the reproduction number (method "si_from_data")
mcmc_seed <- 1
burnin <- 1000
thin <- 10
mcmc_control <- make_mcmc_control(burnin = burnin, thin = thin,
                     seed = mcmc_seed)

incid <- MockRotavirus$incidence
method <- "si_from_data"
overall_seed <- 2
config <- make_config(incid = incid,
                     method = method,
                     si_parametric_distr = "G",
                     mcmc_control = mcmc_control,
                     n1 = 500
                     n2 = 50,
                     seed = overall_seed)

R_si_from_data <- estimate_R(incid,
                             method = method,
                             si_data = MockRotavirus$si_data,
                             config = config)

## End(Not run)
```

`Measles1861` *Data on the 1861 measles epidemic in Hagelloch, 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).

Format

A list of two elements:

incidence a vector containing 48 days of observation,

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 reproduction number (method "non_parametric_si")
res <- estimate_R(Measles1861$incidence, method="non_parametric_si",
          config = make_config(list(
                t_start = seq(17, 42),
                t_end = seq(23, 48),
                si_distr = Measles1861$si_distr)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.
```

MockRotavirus *Mock data on a rotavirus epidemic.*

Description

This data set gives: 1/ the daily incidence of onset of symptoms in a mock outbreak of rotavirus , 2/ mock observations of symptom onset dates for 19 pairs of infector/infected individuals.

Format

A list of two elements:

incidence a vector containing 53 days of observation,

si_distr a dataframe containing a set of 19 observations; each observation corresponds to a pair of infector/infected individuals. EL and ER columns contain the lower an upper bounds of the dates of symptoms onset in the infectors. SL and SR columns contain the lower an upper bounds of the dates of symptoms onset in the infected indiviuals. The type column has entries 0, 1, or 2, corresponding to doubly interval-censored, single interval-censored or exact observations, respectively, see Reich et al. Statist. Med. 2009

Examples

```
## Not run:
## Note the following example uses an MCMC routine
## to estimate the serial interval distribution from data,
## so may take a few minutes to run

## load data
data("MockRotavirus")

## estimate the reproduction number (method "si_from_data")
res <- estimate_R(MockRotavirus$incidence,
          method = "si_from_data",
          si_data = MockRotavirus$si_data,
          config = make_config(list(
            si_parametric_distr = "G",
            mcmc_control = make_mcmc_control(list(burnin = 3000, thin = 10)),
            n1 = 500, n2 = 50)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.

## End(Not run)
```

---

overall_infectivity *Overall Infectivity Due To Previously Infected Individuals*

Description

`overall_infectivity` computes the overall infectivity due to previously infected individuals.

Usage

```
overall_infectivity(incid, si_distr)
```

Arguments

`incid`	One of the following • A vector (or a dataframe with a single column) of non-negative integers containing an incidence time series

- A dataframe of non-negative integers with two columns, so that `incid$local` contains the incidence of cases due to local transmission and `incid$imported` contains the incidence of imported cases (with `incid$local + incid$imported` the total incidence).

Note that the cases from the first time step are always all assumed to be imported cases.

`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, with `I = incid$local + incid$imported` if I is a matrix), weigthed 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

A vector which contains the overall infectivity λ_t at each time step

Author(s)

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

References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics (AJE 2013).

See Also

discr_si, estimate_R

Examples

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

## compute overall infectivity
lambda <- overall_infectivity(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")
```

OverallInfectivity *Function to ensure compatibility with EpiEstim versions <2.0*

Description

Please only use for compatibility; Prefer the new overall_infectivity function instead

Usage

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

Arguments

I	see incid in overall_infectivity
SI.Distr	see si_distr in overall_infectivity

plot.estimate_R *Plot outputs of estimate_r*

Description

The plot method of estimate_r objects can be used to visualise three types of information. The first one shows the epidemic curve. The second one shows the posterior mean and 95% credible interval of the reproduction number. The estimate for a time window is plotted at the end of the time window. The third plot shows the discrete distribution(s) of the serial interval.

Usage

```
## S3 method for class 'estimate_R'
plot(x, what = c("all", "incid", "R", "SI"),
  add_imported_cases = FALSE, options_I = list(col = palette(), transp =
  0.7, xlim = NULL, ylim = NULL), options_R = list(col = palette(), transp =
  0.2, xlim = NULL, ylim = NULL), options_SI = list(prob_min = 0.001, col =
  "black", transp = 0.25, xlim = NULL, ylim = NULL), legend = TRUE, ...)
```

Arguments

x	The output of function estimate_R or function wallinga_teunis, or a list of such outputs. If a list, and what='R' or what='all', all estimates of R are plotted on a single graph.
what	A string specifying what to plot, namely the incidence time series (what='incid'), the estimated reproduction number (what='R'), the serial interval distribution (what='SI', or all three (what='all')).

`add_imported_cases`
: A boolean to specify whether, on the incidence time series plot, to add the incidence of imported cases.

`options_I`
: For what = "incid" or "all". A list of graphical options:

  col A colour or vector of colours used for plotting incid. By default uses the default R colours.

  transp A numeric value between 0 and 1 used to monitor transparency of the bars plotted. Defaults to 0.7.

  xlim A parameter similar to that in `par`, to monitor the limits of the horizontal axis

  ylim A parameter similar to that in `par`, to monitor the limits of the vertical axis

`options_R`
: For what = "R" or "all". A list of graphical options:

  col A colour or vector of colours used for plotting R. By default uses the default R colours.

  transp A numeric value between 0 and 1 used to monitor transparency of the 95%CrI. Defaults to 0.2.

  xlim A parameter similar to that in `par`, to monitor the limits of the horizontal axis

  ylim A parameter similar to that in `par`, to monitor the limits of the vertical axis

`options_SI`
: For what = "SI" or "all". A list of graphical options:

  prob_min A numeric value between 0 and 1. The SI distributions explored are only shown from time 0 up to the time t so that each distribution explored has probability < `prob_min` to be on any time step after t. Defaults to 0.001.

  col A colour or vector of colours used for plotting the SI. Defaults to black.

  transp A numeric value between 0 and 1 used to monitor transparency of the lines. Defaults to 0.25

  xlim A parameter similar to that in `par`, to monitor the limits of the horizontal axis

  ylim A parameter similar to that in `par`, to monitor the limits of the vertical axis

`legend`
: A boolean (TRUE by default) governing the presence / absence of legends on the plots

`...`
: further arguments passed to other methods.

Value

a plot (if `what = "incid"`, `"R"`, or `"SI"`) or a `grob` object (if `what = "all"`).

Author(s)

Rolina van Gaalen <rolina.van.gaalen@rivm.nl> and Anne Cori <a.cori@imperial.ac.uk>; S3 method by Thibaut Jombart

See Also

`estimate_R` and `wallinga_teunis`

Examples

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

## estimate the instantaneous reproduction number
## (method "non_parametric_si")
R_i <- estimate_R(Flu2009$incidence, method = "non_parametric_si",
                  config = list(t_start = seq(2, 26), t_end = seq(8, 32),
                                si_distr = Flu2009$si_distr))

## visualise results
plot(R_i, legend = FALSE)

## estimate the instantaneous reproduction number
## (method "non_parametric_si")
R_c <- wallinga_teunis(Flu2009$incidence, method = "non_parametric_si",
          config = list(t_start = seq(2, 26), t_end = seq(8, 32),
          si_distr = Flu2009$si_distr ))

## produce plot of the incidence
## (with, on top of total incidence, the incidence of imported cases),
## estimated instantaneous and case reproduction numbers
## and serial interval distribution used
p_I <- plot(R_i, "incid", add_imported_cases=TRUE) # plots the incidence
p_SI <- plot(R_i, "SI") # plots the serial interval distribution
p_Ri <- plot(R_i, "R",
          options_R = list(ylim = c(0, 4)))
          # plots the estimated instantaneous reproduction number
p_Rc <- plot(R_c, "R",
          list(ylim = c(0, 4)))
          # plots the estimated case reproduction number
gridExtra::grid.arrange(p_I, p_SI, p_Ri, p_Rc, ncol = 2)
```

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).

Format

A list of two elements:

incidence a vector containing 107 days of observation,

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 reproduction number (method "non_parametric_si")
res <- estimate_R(SARS2003$incidence, method="non_parametric_si",
          config = make_config(list(
                      t_start = seq(14, 101),
                      t_end = seq(20, 107),
                      si_distr = SARS2003$si_distr)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the 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).

Format

A list of two elements:

incidence a vector containing 57 days of observation,

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 reproduction number (method "non_parametric_si")
res <- estimate_R(Smallpox1972$incidence, method="non_parametric_si",
          config = make_config(list(
                      t_start = seq(27, 51),
                      t_end = seq(33, 57),
                      si_distr = Smallpox1972$si_distr)))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the reproduction number
## over the 7-day window finishing on that day.
```

`wallinga_teunis` *Estimation of the case reproduction number using the Wallinga and Teunis method*

Description

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

Usage

```
wallinga_teunis(incid, method = c("non_parametric_si", "parametric_si"),
  config)
```

Arguments

`incid`	One of the following • Vector (or a dataframe with a column named 'incid') of non-negative integers containing an incidence time series. If the dataframe contains a column `incid$dates`, this is used for plotting. `incid$dates` must contains only dates in a row. • An object of class `incidence`
`method`	the method used to estimate R, one of "non_parametric_si", "parametric_si", "uncertain_si", "si_from_data" or "si_from_sample"

`config` a list with the following elements:

- t_start: Vector of positive integers giving the starting 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.
- t_end: Vector of positive integers giving the 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]`.
- method: One of "non_parametric_si" or "parametric_si" (see details).
- mean_si: For method "parametric_si" ; positive real giving the mean serial interval.
- std_si: For method "parametric_si" ; non negative real giving the stadard deviation of the serial interval.
- si_distr: For method "non_parametric_si" ; 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.
- n_sim: A positive integer giving the number of simulated epidemic trees used for computation of the confidence intervals of the case reproduction number (see details).

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 (config$n_sim) of possible transmission trees.

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

——————— `method "non_parametric_si"` ———————

The discrete distribution of the serial interval is directly specified in the argument `config$si_distr`.

——————— `method "parametric_si"` ———————

The mean and standard deviation of the continuous distribution of the serial interval are given in the arguments `config$mean_si` and `config$std_si`. The discrete distribution of the serial interval is derived automatically using `discr_si`.

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.
- si_distr: a vector containing the discrete serial interval distribution used for estimation
- SI.Moments: a vector containing the mean and std of the discrete serial interval distribution(s) used for estimation
- I: the time series of total incidence

- I_local: the time series of incidence of local cases (so that `I_local` + `I_imported` = `I`)
- I_imported: the time series of incidence of imported cases (so that `I_local` + `I_imported` = `I`)
- dates: a vector of dates corresponding to the incidence time series

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References

Cori, A. et al. A new framework and software to estimate time-varying reproduction numbers during epidemics (AJE 2013). Wallinga, J. and P. Teunis. Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures (AJE 2004).

See Also

discr_si, estimate_R

Examples

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

## estimate the case reproduction number (method "non_parametric_si")
res <- wallinga_teunis(Flu2009$incidence,
   method="non_parametric_si",
   config = list(t_start = seq(2, 26), t_end = seq(8, 32),
                 si_distr = Flu2009$si_distr,
                 n_sim = 100))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the case reproduction number over the 7-day window
## finishing on that day.

## estimate the case reproduction number (method "parametric_si")
res <- wallinga_teunis(Flu2009$incidence, method="parametric_si",
   config = list(t_start = seq(2, 26), t_end = seq(8, 32),
                 mean_si = 2.6, std_si = 1.5,
                 n_sim = 100))
plot(res)
## the second plot produced shows, at each each day,
## the estimate of the case reproduction number over the 7-day window
## finishing on that day.
```

WT *Function to ensure compatibility with EpiEstim versions <2.0*

Description

Please only use for compatibility; Prefer the new wallinga_teunis function instead

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	see incid in wallinga_teunis
T.Start	see config$t_start in wallinga_teunis
T.End	see config$t_end in wallinga_teunis
method	see method in wallinga_teunis (but WT uses CamelCase where wallinga_teunis uses snake_case for the method names)
Mean.SI	see config$mean_si in wallinga_teunis
Std.SI	see config$std_si in wallinga_teunis
SI.Distr	see config$si_distr in wallinga_teunis
nSim	see config$n_sim in wallinga_teunis
plot	Not used anymore, only there for compatibility
leg.pos	Not used anymore, only there for compatibility

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