Package 'earlyR'

October 13, 2022

Title Estimation of Transmissibility in the Early Stages of a Disease Outbreak

Version 0.0.5

Description Implements a simple, likelihood-based estimation of the reproduction number (R0) using a branching process with a Poisson likelihood. This model requires knowledge of the serial interval distribution, and dates of symptom onsets. Infectiousness is determined by weighting R0 by the probability mass function of the serial interval on the corresponding day. It is a simplified version of the model introduced by Cori et al. (2013) <doi:10.1093/aje/kwt133>.

Depends R (>= 3.3.0)

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Encoding UTF-8

LazyData true

Imports stats, distcrete, EpiEstim, epitrix, ggplot2

Suggests testthat, vdiffr, roxygen2, incidence, knitr, rmarkdown, projections, covr

RoxygenNote 7.1.1

URL https://www.repidemicsconsortium.org/earlyR/

BugReports https://github.com/reconhub/earlyR/issues

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2020-10-27 08:50:02 UTC

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get_R   *Estimate the Reproduction Number*

Description

This function estimates the (most of the time, 'basic') reproduction number (R) using i) the known distribution of the Serial Interval (delay between primary to secondary onset) and ii) incidence data.

Usage

```
get_R(x, ...)

## Default S3 method:
get_R(x, ...)

## S3 method for class 'integer'
get_R(
  x,
  disease = NULL,
  si = NULL,
  si_mean = NULL,
  si_sd = NULL,
  max_R = 10,
  days = 30,
  ...
)

## S3 method for class 'numeric'
get_R(x, ...)

## S3 method for class 'incidence'
get_R(x, ...)
```

Arguments

x   The daily incidence to be used for inferring the reproduction number. Input can be an `incidence` object, as output by the package `incidence`, or a vector of numbers indicating daily number of cases. Note that 'zero' incidence should be reported as well (see details).

...	Further arguments to be passed to the methods.
disease	A character string indicating the name of the disease studied. If provided, then `si_mean` and `si_sd` will be filled in automatically using value from the literature. Accepted values are: "ebola".
si	A `distcrete` object (see package `distcrete`) containing the discretized distribution of the serial interval.
si_mean	The mean of the serial interval distribution. Ignored if `si` is provided.
si_sd	The standard deviation of the serial interval distribution. Ignored if `si` is provided.
max_R	The maximum value the reproduction number can take.
days	The number of days after the last incidence date for which the force of infection should be computed. This does not change the estimation of the reproduction number, but will affect projections.

Details

The estimation of R relies on all available incidence data. As such, all zero incidence after the first case should be included in x. When using `inidence` from the 'incidence' package, make sure you use the argument `last_date` to indicate where the epicurve stops, otherwise the curve is stopped after the last case. Use `as.data.frame` to double-check that the epicurve includes the last 'zeros'.

Value

A list with the `earlyR` class, containing the following components:

- `$incidence`: the input incidence, in its original format
- `$R_grid`: the grid of R values for which the likelihood has been computed.
- `$R_like`: the values of likelihood corresponding to the `$R_grid`
- `$R_ml`: the maximum likelihood estimate of R
- `$dates`: the dates for which infectiousness has been computed
- `$lambdas`: the corresponding values of force of infection
- `$si`: the serial interval, stored as a `distcrete` object

Author(s)

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Examples

```
if (require(incidence)) {

## example: onsets on days 1, 5, 6 and 12; estimation on day 24
 x <- incidence(c(1, 5, 6, 12), last_date = 24)
 x
 as.data.frame(x)
 plot(x)
```

```
res <- get_R(x, disease = "ebola")
res
plot(res)

}
```

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plot.earlyR   *Plot earlyR objects*

Description

These functions are designed for plotting earlyR objects, output by the function [get_R](#). It can plot either the likelihood of R values, or the force of infection over time (see argument type). For points, the latter is used.

Usage

```
## S3 method for class 'earlyR'
plot(x, type = c("R", "lambdas"), scale = "ml", ...)

## S3 method for class 'earlyR'
points(x, scale = 1, ...)
```

Arguments

x   A earlyR object.

type   The type of graphic to be generated, matching either "R" or "lamdbas"; "R" will plot the likelihood of R values; "lambdas" will plot the force of infection over time; see 'scale' argument to interpret the force of infection.

scale   A numeric value indicating the total number of new cases expected over the time period of the lambdas, or a recognised 'character' string; lambdas will be scaled to correspond to the number of expected cases every day; defaults to 'ml', which tells function to use the maximum likelihood estimate of *R* multiplied by the number of infectious cases

...   Further arguments to be passed to other methods; for the plot of *R*, '...' is passed to 'ggplot2::geom_line()'; for the plot of *lambdas*, '...' is passed to 'ggplot2::geom_bar()'.

Value

A 'ggplot2' object.

if (require(incidence))

example: onsets on days 1, 5, 6 and 12; estimation on day 24 onset <- c(1, 5, 6, 12) x <- incidence(onset, last_date = 24) x

res <- get_R(x, disease = "ebola") res plot(res) plot(res, "lambdas")

Author(s)

Thibaut Jombart <thibautjombart@gmail.com>

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print.earlyR   *Print method for earlyR objects*

Description

This method prints the content of earlyR objects.

Usage

```
## S3 method for class 'earlyR'
print(x, ...)
```

Arguments

x	A earlyR object.
...	further parameters to be passed to other methods (currently not used)

Author(s)

Thibaut Jombart (<thibautjombart@gmail.com>)

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sample_R   *Get a sample of plausible Reproduction Numbers*

Description

This function derives a sample of plausible R values from an earlyR object (as returned by get_R).
The probability of each returned values of R are directly proportional to their likelihood.

Usage

```
sample_R(x, n = 100)
```

Arguments

x	An earlyR object.
n	The number of R values to sample.

Author(s)

Thibaut Jombart <thibautjombart@gmail.com>

Examples

```
if (require(incidence)) {
 x <- incidence(c(1, 5, 5, 12, 45, 65))
 plot(x)
 res <- get_R(x, disease = "ebola")
 res
 plot(res)

 sample_R(res, 10)
 hist(sample_R(res, 1000), col = "grey", border = "white")
}
```

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