Package ‘earlyR’

December 6, 2017

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

Version  0.0.1

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)
License  MIT + file LICENSE
Encoding  UTF-8
LazyData  true
Imports  stats, distcrete, EpiEstim, epitrix
Suggests  testthat, vdiffr, roxygen2, incidence, knitr
RoxygenNote  6.0.1
URL  http://www.repidemicsconsortium.org/earlyR
BugReports  https://github.com/reconhub/earlyR/issues
NeedsCompilation  no
Author  Thibaut Jombart [aut, cre], Anne Cori [aut], Pierre Nouvellet [aut]
Maintainer  Thibaut Jombart <thibautjombart@gmail.com>
Repository  CRAN
Date/Publication  2017-12-06 15:50:22 UTC

R topics documented:

  get_R  .......................................................... 2
  plot.earlyR  ................................................. 4
  print.earlyR  ................................................ 4
  sample_R  .................................................... 5
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 litera-
   ture. Accepted values are: "ebola".
si A distcrete object (see package distcrete) containing the discretized distri-
   bution 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 pro-
   vided.
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.
get_R

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 incidence 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 discrete object

Author(s)

Thibaut Jombart <thibautjombart@gmail.com>

Examples

```r
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)
plot(res, "lambdas")
}
```
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.

```r
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")
plot(res, "lambdas")
plot(res, "lambdas", scaling = 5)
points(onset, 1:4, cex = 3, pch = 20)
```

Arguments

- `x`: A earlyR object.
- `type`: The type of graphic to be generated, matching either "R" or "lambdas"; "R" will plot the likelihood of R values; "lambdas" will plot the force of infection over time.
- `scale`: A numeric value indicating the scaling factor for lambdas on the 'y' axis.
- `...`: Further arguments to be passed to other methods (not used).

Author(s)

Thibaut Jombart <thibautjombart@gmail.com>

Description

This method prints the content of earlyR objects.
sample_R

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>)

---

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

```r
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")
}
```
Index

get_R, 2, 4, 5

plot.earlyR, 4
points.earlyR(plot.earlyR), 4
print.earlyR, 4

sample_R, 5