Package ‘earlyR’

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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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LazyData  true

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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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**get_R** Estimate the Reproduction Number

Description

This function estimates the (mostly 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

```r
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 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 distcrete object

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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)
```

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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**

```r
## 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 "lambdas"; "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.

```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")
  res
  plot(res)
  plot(res, "lambdas")
```
print.earlyR

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**print.earlyR**

*Print method for earlyR objects*

**Description**

This method prints the content of earlyR objects.

**Usage**

```r
## 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)**

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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**

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

**Arguments**

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

**Author(s)**

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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")
}
```
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