Package 'seroincidence'

June 5, 2018

Type Package

Title Estimating Infection Rates from Serological Data

Version 2.0.0

Date 2018-06-05

Maintainer Chantal Quinten <seroincidence@ecdc.europa.eu>

Description Translates antibody levels measured in a (cross-sectional) population sample into an estimate of the frequency with which seroconversions (infections) occur in the sampled population.

Depends R (>= 2.10)

License GPL-3

Imports stats, utils

Suggests knitr, rmarkdown, parallel

VignetteBuilder knitr

LazyData true

Encoding UTF-8

URL https://ecdc.europa.eu/en/publications-data/seroincidence-calculator-tool

RoxygenNote 6.0.1

NeedsCompilation no

Author Peter Teunis [aut] (Author of the method and original code.), Jan van Eijkeren [aut] (Author of the method and original code.), Daniel Lewandowski [com, ctb] (Creator of the R package.), Chantal Quinten [cre, ctb] (Project manager and the package maintainer.)

Repository CRAN

Date/Publication 2018-06-05 16:34:14 UTC

R topics documented:

campylobacterDelftParams1 . . . 2
campylobacterDelftParams3 . . . 3
campylobacterDelftParams4 . . . 3
campylobacterSimLowData . . . 4
campylobacterSSIParams1 . . . 5
campylobacterSSIParams2 . . . 5
campylobacterSSIParams4 . . . 6
estimateSeroincidence . . . 6
getAdditionalData . . . 8
pertussisIgGPTParams1 . . . 9
pertussisIgGPTParams2 . . . 9
pertussisIgGPTParams3 . . . 10
pertussisIgGPTParams4 . . . 10
print.seroincidence . . . 11
print.summary.seroincidence . . . 11
salmonellaSSIParams1 . . . 12
salmonellaSSIParams2 . . . 13
salmonellaSSIParams4 . . . 13
seroincidence . . . 14
summary.seroincidence . . . 16

Index **18**

`campylobacterDelftParams1` *Campylobacter Delft Response Parameters Data for Model 1*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
campylobacterDelftParams1
```

Format

A list of three dataframes:

`IgA` A dataframe containing 4000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 4000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 4000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterDelftParams1
lapply(campylobacterDelftParams1, head)
```

`campylobacterDelftParams3`
Campylobacter Delft Response Parameters Data for Model 3

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
campylobacterDelftParams3
```

Format

A list of three dataframes:

`IgA` A dataframe containing 4000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 4000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 4000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterDelftParams3
lapply(campylobacterDelftParams3, head)
```

`campylobacterDelftParams4`
Campylobacter Delft Response Parameters Data for Model 4

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
campylobacterDelftParams4
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterDelftParams4
lapply(campylobacterDelftParams4, head)
```

`campylobacterSimLowData`

Simulated Cross-sectional Data

Description

Simulated cross-sectional population sample of antibody levels data for Campylobacter and Pertussis for lambda 0.036/yr (low), 0.021/yr (medium) and 1.15/yr (high).

Usage

```
campylobacterSimLowData
```

Format

A data frame with 500 observations on the following 2 to 4 variables:

Age

IgG

IgM

IgA

Examples

```
# Show first rows of the data
head(campylobacterSimLowData)

# Summarize the data
summary(campylobacterSimLowData)
```

`campylobacterSSIParams1`

Campylobacter SSI Response Parameters Data for Model 1

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type

Usage

```
campylobacterSSIParams1
```

Format

A list of three dataframes:

`IgA` A dataframe containing 4000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 4000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 4000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterSSIParams1
lapply(campylobacterSSIParams1, head)
```

`campylobacterSSIParams2`

Campylobacter SSI Response Parameters Data for Model 2

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type

Usage

```
campylobacterSSIParams2
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterSSIParams2
lapply(campylobacterSSIParams2, head)
```

`campylobacterSSIParams4` *Campylobacter SSI Response Parameters Data for Model 4*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
campylobacterSSIParams4
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in campylobacterSSIParams4
lapply(campylobacterSSIParams4, head)
```

`estimateSeroincidence` *Estimate Seroincidence*

Description

Function to estimate seroincidences based on cross-section serology data and longitudinal response model.

Usage

```
estimateSeroincidence(data, antibodies, strata = "", params, censorLimits,
  par0, start = -6, numCores = 1L)
```

Arguments

data	Data frame with cross-sectional serology data per antibody and age, and additional columns to identify possible strata.
antibodies	Character vector with one or more antibody names. Values must match data.
strata	Character vector of strata. Values must match with data. Default = "".
params	List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.
censorLimits	List of cutoffs for one or more named antibody types (corresponding to data).
par0	List of parameters for the (lognormal) distribution of antibody concentrations for true seronegatives (i.e. those who never seroconverted), by named antibody type (corresponding to data).
start	A starting value for log(lambda). Value of -6 corresponds roughly to 1 day (log(1/365.25)), -4 corresponds roughly to 1 week (log(7 / 365.25)). Default = -6.
numCores	Number of processor cores to use for calculations when computing by strata. If set to more than 1 and package **parallel** is available, then the computations are executed in parallel. Default = 1L.

Value

A set of lambda estimates for each strata.

Examples

```
## Not run:
estimateSeroincidence(data = csData,
                      antibodies = c("IgG", "IgM", "IgA"),
                      strata = "",
                      params = campylobacterDelftParams4,
                      censorLimits = cutOffs,
                      par0 = baseLn,
                      start = -4)

estimateSeroincidence(data = csData,
                      antibodies = c("IgG", "IgM", "IgA"),
                      strata = "",
                      params = campylobacterDelftParams4,
                      censorLimits = cutOffs,
                      par0 = baseLn,
                      start = -4,
                      numCores = parallel::detectCores())

## End(Not run)
```

`getAdditionalData` *Get Additional Data*

Description

Retrieves additional data from internet. This can be any file type, but the purpose of this function is to download data such as longitudinal response parameters from an online repository.

Usage

```
getAdditionalData(fileName,
  repoURL = "http://ecdc.europa.eu/sites/portal/files/documents",
  savePath = NULL)
```

Arguments

`fileName`	Name of the file to download. Required.
`repoURL`	Web address of the remote repository of files to download from. Required. Default = `"http://ecdc.europa.eu/sites/portal/files/documents"`
`savePath`	Folder to save the downloaded and unzipped (if needed) file. File is saved only if this argument is not `NULL`. Optional. Default = `NULL`.

Value

Data object

Examples

```
## Not run:
getAdditionalData(fileName = "coxiellaIFAParams4.zip")
getAdditionalData(fileName = "yersiniaSSIParams4.zip")
getAdditionalData(fileName = "coxiellaIFAParams4.zip", savePath = getwd())
getAdditionalData(fileName = "yersiniaSSIParams4.zip", savePath = getwd())

## End(Not run)
```

pertussisIgGPTParams1 *Pertussis IgG-PT Response Parameters Data for Model 1*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
pertussisIgGPTParams1
```

Format

A dataframe `IgG` containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in pertussisIgGPTParams1
lapply(pertussisIgGPTParams1, head)
```

pertussisIgGPTParams2 *Pertussis IgG-PT Response Parameters Data for Model 2*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
pertussisIgGPTParams2
```

Format

A dataframe `IgG` containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in pertussisIgGPTParams2
lapply(pertussisIgGPTParams2, head)
```

pertussisIgGPTParams3 *Pertussis IgG-PT Response Parameters Data for Model 3*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
pertussisIgGPTParams3
```

Format

A dataframe `IgG` containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in pertussisIgGPTParams3
lapply(pertussisIgGPTParams3, head)
```

pertussisIgGPTParams4 *Pertussis IgG-PT Response Parameters Data for Model 4*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
pertussisIgGPTParams4
```

Format

A dataframe `IgG` containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in pertussisIgGPTParams4
lapply(pertussisIgGPTParams4, head)
```

print.seroincidence *Print Method for Seroincidence Object*

Description

Custom `print` function to show output of the seroincidence calculator `estimateSeroincidence`.

Usage

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

Arguments

`x`	A list containing output of function `estimateSeroincidence`.
`...`	Additional arguments affecting the summary produced.

Examples

```
## Not run:
# estimate seroincidence
seroincidence <- estimateSeroincidence(...)

# print the seroincidence object to the console
print(seroincidence)

# or simply type (appropriate print method will be invoked automatically)
seroincidence

## End(Not run)
```

print.summary.seroincidence *Print Method for Seroincidence Summary Object*

Description

Custom `print` function to show output of the seroincidence summary `summary.seroincidence`.

Usage

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

Arguments

x	A list containing output of function summary.seroincidence.
...	Additional arguments affecting the summary produced.

Examples

```
## Not run:
# estimate seroincidence
seroincidence <- estimateSeroincidence(...)

# calculate summary statistics for the seroincidence object
seroincidenceSummary <- summary(seroincidence)

# print the summary of seroincidence object to the console
print(seroincidenceSummary)

# or simply type (appropriate print method will be invoked automatically)
seroincidenceSummary

## End(Not run)
```

---

salmonellaSSIParams1 *Salmonella SSI Response Parameters Data for Model 1*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
salmonellaSSIParams1
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in salmonellaSSIParams1
lapply(salmonellaSSIParams1, head)
```

salmonellaSSIParams2 *Salmonella SSI Response Parameters Data for Model 2*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
salmonellaSSIParams2
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in salmonellaSSIParams2
lapply(salmonellaSSIParams2, head)
```

salmonellaSSIParams4 *Salmonella SSI Response Parameters Data for Model 4*

Description

List of data frames of all longitudinal parameters. Each data frame contains Monte Carlo samples for each antibody type.

Usage

```
salmonellaSSIParams4
```

Format

A list of three dataframes:

`IgA` A dataframe containing 3000 rows with 7 parameters for IgA antibody.

`IgM` A dataframe containing 3000 rows with 7 parameters for IgM antibody.

`IgG` A dataframe containing 3000 rows with 7 parameters for IgG antibody.

Examples

```
# Show first rows of every dataframe contained in salmonellaSSIParams4
lapply(salmonellaSSIParams4, head)
```

`seroincidence` *Estimating Infection Rates from Serological Data*

Description

Translates antibody levels measured in a (cross-sectional) population sample into an estimate of the frequency with which seroconversions (infections) occur in the sampled population.

Details

For detailed documentation type the following in the R console:

```
vignette("installation", package = "seroincidence")
vignette("tutorial", package = "seroincidence")
vignette("methodology", package = "seroincidence")
```

Author(s)

Author: Peter Teunis <<p.teunis@emory.edu>>
Author: Jan van Eijkeren
Contributor: Daniel Lewandowski <<daniel@nextpagesoft.net>>
Maintainer: Chantal Quinten <<seroincidence@ecdc.europa.eu>>

References

Methods for estimating seroincidence

- Teunis, P. F., van Eijkeren, J. C., Ang, C. W., van Duynhoven, Y. T., Simonsen, J. B., Strid, M. A., van Pelt, W.
  "Biomarker dynamics: estimating infection rates from serological data"
  Statistics in Medicine 31, no. 20 (September 9, 2012): 2240–48. doi:10.1002/sim.5322.
- Simonsen, J., Molbak, K., Falkenhorst, G., Krogfelt, K. A., Linneberg, A., Teunis, P. F.
  "Estimation of incidences of infectious diseases based on antibody measurements"
  Statistics in Medicine 28, no. 14 (June 30, 2009): 1882–95. doi:10.1002/sim.3592.

Applications

- Monge, S., Teunis, P. F., Friesema, I., Franz, E., Ang, W., van Pelt, W., Mughini-Gras, L.
  "Immune response-eliciting exposure to Campylobacter vastly exceeds the incidence of clinically overt campylobacteriosis but is associated with similar risk factors: A nationwide serosurvey in the Netherlands"
  Journal of Infection, 2018, 1–7, doi:10.1016/j.jinf.2018.04.016

- Kretzschmar, M., Teunis, P. F., Pebody, R. G.
"Incidence and reproduction numbers of pertussis: estimates from serological and social contact data in five European countries"
PLoS Medicine 7, no. 6 (June 1, 2010):e1000291. doi:10.1371/journal.pmed.1000291.
- Simonsen, J., Strid, M. A., Molbak, K., Krogfelt, K. A., Linneberg, A., Teunis, P.
"Sero-epidemiology as a tool to study the incidence of Salmonella infections in humans"
Epidemiology and Infection 136, no. 7 (July 1, 2008): 895–902. doi:10.1017/S0950268807009314
- Simonsen, J., Teunis, P. F., van Pelt, W., van Duynhoven, Y., Krogfelt, K. A., Sadkowska-Todys, M., Molbak K.
"Usefulness of seroconversion rates for comparing infection pressures between countries"
Epidemiology and Infection, April 12, 2010, 1–8. doi:10.1017/S0950268810000750.
- Falkenhorst, G., Simonsen, J., Ceper, T. H., van Pelt, W., de Valk, H., Sadkowska-Todys, M., Zota, L., Kuusi, M., Jernberg, C., Rota, M. C., van Duynhoven, Y. T., Teunis, P. F., Krogfelt, K. A., Molbak, K.
"Serological cross-sectional studies on salmonella incidence in eight European countries: no correlation with incidence of reported cases"
BMC Public Health 12, no. 1 (July 15, 2012): 523–23. doi:10.1186/1471-2458-12-523.
- Teunis, P. F., Falkenhorst, G., Ang, C. W., Strid, M. A., De Valk, H., Sadkowska-Todys, M., Zota, L., Kuusi, M., Rota, M. C., Simonsen, J. B., Molbak, K., Van Duynhoven, Y. T., van Pelt, W.
"Campylobacter seroconversion rates in selected countries in the European Union"
Epidemiology and Infection 141, no. 10 (2013): 2051–57. doi:10.1017/S0950268812002774.
- de Melker, H. E., Versteegh, F. G., Schellekens, J. F., Teunis, P. F., Kretzschmar, M.
"The incidence of Bordetella pertussis infections estimated in the population from a combination of serological surveys"
The Journal of Infection 53, no. 2 (August 1, 2006): 106–13. doi:10.1016/j.jinf.2005.10.020

Quantification of seroresponse

- de Graaf, W. F., Kretzschmar, M. E., Teunis, P. F., Diekmann, O.
"A two-phase within-host model for immune response and its application to serological profiles of pertussis"
Epidemics 9 (2014):1–7. doi:10.1016/j.epidem.2014.08.002.
- Berbers, G. A., van de Wetering, M. S., van Gageldonk, P. G., Schellekens, J. F., Versteegh, F. G., Teunis, P.F.
"A novel method for evaluating natural and vaccine induced serological responses to Bordetella pertussis antigens"
Vaccine 31, no. 36 (August 12, 2013): 3732–38. doi:10.1016/j.vaccine.2013.05.073.
- Versteegh, F. G., Mertens, P. L., de Melker, H. E., Roord, J. J., Schellekens, J. F., Teunis, P. F.
"Age-specific long-term course of IgG antibodies to pertussis toxin after symptomatic infection with Bordetella pertussis"
Epidemiology and Infection 133, no. 4 (August 1, 2005): 737–48.
- Teunis, P. F., van der Heijden, O. G., de Melker, H. E., Schellekens, J. F., Versteegh, F. G., Kretzschmar, M. E. "Kinetics of the IgG antibody response to pertussis toxin after infection with B. pertussis"
Epidemiology and Infection 129, no. 3 (December 10, 2002):479. doi:10.1017/S0950268802007896.

summary.seroincidence *Summary Method for Seroincidence Object*

Description

Calculate seroincidence from output of the seroincidence calculator estimateSeroincidence.

Usage

```
## S3 method for class 'seroincidence'
summary(object, ..., quantiles = c(0.025, 0.975),
  showDeviance = TRUE, showConvergence = TRUE)
```

Arguments

object	A dataframe containing output of function estimateSeroincidence.
...	Additional arguments affecting the summary produced.
quantiles	A vector of length 2 specifying quantiles for lower (first element) and upper (second element) bounds of lambda. Default = c(0.025, 0.975).
showDeviance	Logical flag (FALSE/TRUE) for reporting deviance (-2*log(likelihood) at estimated seroincidence. Default = TRUE.
showConvergence	Logical flag (FALSE/TRUE) for reporting convergence (see help for optim for details). Default = TRUE.

Value

A list with the following items:

Results Dataframe with maximum likelihood estimate of lambda (the seroincidence) (column Lambda) and corresponding lower (Lambda.lwr) and upper (Lambda.upr bounds.
Optionally Deviance (Negative log likelihood (NLL) at estimated (maximum likelihood) lambda) and Covergence (Convergence indicator returned by optim. Value of 0 indicates convergence) columns are included.

Antibodies Character vector with names of input antibodies used in estimateSeroincidence.

Strata Character with names of strata used in estimateSeroincidence.

CensorLimits List of cutoffs for each of the antibodies used in estimateSeroincidence.

Examples

```
## Not run:
# estimate seroincidence
seroincidence <- estimateSeroincidence(...)

# calculate summary statistics for the seroincidence object
```

```
seroincidenceSummary <- summary(seroincidence)

## End(Not run)
```

Index

campylobacterDelftParams1, 2
campylobacterDelftParams3, 3
campylobacterDelftParams4, 3
campylobacterSimHighData
        *(*campylobacterSimLowData*)*, 4
campylobacterSimLowData, 4
campylobacterSimMediumData
        *(*campylobacterSimLowData*)*, 4
campylobacterSSIParams1, 5
campylobacterSSIParams2, 5
campylobacterSSIParams4, 6

estimateSeroincidence, 6, *11*, *16*

getAdditionalData, 8

optim, *16*

pertussisIgGPTParams1, 9
pertussisIgGPTParams2, 9
pertussisIgGPTParams3, 10
pertussisIgGPTParams4, 10
pertussisSimHighData
        *(*campylobacterSimLowData*)*, 4
pertussisSimLowData
        *(*campylobacterSimLowData*)*, 4
pertussisSimMediumData
        *(*campylobacterSimLowData*)*, 4
print, *11*
print.seroincidence, 11
print.summary.seroincidence, 11

salmonellaSSIParams1, 12
salmonellaSSIParams2, 13
salmonellaSSIParams4, 13
seroincidence, 14
seroincidence-package *(*seroincidence*)*,
        14
summary.seroincidence, *11*, *12*, 16