Package ‘postinfectious’

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Type Package

Title Estimating the Incubation Period Distribution of Post-Infectious Syndrome

Version 0.1.0

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Description Functions to estimate the incubation period distribution of post-infectious syndrome which is defined as the time between the symptom onset of the antecedent infection and that of the post-infectious syndrome.

License GPL-2

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Contents

`pis.fit` *Estimating the incubation period distribution of a post-infectious syndrome*

Description

This function estimates the incubation period distribution of a post-infectious syndrome with maximum likelihood estimation. The incubation period distribution of the antecedent infection and the post-infectious syndrome are allowed to be lognormal (`"LN"`), Weibull (`"WB"`) or gamma (`"GM"`) distributed. The data set is allowed to have cases with the actecedent diseases whose incuation periods come from different distributions (see Examples).

Usage

```
pis.fit(data,postinfect=c("LN","WB","GM"),theta)
```

Arguments

`data`	A data.frame containing at least 4 columns. The first two columns represent (1) the time between the symptom onset of the antecedent infection and post-infectious syndrome and (2) the incubation period distribution of the antecedent infection (only `"LN"`, `"WB"` and `"GM"`). The last two columns refer to the parameters of the incubation period distribution of the antecedent infection; for `"LN"`, they are `meanlog` and `sdlog` as in `dlnorm`; for `"WB"`, they are `shape` and `scale` as in `dweibull`; for `"GM"`, they are `shape` and `rate` as in `dgamma`.
`postinfect`	The incubation period distribution of the post-infectious disease. It can only be `"LN"`, `"WB"` and `"GM"`.
`theta`	A vector of two numbers as the initial value for optimisation.

Details

For each observed case, let S_0 and S be the incubation period of the antecedent infection and post-infectious syndrome, respectively. As the antecedent infection is the antigenic factor of the post-infectious syndrome, they both share the same time of infection exposure. The difference between S_0 and S, denoted by X, is the time between the two symptom onsets. Also let θ_0 and θ be the set of the parameters of the distribution of S_0 and S then the likelihood of such observed case is given by,

$$\int_{-\infty}^{\infty} f_0(S_0,\theta_0)f(S_0+X,\theta)dS_0$$

where f_0 and f are the probability density function of S_0 and S, respectively. θ is then estimated by maximising the sum of likelihood of all observed cases.

Value

`Parameter`	Estimates of the parameters of the incubation period distribution of the post-infectious syndrome.
`SE`	Standard errors of `Parameter`
`AIC`	Akaike Information Criterion.
`Convergence`	The convergence message of `optim`
`Median`	The median incubation period distribution of the post-infectious syndrome.
`Theta.initial`	Initial values used in `optim`
`Distribution`	The Distribution assumed in the estimation, i.e. `"LN"`, `"WB"` or `"GM"`.

Author(s)

Char Leung

Examples

```
#generate artificial data
S<-c(56,37,32,7,8,3,5)
S0<-c(2,1,3,1,1,1,3)
X<-S-S0
f0<-c(rep("LN",4),rep("WB",3))
phi<-matrix(c(rep(c(0,1),4),rep(c(1,2),3)),byrow=TRUE,ncol=2)
data<-data.frame(X,f0,phi)
pis.fit(data,"LN",theta=c(2.5,1))
```

`pis.fit.boots` *Bootstrap estimates of the output in* `pis.fit`

Description

This function creates bootstrap estimates of the output of `pis.fit` by creating bootstrap samples

Usage

```
pis.fit.boots(data,postinfect=c("LN","WB","GM"),theta,n.boots=1000,collective=100)
```

Arguments

`data`	A data.frame containing at least 4 columns. The first two columns represent (1) the time between the symptom onset of the antecedent infection and post-infectious syndrome and (2) the incubation period distribution of the antecedent infection (only `"LN"`, `"WB"` and `"GM"`). The last two columns refer to the parameters of the incubation period distribution of the antecedent infection; for `"LN"`, they are `meanlog` and `sdlog` as in `dlnorm`; for `"WB"`, they are `shape` and `scale` as in `dweibull`; for `"GM"`, they are `shape` and `rate` as in `dgamma`.
`postinfect`	The incubation period distribution of the post-infectious disease. It can only be `"LN"`, `"WB"` and `"GM"`.
`theta`	Text input only and it is an R expression to be evaluated (i.e. `eval`) so as to create initial values used in `optim`. The reason behind this is to allow random numbers as the initial values in optimisation. See Examples.
`n.boots`	The number of bootstrap samples.
`collective`	The number of bootstrap samples to be estimated at once as the estimation process uses the `apply` function.

Value

Same as those in `pis.fit`.

Author(s)

Char Leung

See Also

pis.fit

Examples

```
S<-c(56,37,32,7,8,3,5)
S0<-c(2,1,3,1,1,1,3)
X<-S-S0
f0<-c(rep("LN",4),rep("WB",3))
phi<-matrix(c(rep(c(0,1),4),rep(c(1,2),3)),byrow=TRUE,ncol=2)
data<-data.frame(X,f0,phi)
pis.fit.boots(data,"LN",theta="c(runif(1,2,3),runif(1,0,1))",n.boots=20,collective=15)
```

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