

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.

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pis.fit	<i>Estimating the incubation period distribution of a post-infectious syndrome</i>
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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 antecedent diseases whose incubation 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

<code>data</code>	A <code>data.frame</code> 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 <code>meanlog</code> and <code>sdlog</code> as in <code>dlnorm</code> ; for "WB", they are <code>shape</code> and <code>scale</code> as in <code>dweibull</code> ; for "GM", they are <code>shape</code> and <code>rate</code> as in <code>dgamma</code> .
<code>postinfect</code>	The incubation period distribution of the post-infectious disease. It can only be "LN", "WB" and "GM".
<code>theta</code>	Text input only and it is an R expression to be evaluated (i.e. <code>eval</code>) so as to create initial values used in <code>optim</code> . The reason behind this is to allow random numbers as the initial values in optimisation. See Examples.
<code>n.boots</code>	The number of bootstrap samples.
<code>collective</code>	The number of bootstrap samples to be estimated at once as the estimation process uses the <code>apply</code> function.

Value

Same as those in `pis.fit`.

Author(s)

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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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