

Package ‘DengueRT’

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Type Package

Title Parameter Estimates and Real-Time Prediction of a Single Dengue Outbreak

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Author Carlos Sebrango, Lizet Sanchez, Ziv Shkedy, Ewoud De Troyer

Maintainer Carlos Sebrango <sebrango@uniss.edu.cu>

Description Provides functions for parameter estimation and real-time predictions of a single dengue outbreak taking into account model uncertainty using model averaging.

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allmodelpredict	<i>Real-time predictions of the final size and the turning point at the end of the epidemic, the incidence and the cumulative number of cases in future observations.</i>
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Description

This function provides real-time predictions of the final size and the turning point at the end of the epidemic for each built-in model and model averaged, as well as the incidence and the cumulative number of cases in future observations. Also this function, when all the built-in models are used, gives the AIC of each model, the model averaged weights and predicted incidence and cumulative cases.

Usage

```
## Object of the S3 class dengue
allmodelpredict(inc,time,pred,start=NULL,model)
```

Arguments

inc,time	Vector of equal length specifying incidence (number of reported cases per time unit) and time interval (from the start of outbreak).
pred	Number of observation in which the incidence and the cumulative number of cases will be predicted.
start	A list with the starting values of the model to be used for fitting the data. If model="all" the input must be a list of a list with the starting values of Richards, 3P logistic, Sigmoid Emax, Gompertz, Weibull and 5P logistic model parameters. By default, the initial values are provided by self-starting functions (see argument start in allmodels function).
model	The nonlinear model to be used for fitting the data. Built-in models are "Richards", "Logistic3P", "SigmEmax", "Gompertz", "Weibull" and "Logistic5P" (see argument model in allmodels function). If model = "all" the parameter estimate will be done taking into account all built-in models via model averaging.

Value

An object with the parameter estimate for each built-in model and model averaged estimate for final size and turning point of outbreak. It is a list:

Incidence	All the available incidences
Time	All the available time points
PredTime	Period of time for which the prediction is required
AIC	The AIC for each built-in model and model averaged
tTable	A table with parameter estimates and t test. It is not available when all the model are used.

Weights	Model averaged weights. It is not available when is used only one built-in model
FinalSize	95% confidence interval and point estimate of the final size of outbreak for each built-in model and model averaged estimate
TurningPoint	95% confidence interval and point estimate of the turning point of outbreak for each built-in model and model averaged estimate
Predict	Predicted cumulative cases for each built-in model
PredictMA	Predicted cumulative cases for model averaged
PredInc	Predicted incidence for each built-in model
PredMAInc	Predicted incidence for model averaged
function.type	Name of the function
model.type	models used to estimate

Generic functions such as plot and summary have methods to show the results of the fit

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy

References

- K. Burnham, D. R. Anderson, Model Selection and Multimodel Inference: A Practical Information - theoretic Approach, 2nd Edition, Springer-Verlag, New York, 2002.
- G. Claeskens, N. L. Hjort, Model selection and model averaging, Cambridge University Press, 2008.

Examples

```
## Not run:
## (data example 1)
data("dengueoutbreak1")

## Using only the information until time point 20
## Prediction of the final size and turning point at the end of epidemic,
## the incidence and the cumulative number of cases in the observation
## number 36 using only the Richards model
allmodelpredict(dengueoutbreak1$Incidence[1:20],dengueoutbreak1$Time[1:20],36,
model = "Richards")

## Using only the information until time point 22
## Now using all built-in model, Prediction of the final size and turning point
## at the end of epidemic, the incidence and the cumulative number of cases
## in the observation number 30
allmodelpredict(dengueoutbreak1$Incidence[1:22],dengueoutbreak1$Time[1:22],30,
model = "all")
## End(Not run)

## (data example 2)
data("dengueoutbreak2")
## Using only the information until time point 18, Prediction of the final size and
```

```

## turning point at the end of epidemic, the incidence and the cumulative number
## of cases in the observation number 31 using only the 3P logistic model

allmodelpredict(dengueoutbreak2$Incidence[1:18],dengueoutbreak2$Time[1:18],31,
model = "logistic3P")

## Not run:
## Using only the information until time point 20
## Now using all built-in model, Prediction of the final size and turning point
## at the end of epidemic, the incidence and the cumulative number of cases
## in the observation number 30
allmodelpredict(dengueoutbreak2$Incidence[1:20],dengueoutbreak2$Time[1:20],34,
model = "all")
## End(Not run)

```

allmodels	<i>Parameter estimate for each built-in model and model averaged estimate for final size and turning point of outbreak.</i>
-----------	---

Description

This function gives the parameter estimate for each built-in model and model averaged estimate for final size and turning point of outbreak. Also this function, when all the built-in models are used, gives the AIC of each model, the model averaged weights and predicted incidence and cumulative cases. This function is used retrospectively, that is, when all the data are available.

Usage

```

## Object of the S3 class dengue
allmodels(inc,time,start=NULL,model)

```

Arguments

inc,time	Vector of equal length specifying incidence (number of reported cases per time unit) and time interval (from the start of outbreak).
start	<p>A list with the starting values of the model to be used for fitting the data. If model="all" the input must be a list of a list with the starting values of Richards, 3P logistic, Sigmoid Emax, Gompertz, Weibull and 5P logistic model parameters. By default, the initial values are provided by self-starting functions.</p> <ul style="list-style-type: none"> • 3P Logistic model uses SSlogis selfstart function from the stats package. • Sigmoid Emax model uses LL.4 selfstart function from the drc package. • Gompertz model uses SSgompertz selfstart function from the stats package. • Weibull model uses SSweibull selfstart function from stats package. • 5P Logistic model uses LL.5 and LL.4 selfstart functions from drc package. • Richards model uses SSlogis selfstart function and some ideas of SSRichards selfstart function from NRAIA package now archived.

model

The nonlinear model to be used for fitting the data. Built-in models are "Richards", "Logistic3P", "SigmEmax", "Gompertz", "Weibull" and "Logistic5P". If model = "all" the parameter estimate will be done taking into account all built-in models via model averaging. For all built-in model, $C(t)$ represents the cumulative number of reported cases at time t and also the turning point (η) and the final size of epidemic (α) are parameters in the models. The model expressions of each built-in model are given as follow:

- The Richards model is given by the expression:

$$C(t) = \alpha / [1 + k \cdot \exp(-k \cdot \gamma \cdot (t - \eta))]^{1/k}$$

Where

γ : Per capita growth rate or intrinsic growth rate.

k : Exponent of the deviation from standard logistic curve.

- The three parameter logistic model (3P Logistic), proposed by Verhulst, is given by the expression:

$$C(t) = \alpha / [1 + \exp(-\gamma \cdot (t - \eta))]$$

Where

γ : Per capita growth rate or intrinsic growth rate.

- The Sigmoid Emax model is given by the expression:

$$C(t) = \beta + (t^n)(\alpha - \beta) / (t^n + \eta^n)$$

Where

n : Slope factor or Hill factor.

β : Lower asymptote.

- The Gompertz model is given by the expression :

$$C(t) = \beta + (\alpha - \beta) \cdot \exp(-\exp(-\gamma(t - \eta)))$$

Where

γ : Per capita growth rate or intrinsic growth rate.

β : Lower asymptote.

- The Weibull model is given by the expression:

$$C(t) = \alpha + (\beta - \alpha) \cdot \exp(-(t/\eta)^k)$$

Where

k : Shape factor.

β : Lower asymptote.

- The five parameter logistic model (5P Logistic) is given by the expression:

$$C(t) = \alpha + (\beta - \alpha) / [1 + (2^{1/g} - 1) \cdot (t/\eta)^k]^g$$

Where

g: Asymmetry factor.
 k: Shape factor.
 beta: Lower asymptote.

Value

An object with the parameter estimate for each built-in model and model averaged estimate for final size and turning point of outbreak. It is a list:

Incidence	All the available incidences
Time	All the available time points
AIC	The AIC for each built-in model and model averaged
tTable	A table with parameter estimates and t test. It is not available when all the model are used.
Weights	Model averaged weights. It is not available when is used only one built-in model
FinalSize	95% confidence interval and point estimate of the final size of outbreak for each built-in model and model averaged estimate
TurningPoint	95% confidence interval and point estimate of the turning point of outbreak for each built-in model and model averaged estimate
Predict	Predicted cumulative cases for each built-in model
PredictMA	Predicted cumulative cases for model averaged
PredInc	Predicted incidence for each built-in model
PredMAInc	Predicted incidence for model averaged
function.type	Name of the function
model.type	models used to estimate

Generic functions such as plot and summary have methods to show the results of the fit

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy

References

- K. Burnham, D. R. Anderson, Model Selection and Multimodel Inference: A Practical Information-theoretic Approach, 2nd Edition, Springer-Verlag, New York, 2002.
- J. MacDougall, Analysis of dose responses Studies: Emax model, in: N. Ting (Ed.), Dose Finding in Drug Development, Statistics for Biology and Health, Springer New York, pp. 127, 2006.
- G. Claeskens, N. L. Hjort, Model selection and model averaging, Cambridge University Press, 2008.
- D. Ratkowsky, Handbook of nonlinear regression models, Marcel Dekker, New York, 1990.
- F. Richards, A flexible growth function for empirical use, Journal of Experimental Botany 10 (29), pp 290-301, 1959.
- Y.H. Hsieh, Temporal trend and regional variability of 2001-2002 multiwave DENV-3 epidemic in Havana City: did Hurricane Michelle contribute to its severity?, Tropical Medicine and International Health, Vol. 18, no. 7, pp 830-838, 2013.

A. Tsoularis, J. Wallace, Analysis of logistic growth models, *Mathematical Biosciences*, Vol. 179, no. 1, pp 21-55, 2002.

J. Liao, R. Liu, Re-parameterization of five-parameter logistic function, *Journal of Chemometrics* 23 (5), pp 248-253, 2009.

Examples

```
## (data example 1)
data("dengueoutbreak1")
## Not run:
## Parameter estimate for Richards model (for Incidence data example 1)
allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time,
start=list(alpha=375,k=2.38,gamma=0.76,eta=16), model="Richards")
## End(Not run)
## or
p1<-allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time, model="Richards")
## summary function for a allmodels object
summary(p1)
## plot function for a allmodels object
plot(p1,which=c(1,2))

## Not run:
## Parameter estimate for each built-in model and model averaged
##estimate for final size and turning point of outbreak

allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time,
start=list(list(alpha=375,k=2.38,gamma=0.76,eta=16),
list(alpha=375,gamma=1,eta=16),list(alpha=380,eta=13,beta=7,n=5),
list(alpha=380,eta=20,beta=0,gamma=1),list(alpha=410,eta=12,beta=11,k=3),
list(alpha=380,beta=4,g=1,eta=13,k=15)), model="all")
## or
allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time,model="all")

## (data example 2)
data("dengueoutbreak2")
# Parameter estimate for 3P Logistic model
allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time,
start=list(alpha=375,gamma=1,eta=16), model="logistic3P")
## or
allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time,model="logistic3P")

## Parameter estimate for each built-in model and model averaged estimate
##for final size and turning point of outbreak
##for Incidence data example 2
allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time,
start=list(list(alpha=355,k=1,gamma=1,eta=14),
list(alpha=355,gamma=1,eta=14), list(alpha=355,eta=13,beta=10,n=6),
list(alpha=355,eta=11,beta=20,gamma=1),list(alpha=355,eta=12,beta=22,k=3),
list(alpha=355,beta=15,g=1,eta=13,k=10)),model="all")
## or
allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time,model="all")
## End(Not run)
```

changetimeFSTP	<i>Changes over time of the final size and turning point estimates for each built-in model and model averaged.</i>
----------------	--

Description

This function provides the changes over time of the final size and turning point estimates (for specific models and model average) from the time point required until the last time point available. The output of the function are two tables, one for final size and the other for turning point. the rows represent the data used for the estimation of the model parameters.

Usage

```
## Object of the S3 class dengue
changetimeFSTP(inc, time, ini, start = NULL)
```

Arguments

<code>inc, time</code>	Vector of equal length specifying incidence (number of reported cases per time unit) and time interval (from the start of outbreak).
<code>ini</code>	Time point from which is required to see the changes over time of the final size and turning point estimates
<code>start</code>	A list with the starting values of the model to be used for fitting the data. If <code>model="all"</code> the input must be a list of a list with the starting values of Richards, 3P logistic, Sigmoid Emax, Gompertz, Weibull and 5P logistic model parameters. By default, the initial values are provided by self-starting functions.

Value

An object with the changes over time of the final size and turning point estimates for specific models and model average. It is a list:

<code>Incidence</code>	All the available incidences
<code>Time</code>	All the available time points
<code>Period</code>	Time period required to see the changes over time of the final size and turning point estimates
<code>FSchangetime</code>	A Table with the changes over time of the final size for the time period required
<code>TPchangetime</code>	A Table with the changes over time of the turning point for the time period required
<code>function.type</code>	Name of the function
<code>model.type</code>	models used to estimate

Generic functions such as `plot` and `summary` have methods to show the results of the fit.

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy

References

K. Burnham, D. R. Anderson, Model Selection and Multimodel Inference: A Practical Information-theoretic Approach, 2nd Edition, Springer-Verlag, New York, 2002.
G. Claeskens, N. L. Hjort, Model selection and model averaging, Cambridge University Press, 2008.

Examples

```
## Not run:
## (data example 2)
data("dengueoutbreak2")

##Time point from which is required to see the changes over time
##of the final size and turning point estimates:20

t2<-changetimeFSTP(dengueoutbreak2$Incidence,dengueoutbreak2$Time,20)

##summary function for changetimeFSTP object
summary(t2)

## plot function for changetimeFSTP object
plot(t2,which=c(5,6))

## End(Not run)
```

dengueoutbreak1	<i>Incidence data of the 2001/2002 single dengue outbreak in the health area "26 de julio", Havana City, Cuba.</i>
-----------------	--

Description

This data set gives the incidence (Reported dengue cases) in each time point (in weeks) of the 2001/2002 single dengue outbreak in the health area "26 de julio" of the Playa municipality, Havana City, as compiled by the Institute of Tropical Medicine "Pedro Kouri", Havana City, Cuba.

Usage

```
data("dengueoutbreak1")
```

Format

A data frame with 36 observations on the following 2 variables.

Incidence a numeric vector, representing the incidence of the outbreak.

Time a numeric vector, representing the time vector in weeks.

Source

Institute of Tropical Medicine "Pedro Kouri", Havana City, Cuba.

dengueoutbreak2	<i>Incidence data of the 2001/2002 single dengue outbreak in the health area "J. R. Ramirez", Havana City, Cuba.</i>
-----------------	--

Description

This data set gives the incidence (Reported dengue cases) in each time point (in weeks) of the 2001/2002 single dengue outbreak in the health area "J. R. Ramirez" of the Playa municipality, Havana City, as compiled by the Institute of Tropical Medicine "Pedro Kouri", Havana City, Cuba.

Usage

```
data("dengueoutbreak2")
```

Format

A data frame with 34 observations on the following 2 variables.

Incidence a numeric vector, representing the incidence of the outbreak.

Time a numeric vector, representing the time vector in weeks.

Source

Institute of Tropical Medicine "Pedro Kouri", Havana City, Cuba.

DengueRT	<i>Parameter Estimates and Real-Time Prediction of a Single Dengue Outbreak</i>
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Description

The DengueRT package uses the incidence data from a single dengue outbreak and provides functions to estimate the final size, the turning point of the epidemic and to conduct a real-time prediction for these parameters using several nonlinear models taking into account model uncertainty using model averaging. Graphical tools for a visualization of the results are also included.

Details

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 License: GPL-3

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy, Ewoud De Troyer

Maintainer: Carlos Sebrango <sebrango@uniss.edu.cu>

References

- K. Burnham, D. R. Anderson, *Model Selection and Multimodel Inference: A Practical Information-theoretic Approach*, 2nd Edition, Springer-Verlag, New York, 2002.
- J. MacDougall, Analysis of dose responses Studies: Emax model, in: N. Ting (Ed.), *Dose Finding in Drug Development*, Statistics for Biology and Health, Springer New York, pp. 127, 2006.
- G. Claeskens, N. L. Hjort, *Model selection and model averaging*, Cambridge University Press, 2008.
- D. Ratkowsky, *Handbook of nonlinear regression models*, Marcel Dekker, New York, 1990.
- F. Richards, A flexible growth function for empirical use, *Journal of Experimental Botany* 10 (29), pp 290-301, 1959.
- Y.H. Hsieh, Temporal trend and regional variability of 2001-2002 multiwave DENV-3 epidemic in Havana City: did Hurricane Michelle contribute to its severity?, *Tropical Medicine and International Health*, Vol. 18, no. 7, pp 830-838, 2013.
- A. Tsoularis, J. Wallace, Analysis of logistic growth models, *Mathematical Biosciences*, Vol. 179, no. 1, pp 21-55, 2002.
- J. Liao, R. Liu, Re-parameterization of five-parameter logistic function, *Journal of Chemometrics* 23 (5), pp 248-253, 2009.

plot

Plots for a visualization of the results

Description

plot is a generic function used to produce plots for a visualization of the results of the functions: allmodels, allmodelpredict and changetimeFSTP from the S3 class dengue. The function invokes particular methods of the S3 class dengue.

Usage

```
## S3 method for class 'dengue'
plot(x, which = c(1, 2), xlab = "", ...)
```

Arguments

- x An object for which a plot is desired. It could be any of the following objects: allmodels, allmodelpredict and changetimeFSTP
- which Different graph options, from 1 to 6.

- Option 1 gives a plot with the cumulative number of cases and fitted models for each built-in model and model averaged. This option is only available for `allmodels` and `allmodelpredict` objects.
- Option 2 gives a plot with the incidence and fitted models for each built-in model and model averaged. This option is only available for `allmodels` and `allmodelpredict` objects.
- Option 3 gives a plot with the final size 95% confidence interval and point estimate for each built-in model and model averaged. This option is only available for `allmodels` and `allmodelpredict` objects when all models are used.
- Option 4 gives a plot with the turning point 95% confidence interval and point estimate for each built-in model and model averaged. This option is only available for `allmodels` and `allmodelpredict` objects when all models are used.
- Option 5 gives a plot with the change over time of the final size estimates for each built-in model and model averaged. This option is only available for `changetimeFSTP` objects.
- Option 6 gives a plot with the change over time of the turning point estimates for each built-in model and model averaged. This option is only available for `changetimeFSTP` objects.

`xlab` A title for the x axis. It is not necessary for options 3 y 4.

`...` Additional arguments affecting the plot produced. Arguments to be passed to methods, such as graphical parameters (lines, segment, etc)

Details

When the which options 1, 2, 5 and 6 are used, the plot displays all fitted models with the following colours: (Richards (red), 3P logistic (green), Sigmoid Emax (dark blue), Gompertz (clear blue), Weibull (pink) and 5P logistic (yellow))and the fitted model via model averaging (gray colour). The which options 1, 2, 3 and 4 are only used with the `allmodels` and `allmodelpredict` objects. The which options 5 and 6 are only used with the `changetimeFSTP` object.

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy

References

K. Burnham, D. R. Anderson, *Model Selection and Multimodel Inference: A Practical Information-theoretic Approach*, 2nd Edition, Springer-Verlag, New York, 2002.

G. Claeskens, N. L. Hjort, *Model selection and model averaging*, Cambridge University Press, 2008.

Examples

```
## Not run:
## (data example 1)
data("dengueoutbreak1")
```

```

## plot function for a allmodels object
##Richards model
ee<-allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time, model="Richards")
plot(ee,which=c(1,2))

## (data example 2)
data("dengueoutbreak2")
##using all built-in models
ee2<-allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time, model="all")
plot(ee2,which=c(1,2,3,4))

##plot function for allmodelpredict object
##3P logistic model (Incidence data example 2)
## information available to the time point 20
## observation to predict: 30
ee3<-allmodelpredict(dengueoutbreak2$Incidence[1:20],dengueoutbreak2$Time[1:20],30,
model="logistic3P")
plot(ee3,which=c(1,2))

##using all built-in models (Incidence data example 2)
## information available to the time point 22
## observation to predict: 30
ee4<-allmodelpredict(dengueoutbreak2$Incidence[1:22],dengueoutbreak2$Time[1:22],30,
model="all")
plot(ee4,which=c(1,2,3,4))
## End(Not run)

##plot function for changetimeFSTP object
## See example changetimeFSTP function

```

summary

Result summaries of the functions

Description

summary is a generic function used to produce result summaries of the functions: allmodels, allmodelpredict and changetimeFSTP from the S3 class dengue. The function invokes particular methods of the S3 class dengue.

Usage

```

## S3 method for class 'dengue'
summary(object, ...)

```

Arguments

object	An object for which a summary is desired. It could be any of the following objects: allmodels, allmodelpredict and changetimeFSTP.
...	Additional arguments affecting the summary produced.

Value

The form of the value returned by summary depends on the object of the S3 class dengue. In the case of allmodels returns the AIC, model averaged Weights and model averaged estimates for the final size and turning point of outbreak. If the object is allmodelpredict to the returned value is added a prediction of the incidence and cumulative cases in the required future observation. When the object is changetimeFSTP function the returned values are two tables with the changes over time of the final size and turning point for the time period required.

Author(s)

Carlos Sebrango, Lizet Sanchez, Ziv Shkedy, Ewoud DE Troyer

References

K. Burnham, D. R. Anderson, Model Selection and Multimodel Inference: A Practical Information-theoretic Approach, 2nd Edition, Springer-Verlag, New York, 2002.
G. Claeskens, N. L. Hjort, Model selection and model averaging, Cambridge University Press, 2008.

Examples

```
## Not run:
## (data example 1)
data("dengueoutbreak1")

## summary function for a allmodels object
##Richards model (Incidence data example 1)
ee<-allmodels(dengueoutbreak1$Incidence,dengueoutbreak1$Time, model="Richards")
summary(ee)

## (data example 2)
data("dengueoutbreak2")
##using all built-in models (Incidence data example 2)
ee2<-allmodels(dengueoutbreak2$Incidence,dengueoutbreak2$Time, model="all")
summary(ee2)

##summary function for allmodelpredict object
##3P logistic model (Incidence data example 2)
## information available to the time point 20
## observation to predict: 30
ee3<-allmodelpredict(dengueoutbreak2$Incidence[1:20],dengueoutbreak2$Time[1:20],30,
model="logistic3P")
summary(ee3)

##using all built-in models (Incidence data example 1)
## information available to the time point 22
## observation to predict: 30
ee4<-allmodelpredict(dengueoutbreak1$Incidence[1:22],dengueoutbreak1$Time[1:22],30,
model="all")
summary(ee4)
## End(Not run)
```

```
##summary function for changetimeFSTP object  
## See example changetimeFSTP function
```

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