

Package ‘gamlss.cens’

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Type Package

Title Fitting an interval response variable using gamlss.family distributions

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Depends R (>= 2.2.1), gamlss, gamlss.dist, survival

Imports survival

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Description This is an add on package to GAMLSS. The purpose of this package is to allow users to fit interval response variables in GAMLSS models. The main function gen.cens() generates a censored version of an existing GAMLSS family distribution.

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URL <http://www.gamlss.org/>

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gamlss.cens-package *The GAMLSS Add On Package for Censored Data*

Description

The purpose of this package is to allow the user of the GAMLSS models to be able to fit parametric distributions to data with censored or interval response variable.

Details

Package: gamlss.cens
Type: Package
Version: 1.0
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Author(s)

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References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/i07>.

See Also

[gamlss,gamlss.family](#)

Examples

```
library(survival)
library(gamlss)
library(gamlss.dist)
# comparing results with package survival
# fitting the exponential distribution
```

```

ms1<-survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian,
             dist='exponential')
mg1<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian,
            family=cens(EXP),c.crit=0.00001)
if(abs(-2*ms1$loglik[2]-deviance(mg1))>0.001) stop(paste("discrepancies in exp"))
if(sum(coef(ms1)-coef(mg1))>0.001) warning(paste("discrepancies in coef in exp"))
summary(ms1)
summary(mg1)
# fitting the Weibull distribution
ms2 <-survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull')
mg2 <-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian,
            family=cens(WEI, delta=c(0.001,0.001)), c.crit=0.00001)
if(abs(-2*ms2$loglik[2]-deviance(mg2))>0.005)
  stop(paste("discrepancies in deviance in WEI"))
summary(ms2);summary(mg2)
# compare the scale parameter
  1/exp(coef(mg2,"sigma"))
# now fit the Weibull in different parameterizations
mg21<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian,
            family=cens(WEI2), method=mixed(2,30))
mg21<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian,
            family=cens(WEI3))

```

cens

Function to Fit Censored Data Using a `gamlss.family` Distribution

Description

This function can be used to fit censored or interval response variables. It takes as an argument an existing `gamlss.family` distribution and generates a new `gamlss.family` object which then can be used to fit right, left or interval censored data.

Usage

```

cens(family = "NO", type = c("right", "left", "interval"), name = "cens",
     local = TRUE, delta = NULL, ...)

```

Arguments

family	a <code>gamlss.family</code> object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by <code>gamlss()</code> can be found in <code>gamlss.family</code> and in the package <code>gamlss.dist</code> .
name	the characters you want to add to the name of new functions, by default is <code>cens</code>
type	what type of censoring is required, <code>right</code> , <code>left</code> or <code>interval</code> .
local	if <code>TRUE</code> the function will try to find the environment of <code>gamlss</code> to generate the <code>d</code> and <code>p</code> functions required for the fitting, if <code>FALSE</code> the functions will be generated in the global environment
delta	the delta increment used in the numerical derivatives
...	for extra arguments

Details

This function is created to help users to fit censored data using an existing `gamlss.family` distribution. It does this by taking an existing `gamlss.family` and changing some of the components of the distribution to help the fitting process. In particular it (i) creates a (d) function (for calculating the censored likelihood) and a (p) function (for generating the quantile residuals) within `gamlss`, (ii) changes the global deviance function `G.dev.incr`, the first derivative functions (see note below) and other quantities from the original distribution.

Value

It returns a `gamlss.family` object which has all the components needed for fitting a distribution in `gamlss`.

Note

This function is experimental and could be changed in the future. The function `cens` changes the first derivatives of the original `gamlss` family d function to numerical derivatives for the new censored d function. The default increment `delta`, for this numerical derivatives function, is `eps * pmax(abs(x), 1)` where `eps <- sqrt(.Machine$double.eps)`. The default `delta` could be inappropriate for specific applications and can be overwritten by using the argument `delta`.

Author(s)

Mikis Stasinopoulos <d.stasinopoulos@londonmet.ac.uk> and Bob Rigby <r.rigby@londonmet.ac.uk>

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape, (with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

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Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/i07>.

See Also

[cens.d](#), [cens.p](#), [gen.cens](#)

Examples

```
# comparing output with the survreg() of package survival
library(gamlss.dist)
library(survival)
#-----
# right censoring example
# example from survreg()
# fitting the exponential distribution
```

```

mexp<-survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='exponential')
gexp<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian, family=cens(EXP), c.crit=0.00001)
if(abs(-2*mexp$loglik[2]-deviance(gexp))>0.001) stop(paste("descrepancies in exponential models"))
if(sum(coef(mexp)-coef(gexp))>0.001) warning(paste("descrepancies in coef in exponential models"))
summary(mexp)
summary(gexp)
# fitting different distributions
# weibull
mwei <-survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull')
gwei<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian, family=cens(WEI, delta=c(0.0001,0.0001)), c.crit=
if(abs(-2*mwei$loglik[2]-deviance(gwei))>0.005) stop(paste("descrepancies in deviance in WEI"))
scoef <- sum(coef(mwei)-coef(gwei))
if(abs(scoef)>0.005) warning(cat("descrepancies in coef in WEI of ", scoef, "\n"))
# WEI3 is weibull parametrised with mu as the mean
gwei3 <- gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian, family=cens(WEI3))
# log normal
mlogno <-survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='lognormal')
glogno<-gamlss(Surv(futime, fustat) ~ ecog.ps + rx, data=ovarian, family=cens(LOGNO, delta=c(0.001,0.001)), c.cyc=
if(abs(-2*mlogno$loglik[2]-deviance(glogno))>0.005) stop(paste("descrepancies in deviance in LOGNO"))
coef(mlogno);coef(glogno)
#-----
# now interval response variable
data(lip)
with(lip, y)
mg1<-survreg(y ~ poly(Tem,2)+poly(pH,2)+poly(aw,2), data=lip, dist="weibull")
gg1<- gamlss(y ~ poly(Tem,2)+poly(pH,2)+poly(aw,2), data=lip, family=cens(WEI,type="interval"),
c.crit=0.00001, n.cyc=200, trace=FALSE)

summary(mg1)
summary(gg1)
#-----
# now fitting discretised continuous distribution to count data
# fitting discretised Gamma
data(species)
mGA<-gamlss(Surv(fish,fish+1,type= "interval2")~log(lake)+I(log(lake)^2), sigma.fo=~log(lake),
data=species, family=cens(GA, type="interval"))
# fitting discretised inverse Gaussian
mIG<-gamlss(Surv(fish,fish+1,type= "interval2")~log(lake)+I(log(lake)^2), sigma.fo=~log(lake),
data=species, family=cens(IG, type="interval"))
AIC(mGA,mIG)
plot(fish~log(lake), data=species)
with(species, lines(log(lake)[order(lake)], fitted(mIG)[order(lake)]))
#-----

```

cens.d

Censored probability density function of a `gamlss.family` distribution

Description

Creates a probability density function from a current `gamlss.family` distribution to be used for fitting a censored or interval response variable.

Usage

```
cens.d(family = "NO", type = c("right", "left", "interval"), ...)
```

Arguments

family	a <code>gamlss.family</code> object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by <code>gamlss()</code> can be found in <code>gamlss.family</code> and in the package <code>gamlss.dist</code> .
type	whether right, left or in interval censoring is required, (right is the default)
...	for extra arguments

Details

This function is used to calculate the likelihood function for censored data. This function is not supposed to be used on its own but it is used in function `gen.cens`.

Value

Returns a modified d family function. The argument of the original function d function are the same.

Note

For an example see `gen.cens()`

Author(s)

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References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/i07>.

See Also

[cens.p](#), [gen.cens](#)

Examples

```
#see the help for function cens for an example
```

cens.p	<i>Censored Cumulative Probability Density Function of a <code>gamlss.family</code> Distribution</i>
--------	--

Description

Creates a cumulative density function from a current `gamlss.family` distribution suitable for censored or interval response variable data.

Usage

```
cens.p(family = "NO", type = c("right", "left", "interval"), ...)
```

Arguments

family	a <code>gamlss.family</code> object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by <code>gamlss()</code> can be found in <code>gamlss.family</code> .
type	whether right, left or in interval censoring is required, (right is the default)
...	for extra arguments

Details

This function is used to calculate the quantile residuals for censored data distributions. This function is not supposed to be used on its own but it is used in the function `gen.cens`.

Value

Returns a modified p family function. The argument of the original function d function are the same.

Note

For an example see `gen.cens()`

Author(s)

Mikis Stasinopoulos <d.stasinopoulos@londonmet.ac.uk> and Bob Rigby <r.rigby@londonmet.ac.uk>

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/i07>.

See Also

[cens.d](#), [gen.cens](#)

Examples

```
#see the help for function cens for an example
```

cens.q	<i>Censored Inverse Cumulative Probability Density Function of a <code>gamlss.family</code> Distribution</i>
--------	--

Description

Creates the inverse cumulative density function from a current `gamlss.family` distribution suitable for censored or interval response variable data. This is a dummy function identical to the uncensored one but it is needed for consistency in centile estimation from censored data.

Usage

```
cens.q(family = "NO", ...)
```

Arguments

family	a <code>gamlss.family</code> object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by <code>gamlss()</code> can be found in <code>gamlss.family</code> .
...	for extra arguments

Details

This is dummy function, used only to calculate centiles from censored response variable. This function is not supposed to be used on its own but is used by the function `gen.cens`.

Value

Returns a modified q family function. The argument of the original function q function are the same.

Note

For an example see `gen.cens()`

Author(s)

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References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.

Stasinopoulos D. M., Rigby R.A. and Akantziliotou C. (2006) Instructions on how to use the GAMLSS package in R. Accompanying documentation in the current GAMLSS help files, (see also <http://www.gamlss.org/>).

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <http://www.jstatsoft.org/v23/i07>.

See Also

[cens.d](#), [cens.p](#), [gen.cens](#)

Examples

```
#see the help for function cens for an example
```

gen.cens	<i>A Function to Generate Appropriate Functions to Be Used to Fit a Censored Response variable in GAMLSS</i>
----------	--

Description

The `gen.cens()` function allows the user to generate a `d`, `p`, (dummy) `q` and fitting `gamlss` functions for censor and interval response variables. The function can take any [gamlss.family](#) distribution.

Usage

```
gen.cens(family = "NO", name = "cens",
         type = c("right", "left", "interval"), ...)
```

Arguments

family	a gamlss.family object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by <code>gamlss()</code> can be found in gamlss.family and in the package <code>gamlss.dist</code> .
name	the characters you want to add to the name of new functions, by default is the first letter of type and c i.e WEIc for WEI (weibull) interval response variable
type	whether right, left or in interval censoring is required, (right is the default)
...	for extra arguments

Value

Returns the d, p, (dummy) q and the fitting used in the fitting gamlss algorithm (The one used in the fitting gamlss algorithm) of a gamlss.family distribution.

Author(s)

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References

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See Also

[cens.d](#), [cens.p](#), [cens](#)

Examples

```
library(gamlss.dist)
data(lip)
gen.cens(WEI,type="interval")
WEIic
gg1<- gamlss(y ~ poly(Tem,2)+poly(pH,2)+poly(aw,2), data=lip, family=WEIic, c.crit=0.00001, n.cyc=200, trace=FALSE)
```

lip

Data for lip

Description

The data set used in this package are collected by Dr Peggy Braun (University of Leipzig) and passed on to use by professor Jane Sutherland of London Metropolitan University.

It consists of experimental enzymology results from a research project which attempted to develop a generic food spoilage model.

The data set contains a column called NAMES, which shows the experiment name, three columns with values of the environmental conditions: temperature (Tem), pH and water activity (aw), and the rest of the columns contains the activity of the cocktails, observed at certain days.

The researchers recorded the activity of proteases and lipases in each cocktail and were interested in predicting the time when the activity started given the environmental conditions. The activity is a positive integer and enzymes are considered inactive when activity=0.

Usage

```
data(lip)
```

Format

A data frame with 120 observations on the following 14 variables.

name a factor with levels the different experiment

Tem a numeric vector showing the temperature

pH a numeric vector PH

aw a numeric vector water activity

X0.d a numeric vector if enzyme reacted at day 0

X1.d a numeric vector if enzyme reacted at day 1

X2.d a numeric vector if enzyme reacted at day 2

X4.d a numeric vector if enzyme reacted at days 3 or 4

X11.d a numeric vector if enzyme reacted at days 5 to 11

X18d. a numeric vector if enzyme reacted at days 12 to q18

X25.d a numeric vector if enzyme reacted at days 19 to 25

X32.d a numeric vector if enzyme reacted at days 26 to 32

X39.d a numeric vector if enzyme reacted at days 33 to 39

y a matrix with 3 columns: this is a `Surv()` object indicating the start the finish and censored indicator as defined in function `Surv()` of **survival**.

Source

Prof. Jane Sutherland, London Metropolitan University

Examples

```
data(lip)
with(lip, y)
```

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