Package ‘gamlss’

November 12, 2017

Description Functions for fitting the Generalized Additive Models for Location Scale and Shape introduced by Rigby and Stasinopoulos (2005), <doi:10.1111/j.1467-9876.2005.00510.x>. The models use a distributional regression approach where all the parameters of the conditional distribution of the response variable are modelled using explanatory variables.

Version 5.0-5

Date 2017-11-12

Title Generalised Additive Models for Location Scale and Shape

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Depends R (>= 3.3.0), graphics, stats, splines, utils, grDevices, gamlss.data (>= 5.0-0), gamlss.dist (>= 4.3.1), nlme, parallel

LazyLoad yes

Imports MASS, survival, methods

License GPL-2 | GPL-3

URL http://www.gamlss.org/

NeedsCompilation yes

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Repository CRAN

Date/Publication 2017-11-12 15:17:17 UTC

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The GAMLSS library and datasets

Description

This is a collection of functions to fit Generalized Additive Models for Location Scale and Shape (GAMLSS) and handled gamlss objects.

GAMLSS were introduced by Rigby and Stasinopoulos (2005). GAMLSS is a general framework for univariate regression type statistical problems using new ways of dealing with overdispersion, skewness and kurtosis in the response variable. In GAMLSS the exponential family distribution assumption used in Generalized Linear Model (GLM) and Generalized Additive Model (GAM), (see Nelder and Wedderburn, 1972 and Hastie and Tibshirani, 1990, respectively) is relaxed and replaced by a very general distribution family including highly skew and kurtotic discrete and continuous distributions. The systematic part of the model is expanded to allow modelling not only the mean (or location) but other parameters of the distribution of the response variable as linear parametric, nonlinear parametric or additive non-parametric functions of explanatory variables and/or random effects terms. Maximum (penalized) likelihood estimation is used to fit the models.

Details

Package: gamlss
Type: Package
Version: 1.5-0
Date: 2006-12-13
License: GPL (version 2 or later) See file LICENSE
This package allow the user to model the distribution of the response variable using a variety of one, two, three and four parameter families of distributions. The distributions implemented currently can be found in `gamlss.family`. Other distributions can be easily added. In the current implementation of GAMLSS several additive terms have been implemented including regression splines, smoothing splines, penalized splines, varying coefficients, fractional polynomials and random effects. Other additive terms can be easily added.

Author(s)

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Maintainer: Mikis Stasinopoulos &lt;mikis.stasinopoulos@gamlss.org&gt;

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

Examples

data(abdom)
mod&lt;-gamlss(y~pb(x), sigma.fo=~pb(x), family=BCT, data=abdom, method=mixed(1,20))
plot(mod)
rm(mod)

---

**acfResid**

**ACF plot of the residuals**

Description

This plot display the ACF and PACF of the residuals of a gamlss or other fitted model (provided that they have been standardised appropriately. Is is appropriate for time series data.

Usage

```r
acfResid(obj = NULL, resid = NULL)
```
Arguments

obj A gamlss model or other fitted model where the resid() function applies.
resid if obj does not exist, the argument here will be used.

Details

The ACF and PACF for the residuals r, squared residuals \( r^2 \), \( r^3 \) and \( r^4 \) are plotted.

Value

The relevant plots are displayed.

Author(s)

Mikis Stasinopoulos, Bob Rigby, Vlasios Voudouris, and Majid Djennd.

References


See Also

acf

Examples

library(datasets)
data(co2)
m1<-gamlss(co2-pb(as.numeric(time(co2)))+factor(cycle(co2)))
acfResid(m1)
additive.fit

Usage

additive.fit(x, y, w, s, who, smooth.frame, maxit = 30, tol = 0.001,
        trace = FALSE, se = TRUE, ...)

Arguments

x        the linear part of the explanatory variables
y        the response variable
w        the weights
s        the matrix containing the smoothers
who      the current smoothers
smooth.frame  the data frame used for the smoothers
maxit    maximum number of iterations in the backfitting
tol      the tolerance level for the backfitting
trace    whether to trace the backfitting algorithm
se       whether standard errors are required
...      for extra arguments

Details

This function should not be used on its own

Value

Returns a list with the linear fit plus the smoothers

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and
Regression and Smoothing: Using GAMLSS in R, Chapman and Hall/CRC.
(see also http://www.gamlss.org/).

See Also

gamlss
Functions to fit fractional polynomials in GAMLSS

Description

The function `bfp` generates a power polynomial basis matrix which (for given powers) can be used to fit power polynomials in one x-variable. The function `fp` takes a vector and returns it with several attributes. The vector is used in the construction of the model matrix. The function `fp()` is not used for fitting the fractional polynomial curves but assigns the attributes to the vector to aid gamlss in the fitting process. The function doing the fitting is `gamlss.fp()` which is used at the backfitting function `additive.fit` (but never used on its own). The (experimental) function `pp` can be used to fit power polynomials as in \( a + b_1 x^{p_1} + b_2 x^{p_2} \), where \( p_1 \) and \( p_2 \) have arbitrary values rather restricted as in the `fp` function.

Usage

```r
bfp(x, powers = c(1, 2), shift = NULL, scale = NULL)
fp(x, npoly = 2, shift = NULL, scale = NULL)
pp(x, start = list(), shift = NULL, scale = NULL)
```

Arguments

- `x`: the explanatory variable to be used in functions `bfp()` or `fp()`. Note that this is different from the argument `x` use in `gamlss.fp` (a function used in the backfitting but not by straight by the user).
- `powers`: a vector containing as elements the powers in which the x has to be raised.
- `shift`: a number for shifting the x-variable. The default values is zero, if x is positive, or the minimum of the positive difference in x minus the minimum of x.
- `scale`: a positive number for scaling the x-variable. The default values is \(10^{\lfloor \text{sign}(\log_{10}(\text{range})) \rfloor \times \text{trunc}(\text{abs}(\log_{10}(\text{range})))}\).
- `npoly`: a positive indicating how many fractional polynomials should be considered in the fit. Can take the values 1, 2 or 3 with 2 as default.
- `start`: a list containing the starting values for the non-linear maximization to find the powers. The results from fitting the equivalent fractional polynomials can be used here.

Details

The above functions are an implementation of the fractional polynomials introduced by Royston and Altman (1994). The three functions involved in the fitting are loosely based on the fractional polynomials implementation in S-plus written by Gareth Amber in 1999, (unfortunately the URL link for his work no longer exist). The function `bfp` generates the right design matrix for the fitting a power polynomial of the type \( a + b_1 x^{p_1} + b_2 x^{p_2} + \ldots + b_k x^p \). For given powers \( p_1, p_2, \ldots, p_k \) given as the argument `powers` in `bfp()` the function can be used to fit power polynomials in the same way as the functions `poly()` or `bs()` (of package `splines`) are used to fit orthogonal or piecewise polynomials respectively. The function `fp()`, which is working as a...
smoother in gamlss, is used to fit the best fractional polynomials within a set of power values. Its argument npoly determines whether one, two or three fractional polynomials should used in the fitting. For a fixed number npoly the algorithm looks for the best fitting fractional polynomials in the list c(-2, -1, -0.5, 0, 0.5, 1, 2, 3). Note that npol=3 is rather slow since it fits all possible combinations 3-way combinations at each backfitting interaction. The function gamlss.fp() is an internal function of GAMLSS allowing the fractional polynomials to be fitted in the backfitting cycle of gamlss, and should be not used on its own.

Value

The function bfp returns a matrix to be used as part of the design matrix in the fitting.

The function fp returns a vector with values zero to be included in the design matrix but with attributes useful in the fitting of the fractional polynomials algorithm in gamlss.fp.

Warning

Since the model constant is included in both the design matrix X and in the backfitting part of fractional polynomials, its values is wrongly given in the summary. Its true values is the model constant minus the constant from the fractional polynomial fitting ???. What happens if more that one fractional polynomials are fitted?

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby <b.rigby@londonmet.ac.uk>

References


(see also http://www.gamlss.org/).

See Also

gamlss, gamlss.family

Examples

data(abdom)

# fits polynomials with power 1 and .5
mod1<-.gamlss(y=bfp(x,c(1,0.5)),data=abdom)

# fit the best of one fractional polynomial
m1<-.gamlss(y=fp(x,1),data=abdom)
# fit the best of two fractional polynomials
m2<-gamlss(y~fp(x,2),data=abdom)

# fit the best of three fractional polynomials
m3<-gamlss(y~fp(x,3),data=abdom)

# get the coefficient for the second model
m2$mu.coef$mo

# now power polynomials using the best 2 fp c()
m4 <- gamlss(y ~ pp(x, c(1,3)), data = abdom)

# This is not good idea in this case because
# if you look at the fitted values you see what it went wrong
plot(y~x, data=abdom)
lines(fitted(m2,"mu")~abdom$x,col="red")
lines(fitted(m4,"mu")~abdom$x,col="blue")

calibration

Calibrating centile curves

Description

This function can used when the fitted model centiles do not coincide with the sample centiles.

Usage

calibration(object, xvar, cent = 100 * pnorm((-4:4) * 2/3),
legend = FALSE, fan = FALSE, ...)

Arguments

- **object**: a gamlss fitted object
- **xvar**: The explanatory variable
- **cent**: a vector with elements the % centile values for which the centile curves have to be evaluated
- **legend**: whether legend is required
- **fan**: whether to use the fan version of centiles
- **...**: other argument pass on to centiles() function

Details

The function finds the sample quantiles of the residuals of the fitted model (the z-scores) and use them as sample quantile in the argument cent of the centiles() function. This procedure is appropriate if the fitted model centiles do not coincide with the sample centiles and when this failure is the same in all values of the explanatory variable xvar.

Value

A centile plot is produced and the sample centiles below each centile curve are printed (or saved)
centiles

Author(s)
Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby <r.rigby@londonmet.ac.uk> and Vlasios Voudouris <vlasios.voudouris@abm-analytics.com>

References
(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also
centiles, centiles.fan

Examples
```r
data(abdom)
m1<-gamlss(y~pb(x), sigma.fo~pb(x), family=L0, data=abdom)
calibration(m1, xvar=abdom$x, fan=TRUE)
```

---

Plots the centile curves for a GAMLSS object

Description
This function `centiles()` plots centile curves for distributions belonging to the GAMLSS family of distributions. The function also tabulates the sample percentages below each centile curve (for comparison with the model percentages given by the argument `cent`). The function `centiles.fan()` plots a fan-chart of the centile curves. A restriction of the functions is that it applies to models with one explanatory variable only.

Usage
```r
centiles(obj, xvar = NULL, cent = c(0.4, 2, 10, 25, 50, 75, 90, 98, 99.6),
legend = TRUE, ylab = "y", xlab = "x", main = NULL,
main.gsub = "@", xleg = min(xvar), yleg = max(obj$y),
xlim = range(xvar), ylim = range(obj$y), save = FALSE,
plot = TRUE, points = TRUE, pch = 15, cex = 0.5, col = gray(0.7),
col.centiles = 1:length(cent) + 2, lty.centiles = 1, lwd.centiles = 1,...)
centiles.fan(obj, xvar = NULL, cent = c(0.4, 2, 10, 25, 50, 75, 90, 98, 99.6),
ylab = "y", xlab = "x", main = NULL, main.gsub = "@",
```
Centiles are calculated using the fitted values in `obj` and `xvar` must correspond exactly to the predictor in `obj` to plot correctly.

`col`, `lty` and `lwd` may be vector arguments and are recycled to the length of `cent` if necessary.
A centile plot is produced and the sample centiles below each centile curve are printed (or saved).

This function is appropriate only when one continuous explanatory variable is fitted in the model.

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby <r.rigby@londonmet.ac.uk>
with contribution from Steve Ellison


(see also http://www.gamlss.org/).

See Also

gamlss, centiles.split, centiles.com

Examples

data(abdom)
h<-gamlss(y~pb(x), sigma.formula=~pb(x), family=BCT, data=abdom)
# default plot
centiles(h,xvar=abdom$x)
# control of colours and lines
centiles(h, xvar=abdom$x, col.cent=c(2,3,4,5,1,5,4,3,2,1),
         lwd.cent=c(1,1,1,1,1,2,1,1,1,1))
#Control line types
centiles(h, xvar=abdom$x, col.cent=1, cent=c(.5,2.5,50,97.5,99.5),
         lty.centiles=c(3,2,1,2,3),lwd.cent=c(1,1,2,1,1))
# control of the main title
centiles(h, xvar=abdom$x, main="Abdominal data 
")
# the fan-chart
centiles.fan(h,xvar=abdom$x, colors="rainbow")
rm(h)
**Description**

This function compares centiles curves for more than one GAMLSS objects. It is based on the centiles function. The function also tabulates the sample percentages below each centile curve (for comparison with the model percentages given by the argument `cent`). A restriction of the function is that it applies to models with one explanatory variable only.

**Usage**

```r
centiles.com(obj, ..., xvar = NULL, cent = c(0.4, 10, 50, 90, 99.6), legend = TRUE, ylab = "y", xlab = "x", xleg = min(xvar), yleg = max(obj$y), xlim = range(xvar), ylim = NULL, no.data = FALSE, color = TRUE, main = NULL, plot = TRUE)
```

**Arguments**

- `obj`: a fitted gamlss object from fitting a gamlss continuous distribution
- `...`: optionally more fitted GAMLSS model objects
- `xvar`: the unique explanatory variable
- `cent`: a vector with elements the % centile values for which the centile curves have to be evaluated
- `legend`: whether a legend is required in the plot or not, the default is `legend=TRUE`
- `ylab`: the y-variable label
- `xlab`: the x-variable label
- `xleg`: position of the legend in the x-axis
- `yleg`: position of the legend in the y-axis
- `xlim`: the limits of the x-axis
- `ylim`: the limits of the y-axis
- `no.data`: whether the data should plotted, default `no.data=FALSE` or not `no.data=TRUE`
- `color`: whether the fitted centiles are shown in colour, `color=TRUE` (the default) or not `color=FALSE`
- `main`: the main title
- `plot`: whether to plot the centiles

**Value**

Centile plots are produced for the different fitted models and the sample centiles below each centile curve are printed.
centiles.pred

Warning

This function is appropriate only when one continuous explanatory variable is fitted in the model

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> and Bob Rigby <r.rigby@londonmet.ac.uk>

References

(see also http://www.gamlss.org/).

See Also

gamlss.centiles, centiles.split

Examples

data(abdom)
h1<-gamlss(y~cs(x,df=3), sigma.formula=-cs(x,1),family=BCT, data=abdom)
h2<-gamlss(y~pb(x), sigma.formula=-pb(x), family=BCT, data=abdom)
centiles.com(h1,h2,xvar=abdom$x)
rm(h1,h2)

---

centiles.pred Creating predictive centiles values

Description

This function creates predictive centiles curves for new x-values given a GAMLSS fitted model. The function has three options: i) for given new x-values and given percentage centiles calculates a matrix containing the centiles values for y, ii) for given new x-values and standard normalized centile values calculates a matrix containing the centiles values for y, iii) for given new x-values and new y-values calculates the z-scores. A restriction of the function is that it applies to models with only one explanatory variable.

Usage

centiles.pred(obj, type = c("centiles", "z-scores", "standard-centiles"),
  xname = NULL, xvalues = NULL, power = NULL, yval = NULL,
  cent = c(0.4, 2, 10, 25, 50, 75, 90, 98, 99.6),
  dev = c(-4, -3, -2, -1, 0, 1, 2, 3, 4),
  plot = FALSE, legend = TRUE,
  ...)

**Arguments**

- **obj**: a fitted gamlss object from fitting a gamlss continuous distribution.
- **type**: the default, "centiles", gets the centiles values given in the option `cent`. `type="standard-centiles"` gets the standard centiles given in the dev. `type="z-scores"` gets the z-scores for given y and x new values.
- **xname**: the name of the unique explanatory variable (it has to be the same as in the original fitted model).
- **xvalues**: the new values for the explanatory variable where the prediction will take place.
- **power**: if power transformation is needed (but read the note below).
- **yval**: the response values for a given x required for the calculation of "z-scores".
- **cent**: a vector with elements the % centile values for which the centile curves have to be evaluated.
- **dev**: a vector with elements the standard normalized values for which the centile curves have to be evaluated in the option `type="standard-centiles"`.
- **plot**: whether to plot the "centiles" or the "standard-centiles", the default is `plot=FALSE`.
- **legend**: whether a legend is required in the plot or not, the default is `legend=TRUE`.
- **...**: for extra arguments.

**Value**

A vector (for option `type="z-scores"`) or a matrix for options `type="centiles"` or `type="standard-centiles"` containing the appropriate values.

**Warning**

See example below of how to use the function when power transformation is used for the x-variables.

**Note**

The power option should be only used if the model.

**Author(s)**

Mikis Stasinopoulos, <mikis.stasinopoulos@gamlss.org>, based on ideas of Elaine Borghie from the World Health Organization.

**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).
See Also
gamlss, centiles, centiles.split

Examples

```r
## bring the data and fit the model
data(abdom)
a <- gamlss(y~pb(x), sigma.fo=-pb(x), data=abdom, family=BCT)
## plot the centiles
centiles(a,xvar=abdom$x)
## first use of centiles.pred()
## to calculate the centiles at new x values
##
newx <- seq(12,40,2)
mat <- centiles.pred(a, xname="x", xvalues=newx )
mat
## now plot the centile curves
mat <- centiles.pred(a, xname="x", xvalues=newx, plot=TRUE )
## second use of centiles.pred()
## to calculate (normalised) standard-centiles for new x
## values using the fitted model
##
newx <- seq(12,40,2)
mat <- centiles.pred(a, xname="x", xvalues=newx, type="standard-centiles" )
mat
## now plot the standard centiles
mat <- centiles.pred(a, xname="x", xvalues=newx, type="standard-centiles", plot = TRUE )
## third use of centiles.pred()
## if we have new x and y values what are their z-scores?
##
# create new y and x values and plot them in the previous plot
newx <- c(20,21,2,23,20,9,24,2,24,1,25)
newy <- c(130,121,123,125,140,145,150)
for(i in 1:7) points(newx[i],newy[i],col="blue")
## now calculate their z-scores
znewx <- centiles.pred(a, xname="x", xvalues=newx,yval=newy, type="z-scores" )
znewx
## Not run:
## What we do if the x variables is transformed?
##
## case 1 : transformed x-variable within the formula
##
## fit model
aa <- gamlss(y~pb(x^0.5), sigma.fo=-pb(x^0.5), data=abdom, family=BCT)
## centiles works
centiles(aa,xvar=abdom$x, legend = FALSE)
newx <- seq(12,40,2)
```
**centiles.split**

Plots centile curves split by x for a GAMLSS object

**Description**

This function plots centiles curves for separate ranges of the unique explanatory variable x. It is similar to the `centiles` function but the range of x is split at a user defined values `xcut.points` into r separate ranges. The functions also tabulates the sample percentages below each centile curve for each of the r ranges of x (for comparison with the model percentage given by cent) The model should have only one explanatory variable.

**Usage**

```r
centiles.split(obj, xvar = NULL, xcut.points = NULL, n.inter = 4,
   cent = c(0.4, 2, 10, 25, 50, 75, 90, 98, 99.6),
   legend = FALSE, main = NULL, main.gsub = "@",
   ylab = "y", xlab = "x", ylim = NULL, overlap = 0,
   save = TRUE, plot = TRUE, ...)
```

**Arguments**

- **obj**
  - a fitted gamlss object from fitting a gamlss continuous distribution
- **xvar**
  - the unique explanatory variable
- **xcut.points**
  - the x-axis cut off points e.g. c(20, 30). If `xcut.points=NULL` then the `n.inter` argument is activated
- **n.inter**
  - if `xcut.points=NULL` this argument gives the number of intervals in which the x-variable will be splited, with default 4
- **cent**
  - a vector with elements the % centile values for which the centile curves are to be evaluated
legend: whether a legend is required in the plots or not, the default is `legend=FALSE`.

main: the main title as character. If `NULL` the default title (shown the intervals) is shown.

main.gsub: if the `main.gsub` (with default "@") appears in the main title then it is substituted with the default title.

ylab: the y-variable label.

xlab: the x-variable label.

ylim: the range of the y-variable axis.

overlap: how much overlapping in the `xvar` intervals. Default value is `overlap=0` for non overlapping intervals.

save: whether to save the sample percentages or not with default equal to `TRUE`. In this case the functions produce a matrix giving the sample percentages for each interval.

plot: whether to plot the centiles. This option is usefull if the sample statistics only are to be used.

... for extra arguments.

Value

Centile plots are produced and the sample centiles below each centile curve for each of the r ranges of x can be saved into a matrix.

Warning

This function is appropriate when only one continuous explanatory variable is fitted in the model.

Author(s)

Mikis Stasinopoulos, <mikis.stasinopoulos@gamlss.org>, Bob Rigby <r.rigby@londonmet.ac.uk>, with contributions from Elaine Borghie

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

gamlss centiles, centiles.com
coef.gamlss

Examples

data(abdom)
h<-gamlss(y~pb(x), sigma.formula=~pb(x), family=BCT, data=abdom)
mout <- centiles.split(h,xvar=abdom$x)
mout
rm(h,mout)

coef.gamlss  Extract Model Coefficients in a GAMLSS fitted model

Description

coef.gamlss is the GAMLSS specific method for the generic function coef which extracts model coefficients from objects returned by modelling functions. ‘coefficients’ is an alias for coef.

Usage

## S3 method for class 'gamlss'
coef(object, what = c("mu", "sigma", "nu", "tau"),
parameter = NULL, ...)

Arguments

object a GAMLSS fitted model
what which parameter coefficient is required, default what="mu"
parameter equivalent to what (more obvious name)
... for extra arguments

Value

Coefficients extracted from the GAMLSS model object.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


(see also http://www.gamlss.org/).
See Also

gamlss, deviance.gamlss, fitted.gamlss

Examples

data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
coef(h)
rm(h)

Description

The functions cs() and scs() are using the cubic smoothing splines function smooth.spline() to do smoothing. They take a vector and return it with several attributes. The vector is used in the construction of the model matrix. The functions do not do the smoothing, but assigns the attributes to the vector to aid gamlss in the smoothing. The function doing the smoothing is gamlss.cs(). This function use the R function smooth.spline() which is then used by the backfitting function additive.fit() which is based on the original GAM implementation described in Chambers and Hastie (1992). The function gamlss.scs() differs from the function cs() in that allows cross validation of the smoothing parameters unlike the cs() which fixes the effective degrees of freedom, df. Note that the recommended smoothing function is now the function pb() which allows the estimation of the smoothing parameters using a local maximum likelihood. The function pb() is based on the penalised beta splines (P-splines) of Eilers and Marx (1996).

The (experimental) function vc is now defunct. For fitting varying coefficient models, Hastie and Tibshirani (1993) use the function pvc().

Usage

cs(x, df = 3, spar = NULL, c.spar = NULL, control = cs.control(...), ...)
scs(x, df = NULL, spar = NULL, control = cs.control(...), ...)
cs.control(cv = FALSE, all.knots = TRUE, nknots = NULL, keep.data = TRUE,
        df.offset = 0, penalty = 1.4, control.spar = list(), ...)

Arguments

x the univariate predictor, (or expression, that evaluates to a numeric vector). For the function vc the x argument is the vector which has its (linear) coefficient change with r

df the desired equivalent number of degrees of freedom (trace of the smoother matrix minus two for the constant and linear fit). The real smoothing parameter (spar below) is found such that df=tr(S)-2, where S is the implicit smoother matrix. Values for df should be greater than 0, with 0 implying a linear fit.
spar smoothing parameter, typically (but not necessarily) in (0,1]. The coefficient
lambda of the integral of the squared second derivative in the fit (penalised
log likelihood) criterion is a monotone function of `spar`, see the details in
smooth.spline.

c.spar This is an option to be used when the degrees of freedom of the fitted gamlss
object are different from the ones given as input in the option df. The
default values used are the ones given the option control.spar in the R func-
tion smooth.spline() and they are c.spar=c(-1.5, 2). For very large data
sets e.g. 10000 observations, the upper limit may have to increase for example
to c.spar=c(-1.5, 2.5). Use this option if you have received the warning
'The output df are different from the input, change the control.spar'. c.spar
can take both vectors or lists of length 2, for example c.spar=c(-1.5, 2.5) or
c.spar=list(-1.5, 2.5) would have the same effect.

control control for the function smooth.spline, see below
cv see the R function smooth.spline()
all.knots see the R function smooth.spline()
nknots see the R function smooth.spline()
keep.data see the R function smooth.spline()

df.offset see the R function smooth.spline()
penalty see the R function smooth.spline(), here the default value is 1.4
control.spar see above c.spar or the equivalent argument in the function smooth.spline
... for extra arguments

Details

Note that cs itself does no smoothing; it simply sets things up for the function gamlss() which in
turn uses the function additive.fit() for backfitting which in turn uses gamlss.cs()

Note that cs() and scs() functions behave differently at their default values that is if df and lambda
are not specified. cs(x) by default will use 3 extra degrees of freedom for smoothing for x. scs(x)
by default will estimate lambda (and the degrees of freedom) automatically using generalised cross
validation (GCV). Note that if GCV is used the convergence of the gamlss model can be less stable
compared to a model where the degrees of freedom are fixed. This will be true for small data sets.

Value

the vector x is returned, endowed with a number of attributes. The vector itself is used in the
construction of the model matrix, while the attributes are needed for the backfitting algorithms
additive.fit(). Since smoothing splines includes linear fits, the linear part will be efficiently
computed with the other parametric linear parts of the model.

Warning

For a user who wishes to compare the gamlss() results with the equivalent gam() results in S-plus:
makesure when using S-plus that the convergence criteria epsilon and bf.epsilon in control.gam() are
decreased sufficiently to ensure proper convergence in S-plus. Also note that the degrees
of freedom are defined on top of the linear term in gamlss, but on top of the constant term in S-plus,
(so use an extra degrees of freedom in S-plus in order to obtain comparable results to those in gamlss).

Change the upper limit of spar if you received the warning ’The output df are different from the input, change the control.spar’.

For large data sets do not use expressions, e.g. cs(x*0.5) inside the gamlss function command but evaluate the expression, e.g. nx=x**0.5, first and then use cs(nx).

Note

The degrees of freedom df are defined differently from that of the gam() function in S-plus. Here df are the additional degrees of freedom excluding the constant and the linear part of x. For example df=4 in gamlss() is equivalent to df=5 in gam() in S-plus

Author(s)

Mikis Stasinopoulos and Bob Rigby (see also the documentation of the functionsmooth.spline() for the original authors of the cubic spline function.)

References

(see also http://www.gamlss.org/).

See Also

gamlss, gamlss.cs, pb, pvc

Examples

# cubic splines example
data(aids)
# fitting a smoothing cubic spline with 7 degrees of freedom
# plus the a quarterly effect
aids1 < gamlss(y~cs(x,df=7)+qrt, data=aids, family=PO) #
aids2 < gamlss(y~scs(x,df=5)+qrt, data=aids, family=PO) #
aids3 < gamlss(y~scs(x)+qrt, data=aids, family=PO) # using GCV
with(aids, plot(x,y))
deviance.gamlss

Returns the global, \(-2\log(\text{likelihood})\), or the penalized, \(-2\log(\text{likelihood})+\) penalties, deviance of a fitted GAMLSS model object.

Usage

```r
## S3 method for class 'gamlss'
deviance(object, what = c("G", "P"), ...)
```

Arguments

- `object`: a GAMLSS fitted model
- `what`: put "G" for Global or "P" for Penalized deviance
- `...`: for extra arguments

Details

deviance is a generic function which can be used to extract deviances for fitted models. deviance.gamlss is the method for a GAMLSS object.

Value

The value of the global or the penalized deviance extracted from a GAMLSS object.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


(see also http://www.gamlss.org/).
See Also

gamlss.family, coef.gamlss, fitted.gamlss

Examples

data(aids)
ho <- gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
deviance(h)
rm(h)

devianceIncr The global deviance increment

Description

The global deviance increment is the contribution of each individual observation to the global deviance. The function devianceIncr() can be used to extract the global deviance increment for a fitted gamlss model or for a new (test/validation) data set. Large values for global deviance increment indicate a bad fit and for new data a bad prediction.

Usage

devianceIncr(obj, newdata = NULL)

Arguments

obj a gamlss object
newdata test data set to check the global deviance increment.

Value

Returns a vector of the global deviance increments for each observation.

Author(s)

Mikis Stasinopoulos

References


(see also http://www.gamlss.org/).
See Also
deviance

Examples

```r
# Count data set
# fit Poisson model
h1 <- gamlss(Claims~L_Population+L_Accidents+L_KI+L_Popdensity,
data=LGac1aims, family=PO)
p1<-devianceIncr(h1)
# fit negative binomial model
h2 <- gamlss(Claims~L_Population+L_Accidents+L_KI+L_Popdensity,
data=LGac1aims, family=NBI)
p2<-devianceIncr(h2)
# comparing using boxplots
boxplot(cbind(p1,p2))
# comparing using empirirical cdf
plot(ecdf(p1))
lines(ecdf(p2), col=2)
# comparing against the y-values
plot(p1~LGac1aims$Claims, pch=20, col="gray")
points(p2~LGac1aims$Claims, pch="-", col="orange")
# Continuous data sets
## Not run:
m1 <- gamlss(head~pb(age), data=db[1:6000,])
m1<-devianceIncr(m1)
m2 <- gamlss(head~pb(age), sigma.fo=-pb(age), nu.fo=-pb(age),
               tau.fo=-pb(age), data=db[1:6000,], family=BCT)
p2<d.evianceIncr(m2)
# comparing using summaries
summary(p1); summary(p2)
# comparing using boxplots
boxplot(cbind(p1,p2))
# comparing using histograms
hist(p1, col=rgb(1,0,0,0.5), xlim=c(0,50), breaks=seq(0,50,2))
hist(p2, col=rgb(0,0,1,0.5), add=T)
# comparing using empirirical cdf
plot(ecdf(p1))
lines(ecdf(p2), col=2)
## End(Not run)
```

---

dtop

Detrended transformed Owen’s plot
Description

Provides single or multiple detrended transformed Owen’s plot, Owen (1995), for a GAMLSS fitted objects or any other fitted object which has the method resid(). This is a diagnostic tool for checking whether the normalised quantile residuals are coming from a normal distribution or not. This could be true if the horizontal line is within the confidence intervals.

Usage

dtop(object = NULL, xvar = NULL, resid = NULL,
     type = c("Owen", "JW"),
     conf.level = c("95", "99"), n.inter = 4,
     xcut.points = NULL, overlap = 0,
     show.given = TRUE, cex = 1, pch = 21,
     line = TRUE, ...)

Arguments

- **object**: a GAMLSS fitted object or any other fitted object which has the method resid().
- **xvar**: the explanatory variable against which the detrended Owen’s plots will be plotted.
- **resid**: if the object is not specified the residual vector can be given here.
- **conf.level**: 95 (default) or 99 percent confidence interval for the plots.
- **n.inter**: the number of intervals in which the explanatory variable xvar will be cut.
- **xcut.points**: the x-axis cut off points e.g. c(20,30). If xcut.points=NULL then the n.inter argument is activated.
- **overlap**: how much overlapping in the xvar intervals. Default value is overlap=0 for non overlapping intervals.
- **show.given**: whether to show the x-variable intervals in the top of the graph, default is show.given=TRUE.
- **cex**: the cex plotting parameter with default cex=1.
- **pch**: the pch plotting parameter with default pch=21.
- **line**: whether the detrended empirical cdf should be plotted or not.
- **...**: for extra arguments.

Details

If the xvar argument is not specified then a single detrended Owen’s plot is used, see Owen (1995). In this case the plot is a detrended nonparametric likelihood confidence band for a distribution function. That is, if the horizontal lines lies within the confidence band then the normalised residuals could have come from a Normal distribution and consequently the assumed response variable distribution is reasonable. If the xvar is specified then we have as many plots as n.iter. In this case the x-variable is cut into n.iter intervals with an equal number observations and detrended Owen’s plots for each interval are plotted. This is a way of highlighting failures of the model within different ranges of the explanatory variable.
**Value**

A plot is returned.

**Author(s)**

Mikis Stasinopoulos, Bob Rigby and Vlassios Voudouris

**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

**See Also**

*wp*

**Examples**

```r
data(abdom)
a<-gamlss(y~pb(x),sigma.fo~pb(x,1),family=LO, data=abdom)
dtop(a)
dtop(a, xvar=abdom$x)
rm(a)
```

<table>
<thead>
<tr>
<th>edf</th>
<th>Effective degrees of freedom from gamlss model</th>
</tr>
</thead>
</table>

**Description**

The functions `edf()` and `edfAll()` can be used to obtained the effective degrees of freedom for different additive terms for the distribution parameters in a gamlss model.

**Usage**

```r
edf(obj, what = c(“mu”, “sigma”, “nu”, “tau”),
     parameter= NULL, print = TRUE, ...)
edfAll(obj, ...)
```
Arguments

- `obj` A gamlss fitted model
- `what` which of the four parameters mu, sigma, nu or tau.
- `parameter` equivalent to what
- `print` whether to print the label
- `...` for extra arguments

Value

The function `edfAll()` returns a list of edf for all the fitted parameters. The function `edf()` a vector of edf.

Note

The edf given are the ones fitted in the backfitting so the usually contained (depending on the additive term) the contactnt and the linear part.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References

  (see also http://www.gamlss.org/).

See Also

- `gamlss`

Examples

```r
library(gamlss.data)
data(usair)
m1<- gamlss(y~pb(x1)+pb(x2)+pb(x6), data=usair)
edfAll(m1)
edf(m1)
```
find.hyper

A function to select values of hyper-parameters in a GAMLSS model

Description

This function selects the values of hyper parameters and/or non-linear parameters in a GAMLSS model. It uses the R function `optim` which then minimises the generalised Akaike information criterion (GAIC) with a user defined penalty.

Usage

```r
find.hyper(model = NULL, parameters = NULL, other = NULL, k = 2,
            steps = c(0.1), lower = -Inf, upper = Inf, method = "L-BFGS-B",
            ...)
```

Arguments

- `model`: this is a GAMLSS model in `quote()`. e.g. `quote(gamlss(y~cs(x,df=p[1]),sigma.fo=~cs(x,df=p[2]),data=abdom))` where `p[1]` and `p[2]` denote the parameters to be estimated.
- `parameters`: the starting values in the search of the optimum hyper-parameters and/or non-linear parameters e.g. `parameters=c(3,3)`
- `other`: this is used to optimise other non-parameters, for example a transformation of the explanatory variable of the kind `x^{p[3]}`, `others=quote(nx<-x^{p[3]})` where `nx` is now in the model formula.
- `k`: specifies the penalty in the GAIC. (the default is 2) e.g. `k=3`.
- `steps`: the steps taken in the optimisation procedure [see the `ndeps` option in `optim()`], by default is set to 0.1 for all hyper parameters and non-linear parameters.
- `lower`: the lower permissible level of the parameters i.e. `lower=c(1,1)` this does not apply if a method other than the default method "L-BFGS-B" is used.
- `upper`: the upper permissible level of the parameters i.e. `upper=c(30,10)`, this is not apply if a method other than the default method "L-BFGS-B" is used.
- `method`: the method used in `optim()` to numerically minimise the GAIC over the hyper-parameters and/or non-linear parameters. By default this is "L-BFGS-B" to allow box-restriction on the parameters.
- `...`: for extra arguments to be passed to the R function `optim()` used in the optimisation.

Details

This historically was an experimental function which worked well for the search of the optimum degrees of freedom and non-linear parameters (e.g. power parameter \( \lambda \) used to transform \( x \) to \( x^\lambda \)). With the introduction of the P-Spline smoothing function `pb()` the function `find.hyper()` became almost redundant. `find.hyper()` takes lot longer than `pb()` to find automatically the hyper parameters while both method produce similar results. See below the examples for a small demonstration.
Value

The function turns the same output as the function optim()

- **par** the optimum hyper-parameter values
- **value** the minimised value of the GAIC
- **counts** A two-element integer vector giving the number of calls to ‘fn’ and ‘gr’ respectively
- **convergence** An integer code. ‘0’ indicates successful convergence. see the function optim() for other errors
- **message** A character string giving any additional information returned by the optimiser, or ‘NULL’

Warning

It may be slow to find the optimum

Author(s)

Mikis Stasinopoulos

References


(see also http://www.gamlss.org/).

See Also

gamlss, plot.gamlss, optim

Examples

```r
## Not run:
data(abdom)
# Example estimating the smoothing parameters for mu and
# the transformation parameters for x
# declare the model
mod1<-quote(gamlss(y~cs(nx,df=p[1]),family=BCT, data=abdom,
  control=gamlss.control(trace=FALSE)))
# since we want also to find the transformation for x
# we use the "other" option
op <- find.hyper(model=mod1, other=quote(nx~x^p[2]), parameters=c(3,0.5),
  lower=c(1,0.001), steps=c(0.1,0.001))
```
fitDist

Fits Different Parametric gamlss.family distributions to data

Description

This function is using the function `gamlssML()` to fit all relevant parametric gamlss.family distributions to a data vector. The final model is the one which is selected by the generalised Akaike information criterion with penalty $k$. 
Usage

fitDist(y, k = 2,
   type = c("realAll", "realline", "realplus", "real0to1", "counts", "binom"),
   try.gamlss = FALSE, extra = NULL, data = NULL, ...)

Arguments

y 
the data vector

k 
the penalty for the GAIC with default values k=2 the standard AIC

type 
the type of distribution to be tried see details

try.gamlss 
if gamlssML() failed whether should try gamlss instead. This will slow up things for big data.

extra 
whether extra distribution should be tried which are not in the type list

data 
the data frame where y ca be found

... 
for extra arguments to be passed to gamlssML() to gamlss()

Details

The following are the different type argument:

- realAll all the gamlss.family continuous distributions defined on the real line, i.e. realline plus realplus
- realplus the gamlss.family continuous distributions in the positive real line: "EXP", "GA", "IG", "LNO", "WEI3", "BCCGo", "exGAUS", "GG", "GIG", "BCTo", "BCPeo"
- real0to1 the gamlss.family continuous distributions from 0 to 1: "BE", "BEINF", "BEINF0", "BEINF1", "BE01", "BEZI", "GBI"
- binom the gamlss.family distributions for binomial type data: "BI", "BB", "ZIBI", "ZIBB", "ZABI", "ZABB"

Value

A gamlssML object with two extra components:

fits an ordered list according to the GAIC of the fitted distribution

failed the distributions where the gamlssML() (or gamlss()) fits have failed

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby, Vlasis Voudouris <v.voudouris@londonmet.ac.uk> and Majid Djennad <m.djennad.londonmet.ac.uk>
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

`gamlss`, `gamlssML`

Examples

```r
y <- rt(100, df=1)
mi<-fitDist(y, type="realline")
mi$fits
mi$failed
# an example of using extra
## Not run:
library(gamlss.tr)
data(tensile)
gen.trun(par=1,family="GA", type="right")
gen.trun(par=1,"LOGNO", type="right")
gen.trun(par=c(0,1),"TF", type="both")
ma<-fitDist(str, type="reallto1", extra=c("GAttr", "LOGNObtr", "TFtr"), data=tensile)
## End(Not run)
```

---

**fitted.gamlss**

Extract Fitted Values For A GAMLSS Model

Description

`fitted.gamlss` is the GAMLSS specific method for the generic function `fitted` which extracts fitted values for a specified parameter from a GAMLSS objects. `fitted.values` is an alias for it. The function `fv()` is similar to `fitted.gamlss()` but allows the argument `what` not to be character.

Usage

```r
## S3 method for class 'gamlss'
fitted(object, what = c("mu", "sigma", "nu", "tau"),
       parameter= NULL, ...)
fv(obj, what = c("mu", "sigma", "nu", "tau"), parameter= NULL, ... )
```
fitted.gamlss

Arguments

object   a GAMLSS fitted model
obj      a GAMLSS fitted model
what     which parameter fitted values are required, default what="mu"
parameter equivalent to what
...      for extra arguments

Value

Fitted values extracted from the GAMLSS object for the given parameter.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


(see also http://www.gamlss.org/).

See Also

print.gamlss, summary.gamlss, fitted.gamlss, coef.gamlss, residuals.gamlss, update.gamlss, plot.gamlss, deviance.gamlss, formula.gamlss

Examples

data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
fitted(h)
rm(h)
fittedPlot

Plots The Fitted Values of a GAMLSS Model

Description

This function, applicable only to a models with a single explanatory variable, plots the fitted values for all the parameters of a GAMLSS model against the (one) explanatory variable. It is also useful for comparing the fits for more than one model.

Usage

fittedPlot(object, ..., x = NULL, color = TRUE, line.type = FALSE, xlab = NULL)

Arguments

object a fitted GAMLSS model object(with only one explanatory variable)

... optionally more fitted GAMLSS model objects

x The unique explanatory variable

color whether the fitted lines plots are shown in colour, color=TRUE (the default) or not color=FALSE

line.type whether the line type should be different or not. The default is color=FALSE

xlab the x-label

Value

A plot of the fitted values against the explanatory variable

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@mikis.org>, Bob Rigby and Calliope Akantziliotou

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

gamlss, centiles, centiles.split
Examples

```r
data(abdom)
h1<-gamlss(y~pb(x), sigma.formula=-x, family=BCT, data=abdom)
h2<-gamlss(y~pb(x), sigma.formula=-pb(x), family=BCT, data=abdom)
fittedPlot(h1, h2, x=abdom$x)
rm(h1, h2)
```

**Description**

`formula.gamlss` is the GAMLSS specific method for the generic function `formula` which extracts the model formula from objects returned by modelling functions.

**Usage**

```r
## S3 method for class 'gamlss'
formula(x, what = c("mu", "sigma", "nu", "tau"),
        parameter = NULL, ...)
```

**Arguments**

- `x` a GAMLSS fitted model
- `what` which parameter coefficient is required, default `what="mu"`
- `parameter` equivalent to `what`
- `...` for extra arguments

**Value**

Returns a model formula

**Author(s)**

Mikis Stasinopoulos &lt;mikis.stasinopoulos@gamlss.org&gt;

**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).
See Also

`gamlss.deviance.gamlss, fitted.gamlss`

Examples

```r
data(aids)
h <- gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
formula(h, "mu")
rm(h)
```

Description

Returns an object of class "gamlss", which is a generalized additive model for location scale and shape (GAMLSS). The function `gamlss()` is very similar to the `gam()` function in S-plus (now also in R in package `gam`), but can fit more distributions (not only the ones belonging to the exponential family) and can model all the parameters of the distribution as functions of the explanatory variables (e.g. using linear, non-linear, smoothing, loess and random effects terms).

This implementation of `gamlss()` allows modelling of up to four parameters in a distribution family, which are conventionally called mu, sigma, nu and tau.

The function `gamlssNews()` shows what is new in the current implementation.

Usage

```r
gamlss(formula = formula(data), sigma.formula = ~1,
        nu.formula = ~1, tau.formula = ~1, family = NO(),
        data = sys.parent(), weights = NULL,
        contrasts = NULL, method = RS(), start.from = NULL,
        mu.start = NULL, sigma.start = NULL,
        nu.start = NULL, tau.start = NULL,
        mu.fix = FALSE, sigma.fix = FALSE, nu.fix = FALSE,
        tau.fix = FALSE, control = gamlss.control(...),
        i.control = glim.control(...), ...)
```

Arguments

- `formula` a formula object, with the response on the left of an ~ operator, and the terms, separated by + operators, on the right. Nonparametric smoothing terms are indicated by pb() for penalised beta splines, cs for smoothing splines, lo for loess smooth terms and random or ra for random terms, e.g. y~cs(x, df=5)+x1+x2+x3. Additional smoothers can be added by creating the appropriate interface. Interactions with nonparametric smooth terms are not fully supported, but will not produce errors; they will simply produce the usual parametric interaction
sigma.formula  a formula object for fitting a model to the sigma parameter, as in the formula above, e.g. `sigma.formula=~cs(x,df=5)`. It can be abbreviated to `sigma.formula~cs(x,df=5)`.

nu.formula  a formula object for fitting a model to the nu parameter, e.g. `nu.formula=x`

tau.formula  a formula object for fitting a model to the tau parameter, e.g. `tau.formula=~cs(x,df=2)`

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 `gamlss()` can be found in `gamlss.family`. Functions such as `BI()` (binomial) produce a family object. Also can be given without the parentheses i.e. `BI()`. Family functions can take arguments, as in `BI(mu.link=probit)`

data  a data frame containing the variables occurring in the formula. If this is missing, the variables should be on the search list. e.g. `data=aids`

weights  a vector of weights. Note that this is not the same as in the `glm()` or `gam()` function. Here weights can be used to weight out observations (like in `subset`) or for a weighted likelihood analysis where the contribution of the observations to the likelihood differs according to weights. The length of weights must be the same as the number of observations in the data. By default, the weight is set to one. To set weights to vector w use `weights=w`

contrasts  list of contrasts to be used for some or all of the factors appearing as variables in the model formula. The names of the list should be the names of the corresponding variables. The elements should either be contrast-type matrices (matrices with as many rows as levels of the factor and with columns linearly independent of each other and of a column of ones), or else they should be functions that compute such contrast matrices.

method  the current algorithms for GAMLSS are RS(), CG() and mixed(). i.e. `method=RS()` will use the Rigby and Stasinopoulos algorithm, `method=CG()` will use the Cole and Green algorithm and `mixed(2,10)` will use the RS algorithm twice before switching to the Cole and Green algorithm for up to 10 extra iterations

start.from  a fitted GAMLSS model which the fitted values will be used as staring values for the current model

mu.start  vector or scalar of initial values for the location parameter mu e.g. `mu.start=4`

sigma.start  vector or scalar of initial values for the scale parameter sigma e.g. `sigma.start=1`

nu.start  vector or scalar of initial values for the parameter nu e.g. `nu.start=3`

tau.start  vector or scalar of initial values for the location parameter tau e.g. `tau.start=2`

mu.fix  whether the mu parameter should be kept fixed in the fitting processes e.g. `mu.fix=FALSE`

sigma.fix  whether the sigma parameter should be kept fixed in the fitting processes e.g. `sigma.fix=FALSE`

nu.fix  whether the nu parameter should be kept fixed in the fitting processes e.g. `nu.fix=FALSE`

tau.fix  whether the tau parameter should be kept fixed in the fitting processes e.g. `tau.fix=FALSE`

control  this sets the control parameters of the outer iterations algorithm. The default setting is the `gamlss.control` function

i.control  this sets the control parameters of the inner iterations of the RS algorithm. The default setting is the `glim.control` function
... for extra arguments
x an object

Details

The Generalized Additive Model for Location, Scale and Shape is a general class of statistical models for a univariate response variable. The model assumes independent observations of the response variable y given the parameters, the explanatory variables and the values of the random effects. The distribution for the response variable in the GAMLSS can be selected from a very general family of distributions including highly skew and/or kurtotic continuous and discrete distributions, see \texttt{gamlss.family}. The systematic part of the model is expanded to allow modelling not only of the mean (or location) parameter, but also of the other parameters of the distribution of y, as linear parametric and/or additive nonparametric (smooth) functions of explanatory variables and/or random effects terms. Maximum (penalized) likelihood estimation is used to fit the (non)parametric models. A Newton-Raphson/Fisher scoring algorithm is used to maximize the (penalized) likelihood. The additive terms in the model are fitted using a backfitting algorithm.

\texttt{is.gamlss} is a short version is \texttt{is(object,"gamlss")}

Value

Returns a \texttt{gamlss} object with components

- \texttt{family} the distribution family of the \texttt{gamlss} object (see \texttt{gamlss.family})
- \texttt{parameters} the name of the fitted parameters i.e. \texttt{mu, sigma, nu, tau}
- \texttt{call} the call of the \texttt{gamlss} function
- \texttt{y} the response variable
- \texttt{control} the \texttt{gamlss} fit control settings
- \texttt{weights} the vector of weights
- \texttt{G.deviance} the global deviance
- \texttt{N} the number of observations in the fit
- \texttt{rqres} a function to calculate the normalized (randomized) quantile residuals of the object
- \texttt{iter} the number of external iterations in the fitting process
- \texttt{type} the type of the distribution or the response variable (continuous or discrete)
- \texttt{method} which algorithm is used for the fit, \texttt{RS()}, \texttt{CG()} or \texttt{mixed()}
- \texttt{converged} whether the model fitting has have converged
- \texttt{residuals} the normalized (randomized) quantile residuals of the model
- \texttt{mu.fv} the fitted values of the \texttt{mu} model, also \texttt{sigma.fv, nu.fv, tau.fv} for the other parameters if present
- \texttt{mu.lp} the linear predictor of the \texttt{mu} model, also \texttt{sigma.lp, nu.lp, tau.lp} for the other parameters if present
- \texttt{mu.wv} the working variable of the \texttt{mu} model, also \texttt{sigma.wv, nu.wv, tau.wv} for the other parameters if present
mu.wt  the working weights of the mu model, also sigma.wt, nu.wt, tau.wt for the other
parameters if present
mu.link the link function for the mu model, also sigma.link, nu.link, tau.link for the other
parameters if present
mu.terms the terms for the mu model, also sigma.terms, nu.terms, tau.terms for the other
parameters if present
mu.x  the design matrix for the mu, also sigma.x, nu.x, tau.x for the other parameters
if present
mu.qr  the QR decomposition of the mu model, also sigma.qr, nu.qr, tau.qr for the other
parameters if present
mu.coefficients the linear coefficients of the mu model, also sigma.coefficients, nu.coefficients,
tau.coefficients for the other parameters if present
mu.formula the formula for the mu model, also sigma.formula, nu.formula, tau.formula for
the other parameters if present
mu.df the mu degrees of freedom also sigma.df, nu.df, tau.df for the other parameters
if present
mu.nl.df the non linear degrees of freedom, also sigma.nl.df, nu.nl.df, tau.nl.df for the
other parameters if present
df.fit the total degrees of freedom use by the model
df.residual the residual degrees of freedom left after the model is fitted
aic  the Akaike information criterion
sbc  the Bayesian information criterion

Warning

Respect the parameter hierarchy when you are fitting a model. For example a good model for mu
should be fitted before a model for sigma is fitted

Note

The following generic functions can be used with a GAMLSS object: print, summary, fitted,
coef, residuals, update, plot, deviance, formula

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby, Calliope Akantziliotou
and Vlasios Voudouris <vlasios.voudouris@abm-analytics.com>.

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and
(see also http://www.gamlss.org/).

See Also
gamlss.family, pdf, plot, find.hyper

Examples

data(abdom)
mod<-gamlss(y~pb(x),sigma.fo~pb(x),family=BCT, data=abdom, method=mixed(1,20))
plot(mod)
rm(mod)

---

**gamlss.control**  
*Auxiliary for Controlling GAMLSS Fitting*

**Description**
Auxiliary function as user interface for `gamlss` fitting. Typically only used when calling `gamlss` function with the option control.

**Usage**
gamlss.control(c.crit = 0.001, n.cyc = 20, mu.step = 1, sigma.step = 1, nu.step = 1, tau.step = 1, gd.tol = Inf, iter = 0, trace = TRUE, autostep = TRUE, save = TRUE, ...)

**Arguments**
c.crit  the convergence criterion for the algorithm
n.cyc  the number of cycles of the algorithm
mu.step  the step length for the parameter mu
sigma.step  the step length for the parameter sigma
nu.step  the step length for the parameter nu
tau.step  the step length for the parameter tau
gd.tol  global deviance tolerance level (set more recently to Inf to allow the algorithm to converged even if the global deviance change dramatically during the iterations)
iter  starting value for the number of iterations, typically set to 0 unless the function refit is used
trace  whether to print at each iteration (TRUE) or not (FALSE)
gamlss.control

autostep  whether the steps should be halved automatically if the new global deviance is greater than the old one, the default is autostep=TRUE
save    save=TRUE, (the default), saves all the information on exit. save=FALSE saves only limited information as the global deviance and AIC. For example fitted values, design matrices and additive terms are not saved. The latest is useful when gamlss() is called several times within a procedure.

... for extra arguments

Details

The step length for each of the parameters mu, sigma, nu or tau is very useful to aid convergence if the parameter has a fully parametric model. However using a step length is not theoretically justified if the model for the parameter includes one or more smoothing terms, (even thought it may give a very approximate result).

The crit can be increased to speed up the convergence especially for a large set of data which takes longer to fit. When ‘trace’ is TRUE, calls to the function cat produce the output for each outer iteration.

Value

A list with the arguments as components.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

References


(see also http://www.gamlss.org/).

See Also

gamlss

Examples

data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
con<-gamlss.control(mu.step=0.1)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids, control=con) #
rm(h,con)
Support for Function cs() and scs()

Description

This is support for the functions cs(), and scs(). It is not intended to be called directly by users. The function gamlss.cs is using the R function smooth.spline

Usage

gamlss.cs(x, y, w, df = NULL, spar = NULL, xeval = NULL, ...)

Arguments

x the design matrix
y the response variable
w prior weights
df effective degrees of freedom
spar spar the smoothing parameter
xeval used in prediction
... for extra arguments

Value

Returns a class "smooth.spline" object with

residuals The residuals of the fit
fitted.values The smoothing values
var the variance for the fitted smoother
lambda the final value for spar
nl.df the smoothing degrees of freedom excluding the constant and linear terms, i.e. (df-2)
coefsmo this is a list containing among others the knots and the coefficients

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

See Also

gamlss.cs
Support for Function `fp()`

**Description**

Those are support for the functions `fp()` and `pp`. It is not intended to be called directly by users.

**Usage**

```r

gamlss.fp(x, y, w, npoly = 2, xeval = NULL)
gamlss.pp(x, y, w)
```

**Arguments**

- **x**: the `x` for function `gamlss.fp` is referred to the design matrix of the specific parameter model (not to be used by the user)
- **y**: the `y` for function `gamlss.fp` is referred to the working variable of the specific parameter model (not to be used by the user)
- **w**: the `w` for function `gamlss.fp` is referred to the iterative weight variable of the specific parameter model (not to be used by the user)
- **npoly**: a positive indicating how many fractional polynomials should be considered in the fit. Can take the values 1, 2 or 3 with 2 as default
- **xeval**: used in prediction

**Value**

Returns a list with

- `fitted.values`: fitted
- `residuals`: residuals
- `var`: the trace of the smoothing matrix
- `lambda`: the value of the smoothing parameter
- `coefSmo`: the coefficients from the smoothing fit
- `varcoeff`: the variance of the coefficients

**Author(s)**

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby
References


(see also http://www.gamlss.org/).

See Also
gamlss, fp

gamlss.lo  Support for Function lo()

Description
This is support for the loess function lo(). It is not intended to be called directly by users. The function gamlss.lo is calling the R function loess.

Usage
gamlss.lo(x, y, w, xeval = NULL, ...)

Arguments
x the design matrix
y the response variable
w prior weights
xeval used in prediction
... further arguments passed to or from other methods.

Value
Returns an object
fitted the smooth values
residuals the residuals
var the variance of the smoother
nl.df the non-linear degrees of freedom
coefs the value of lambda
...
Author(s)
Mikis Stasinopoulos based on Brian Ripley implementation of loess function in R

See Also
gamlss, lo

Description
Those functions are support for the functions pb(), pbo(), ps(), ridge(), ri(), cy(), pvc(), and pbm(). The functions are not intended to be called directly by users.

Usage

gamlss.pb(x, y, w, xeval = NULL, ...)
gamlss.pbo(x, y, w, xeval = NULL, ...)
gamlss.ps(x, y, w, xeval = NULL, ...)
gamlss.ri(x, y, w, xeval = NULL, ...)
gamlss.cy(x, y, w, xeval = NULL, ...)
gamlss.pvc(x, y, w, xeval = NULL, ...)
gamlss.pbm(x, y, w, xeval = NULL, ...)
gamlss.pbz(x, y, w, xeval = NULL, ...)
gamlss.pbc(x, y, w, xeval = NULL, ...)
gamlss.pbp(x, y, w, xeval = NULL, ...)

Arguments

x the x for function gamlss.fp is referred to the design matric of the specific parameter model (not to be used by the user)
y the y for function gamlss.fp is referred to the working variable of the specific parameter model (not to be used by the user)
w the w for function gamlss.fp is referred to the iterative weight variable of the specific parameter model (not to be used by the user)
xeval used in prediction
... further arguments passed to or from other methods.

Value
All function return fitted smoothers.

Author(s)
Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

gamlss, pb, ps, ri, ridge, cy, pvc, pbm

gamlss.random

Support for Functions random() and re()

Description

This is support for the functions random() and re() respectively. It is not intended to be called directly by users.

Usage

```r
gamlss.random(x, y, w)
gamlss.re(x, y, w, xeval = NULL, ...)
```

Arguments

- **x**: the explanatory design matrix
- **y**: the response variable
- **w**: iterative weights
- **xeval**: it used internally for prediction
- **...**: for extra arguments

Value

Returns a list with

- **y**: the fitted values
- **residuals**: the residuals
- **var**: the variance of the fitted values
- **lambda**: the final lambda, the smoothing parameter
- **coefSmo**: with value NULL
Author(s)

Mikis Stasinopoulos, based on Trevor Hastie function gam.random

References


(see also http://www.gamlss.org/).

See Also

gamlss, random

gamlss.scope

Generate a Scope Argument for Stepwise GAMLSS

Description

Generates a scope argument for a stepwise GAMLSS.

Usage

gamlss.scope(frame, response = 1, smoother = "cs", arg = NULL, form = TRUE)

Arguments

frame a data or model frame
response which variable is the response; the default is the first
smoother what smoother to use; default is cs
arg any additional arguments required by the smoother
form should a formula be returned (default), or else a character version of the formula

Details

Each formula describes an ordered regimen of terms, each of which is eligible on their own for inclusion in the gam model. One of the terms is selected from each formula by step.gam. If a 1 is selected, that term is omitted.
### Value

A list of formulas is returned, one for each column in frame (excluding the response). For a numeric variable, say $x_1$, the formula is

$$
\sim 1 + x_1 + cs(x_1)
$$

If $x_1$ is a factor, the last smooth term is omitted.

### Author(s)

Mikis Stasinopoulos: a modified function from Statistical Models in S

### References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

### See Also

*stepGAIC*

### Examples

```r
data(usa1r)
gs1 <- gamlss.scope(model.frame(y=x1+x2+x3+x4+x5+x6, data=usa1r))
gs2 <- gamlss.scope(model.frame(usa1r))
gs1
gs2
gs3 <- gamlss.scope(model.frame(usa1r), smooth="fp", arg="3")
gs3
```

---

**gamlssML**  
*Maximum Likelihood estimation of a simple GAMLSS model*

### Description

This is a function for fitting a *gamlss.family* distribution to single data set using a non linear maximisation algorithm in R. This is relevant only when there are not explanatory variables.
Usage

`gamlssML(formula, family = NO, weights = NULL, mu.start = NULL, sigma.start = NULL, nu.start = NULL, tau.start = NULL, mu.fix = FALSE, sigma.fix = FALSE, nu.fix = FALSE, tau.fix = FALSE, data = sys.parent(), start.from = NULL, ...)`

Arguments

- **formula**: a vector of data requiring the fit of a `gamlss.family` distribution or a formula, for example, y ~ 1 (explanatory variables are ignored).
- **family**: `gamlss.family` object, which is used to define the distribution and the link functions of the various parameters. The distribution families supported by `gamlssML()` can be found in `gamlss.family`.
- **weights**: a vector of weights. Here weights can be used to weight out observations (like in `subset`) or for a weighted likelihood analysis where the contribution of the observations to the likelihood differs according to weights. The length of weights must be the same as the number of observations in the data. By default, the weight is set to one. To set weights to vector w use `weights = w`.
- **mu.start**: a scalar of initial values for the location parameter mu e.g. `mu.start = 4`.
- **sigma.start**: a scalar of initial values for the scale parameter sigma e.g. `sigma.start = 1`.
- **nu.start**: a scalar of initial values for the parameter nu e.g. `nu.start = 3`.
- **tau.start**: a scalar of initial values for the parameter tau e.g. `tau.start = 3`.
- **mu.fix**: whether the mu parameter should be kept fixed in the fitting processes e.g. `mu.fix = FALSE`.
- **sigma.fix**: whether the sigma parameter should be kept fixed in the fitting processes e.g. `sigma.fix = FALSE`.
- **nu.fix**: whether the nu parameter should be kept fixed in the fitting processes e.g. `nu.fix = FALSE`.
- **tau.fix**: whether the tau parameter should be kept fixed in the fitting processes e.g. `tau.fix = FALSE`.
- **data**: a data frame containing the variable y. If this is missing, the variable should be on the search list e.g. `data = aids`.
- **start.from**: a `gamlss` object to start from the fitting or vector of length as many parameters in the distribution.
- **...**: for extra arguments.

Details

This function which fits a `gamlss.family` distribution to a single data set is using a non linear maximisation. In fact it uses the internal function `mle()`, which is a copy of the `mle()` function of package `stat4`. The function `gamlssML()` could be for large data faster than the equivalent `gamlss()` function which is designed for regression type of models.

Value

Returns a `gamlssML` object which behaves like a `gamlss` fitted object.
Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby, Vlasis Voudouris and Majid Djennad

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

`gamlss.family`, `gamlss`

Examples

```r
#-------- negative binomial 1000 observations
y <- rNBI(1000)
  system.time(m1 <- gamlss(y ~ 1, family = NBI))
  system.time(mla <- gamlss(y ~ 1, family = NBI, trace = FALSE))
  system.time(mll <- gamlssML(y, family = NBI))
  AIC(m1, mla, mll, k = 0)
  # neg. binomial n=10000
y <- rNBI(10000)
  system.time(m1 <- gamlss(y ~ 1, family = NBI))
  system.time(mla <- gamlss(y ~ 1, family = NBI, trace = FALSE))
  system.time(mll <- gamlssML(y, family = NBI))
  AIC(m1, mla, mll, k = 0)
  # binomial type data
data(aep)
m1 <- gamlssML(aep$y, family = BB) # ok
m2 <- gamlssML(y, data = aep, family = BB) # ok
m3 <- gamlssML(y ~ 1, data = aep, family = BB) # ok
m4 <- gamlssML(aep$y ~ 1, family = BB) # ok
AIC(m1, m2, m3, m4)
```
Description

This is a set of functions useful for selecting appropriate models.

The functions `gamlssVGD`, `VGD`, `getTGD`, `TGD` can be used when a subset of the data is used for validation or testing.

The function `stepVGD()` is a stepwise procedure for selecting an appropriate model for any of the parameters of the model minimising the test global deviance. The function `stepVGDallA()` can select a model using strategy A for all the parameters.

The functions `gamlssCV`, `CV` can be used for a k-fold cross validation.

Usage

```r
# gamlssVGD
formula = NULL, sigma.formula = ~1, nu.formula = ~1,
  tau.formula = ~1, data = NULL, family = NO,
  control = gamlss.control(trace = FALSE),
  rand = NULL, newdata = NULL, ...)

gamlssVGD(formula = NULL, sigma.formula = ~1, nu.formula = ~1,
  tau.formula = ~1, data = NULL, family = NO,
  control = gamlss.control(trace = FALSE),
  rand = NULL, newdata = NULL, ...)

gamlssVGD(formula = NULL, sigma.formula = ~1, nu.formula = ~1,
  tau.formula = ~1, data = NULL, family = NO,
  control = gamlss.control(trace = FALSE),
  rand = NULL, newdata = NULL, ...)

# VGD(object, ...)                 # getTGD(object, newdata = NULL, ...)

# TGD(object, ...)                 # gamlssCV(formula = NULL, sigma.formula = ~1, nu.formula = ~1,
#          tau.formula = ~1, data = NULL, family = NO,
#          control = gamlss.control(trace = FALSE),
#          K.fold = 10, set.seed = 123, rand = NULL,
#          parallel = c("no", "multicore", "snow"),
#          ncpus = 1L, cl = NULL, ...)          # CV(object, ...)

# dropTGD(object, scope, newdata, parameter = c("mu", "sigma", "nu", "tau"),
#          sorted = FALSE, trace = FALSE,
#          parallel = c("no", "multicore", "snow"),
#          ncpus = 1L, cl = NULL, ...)          # addTGD(object, scope, newdata, parameter = c("mu", "sigma", "nu", "tau"),
#        sorted = FALSE, trace = FALSE,
#        parallel = c("no", "multicore", "snow"),
#        ncpus = 1L, cl = NULL, ...)          # stepTGD(object, scope, newdata,
#        direction = c("both", "backward", "forward"),
#        trace = TRUE, keep = NULL, steps = 1000,
#        parameter = c("mu", "sigma", "nu", "tau"),
#        parallel = c("no", "multicore", "snow"),
#        ncpus = 1L, cl = NULL, ...)          # stepTGD(object, scope, newdata,
```
Argument

formula A \text{gamlss mu} formula.
sigma.formula Formula for \sigma.
nu.formula Formula for \nu.
tau.formula Formula for \tau.
data The data frame required for the fit.
family The \text{gamlss.family} distribution.
control The control for fitting the \text{gamlss} model.
rand For \text{gamlssVGD} a variable with values 1 (for fitting) and 2 (for predicting). For \text{gamlssCV} a variable with k values indicating the cross validation sets.
newdata The new data set (validation or test) for prediction.
object A relevant R object.
scope defines the range of models examined in the stepwise selection similar to \text{stepGAIC}.
sigma.scope defines the range of models examined in the stepwise selection for \sigma
nu.scope defines the range of models examined in the stepwise selection for \nu
tau.scope defines the range of models examined in the stepwise selection for \tau
mu.try whether should try fitting models for \mu
sigma.try whether should try fitting models for \sigma
nu.try whether should try fitting models for \nu
tau.try whether should try fitting models for \tau
parameter which distribution parameter is required, default what=\text{\mu}
sorted should the results be sorted on the value of TGD
trace if \text{TRUE} additional information may be given on the fits as they are tried.
direction The mode of stepwise search, can be one of both, backward, or forward, with a default of both. If the scope argument is missing the default for direction is backward
keep see \text{stepGAIC} for explanation
steps the maximum number of steps to be considered. The default is 1000.
K.fold the number of subsets of the data used
set.seed the seed to be used in creating \text{rand}
parallel
ncpus
cl
...


See Also

stepGAIC

Examples

data(abdom)
# generate the random split of the data
rand <- sample(2, 610, replace=TRUE, prob=c(0.6,0.4))
# the proportions in the sample
table(rand)/610
olddata<abdom[rand==1,] # training data
newdata<abdom[rand==2,] # validation data

# gamlssVGD
#---------------------------------------------------------------
# Using rand
v1 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=abdom, family=NO, rand=rand)
v2 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=abdom, family=LO, rand=rand)
v3 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=abdom, family=TF, rand=rand)

VGD(v1,v2,v3)
#---------------------------------------------------------------
## Not run:
#---------------------------------------------------------------
# using two data set
v11 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=NO, newdata=newdata)
v12 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=LO, newdata=newdata)
v13 <- gamlssVGD(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=TF, newdata=newdata)

VGD(v11,v12,v13)
#---------------------------------------------------------------
# function getTGD
#---------------------------------------------------------------
# fit gamlss models first
g1 <- gamlss(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=NO)
g2 <- gamlss(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=LO)
g3 <- gamlss(y~pb(x,df=2), sigma.formula=-pb(x,df=1), data=olddata, family=TF)
# and then use
g11 <-getTGD(g1, newdata=newdata)
g22 <-getTGD(g2, newdata=newdata)
g33 <-getTGD(g3, newdata=newdata)
TGDr(gg1, gg2, gg3)
#---------------------------------------------------------------
# function gamlssCV
#---------------------------------------------------------------
set.seed(123)
rand1 <- sample(10, 610, replace=TRUE)
g1 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, family=NO, 
rand=rand1)
g2 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, family=LO, 
rand=rand1)
g3 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, family=TF, 
rand=rand1)
CV(g1,g2,g3)
CV(g1)
# using parallel
set.seed(123)
rand1 <- sample(10, 610, replace=TRUE)
nc <- detectCores()

system.time(g21 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, 
family=NO, rand=rand1, parallel = "no", ncpus = nc ))

system.time(g22 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, 
family=LO, rand=rand1, parallel = "multicore", ncpus = nc ))

system.time(g23 <- gamlssCV(y~pb(x, df=2), sigma.formula=-pb(x, df=1), data=abdom, 
family=TF, rand=rand1, parallel = "snow", ncpus = nc ))

CV(g21,g22,g23)
#---------------------------------------------------------------
# functions add1TGDr() drop1TGDr() and stepTGDr()
#---------------------------------------------------------------
# the data
data(rent)
rand <- sample(2, dim(rent)[1], replace=TRUE, prob=c(0.6, 0.4))
# the proportions in the sample
table(rand)/dim(rent)[1]
oldrent<-rent[rand==1,] # training set
newrent<-rent[rand==2,] # validation set

# null model
v0 <- gamlss(R-1, data=oldrent, family=GA)
# complete model
v1 <- gamlss(R~pb(Fl)+pb(A)+H+loc, sigma.f0=-pb(Fl)+pb(A)+H+loc, 
data=oldrent, family=GA)

# drop1TGDr
system.time(v3<- drop1TGDr(v1, newdata=newrent, parallel="no"))
system.time(v4<- drop1TGDr(v1, newdata=newrent, parallel="multicore", 
ncpus=nC ) )
system.time(v5<- drop1TGDr(v1, newdata=newrent, parallel="snow", ncpus=nC))
cbind(v3,v4,v5)
# addTGD
system.time(d3<- addTGD(v0,scope=-pb(F1)+pb(A)+H+loc, newdata=newrent, parallel="no"))
system.time(d4<- addTGD(v0,scope=-pb(F1)+pb(A)+H+loc, newdata=newrent, parallel="multicore", ncpus=nC))
system.time(d5<- addTGD(v0,scope=-pb(F1)+pb(A)+H+loc, newdata=newrent, parallel="snow", ncpus=nC))

# stepTGD
system.time(d6<- stepTGD(v0, scope=-pb(F1)+pb(A)+H+loc,newdata=newrent))
system.time(d7<- stepTGD(v0, scope=-pb(F1)+pb(A)+H+loc,newdata=newrent, parallel="multicore", ncpus=nC))
system.time(d8<- stepTGD(v0, scope=-pb(F1)+pb(A)+H+loc,newdata=newrent, parallel="snow", ncpus=nC))

## End(Not run)

general.likelihood

A function to generate the likelihood function from a GAMLLSS object

Description

This function generates a function with argument the parameters of the GAMLLSS model which can evaluate the log-likelihood function.

Usage

gen.likelihood(object)

Arguments

object A gamlls fitted model

Details

The purpose of this function is to help the function vcov() to get the right Hessian matrix after a model has fitted. Note that at the moment smoothing terms are considered as fixed.

Value

A function of the log-likelihood

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> Bob Rigby and Vlasios Voudouris
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

`vcov`

Examples

```r
data(aids)
m1 <- gamlss(y~x+qrt, data=aids, family=NBI)
logl<-gen.likelihood(m1)
logL()
logLik(m1)
```

```r
getPEF               Getting the partial effect function from a continuous term in a GAMLSS model
```

Description

This function can be used to calculate the partial effect and the elasticity of a continuous explanatory variable `x`.

By 'partial effect' function we mean how `x` is influence the parameter of interest given that the rest of explanatory terms for this parameter are on (specified) fixed values.

The function takes a GAMLSS object and for the range of the continuous variable `x`, (by fixing the rest of the explanatory terms at specified values), calculates the effect that `x` has on the specific distribution parameter (or its predictor). The resulting function shows the effect that `x` has on the distribution parameter. The partial effect function which is calculated on a finite grid is then approximated using the `splinefun()` in R and its is saved.

The saved function can be used to calculate the elasticity of `x`. The elasticity is the first derivative of the partial effect function and shows the chance of the parameter of interest for a small change in `x`, by fixing the rest of the explanatory variables at specified values.

Usage

```r
getPEF(obj = NULL, term = NULL, data = NULL, n.points = 100, parameter = c("mu", "sigma", "nu", "tau"), type = c("response", "link"), how = c("median", "last"), fixed.at = list(), plot = FALSE)
```
**getPEF**

**Arguments**

- `obj` A `gamlss` object
- `term` the continuous explanatory variable
- `data` the data.frame (not needed if is declared on `obj`)
- `n.points` the number of points in which the influence function for `x` need to be evaluated
- `parameter` which distribution parameter
- `type` whether against the parameter, "response", or the predictor "link"
- `how` whether for continuous variables should use the median or the last observation in the data
- `fixed.at` a list indicating at which values the rest of the explanatory terms should be fixed
- `plot` whether to the plot the influence function and its first derivatives

**Value**

A function is created which can be used to evaluate the partial effect function at different values of `x`.

**Author(s)**

Mikis Stasinopoulos, Vlasios Voudouris, Daniil Kiose

**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

**See Also**

- `gamlss`

**Examples**

```r
m1 <- gamlss(R~pb(Fl)+pb(A), data=rent, family=GA) # getting the Partial Efect function
pef <- getPEF(obj=m1,term="A", plot=TRUE) # the value at 1980
pef(1980) # the first derivative at 1980
```
Description

The function `getsmo()` extracts information from a fitted smoothing additive term.

Usage

```
getsmo(object, what = c("mu", "sigma", "nu", "tau"),
       parameter= NULL, which = 1)
```

Arguments

- **object**: a GAMLSS fitted model
- **what**: which distribution parameter is required, default what="mu"
- **parameter**: equivalent to what
- **which**: which smoothing term i.e. 1, 2 etc. Note that 0 means all.

Details

This function facilitates the extraction of information from a fitted additive terms. For example `getsmo(m1, "sigma", 2)` is equivalent of `m1$coefSmo[[2]]`. To get the actual fitted values type `m1$sigma.s[[2]]`

Value

A list containing information about a fitted smoother or a fitted objects

Author(s)

Mikis Stasinopoulos and Bob Rigby

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).
glim.control

Examples

data(usair)
t1 <- gamlss(y ~ x1 + pb(x5) + pb(x6), data = usair, family = GA)
# get the value for lambda for the second fitted term in mu
getSmo(t1, parameter = "mu", 2)$lambda

---

glim.control

Auxiliary for Controlling the inner algorithm in a GAMLSS Fitting

Description

Auxiliary function used for the inner iteration of gamlss algorithm. Typically only used when calling gamlss function through the option i.control.

Usage

glim.control(cc = 0.001, cyc = 50, glm.trace = FALSE,
bf.cyc = 30, bf.tol = 0.001, bf.trace = FALSE,
...)

Arguments

cc the convergence criterion for the algorithm
cyc the number of cycles of the algorithm
glm.trace whether to print at each iteration (TRUE) or not (FALSE)
bf.cyc the number of cycles of the backfitting algorithm
bf.tol the convergence criterion (tolerance level) for the backfitting algorithm
bf.trace whether to print at each iteration (TRUE) or not (FALSE, the default)
... for extra arguments

Value

A list with the arguments as components

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby
References


(see also http://www.gamlss.org/).

See Also

gamlss

Examples

data(aids)
con<-glim.control(glm.trace=TRUE)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids, i.control=con) #
rm(h,con)

histDist

This function plots the histogram and a fitted (GAMLSS family) distribution to a variable

Description

This function fits constants to the parameters of a GAMLSS family distribution and them plot the histogram and the fitted distribution.

Usage

histDist(y, family = NO, freq = NULL,
       density = FALSE, nbins = 10, xlim = NULL,
       ylim = NULL, main = NULL, xlab = NULL,
       ylab = NULL, data = NULL, line.wd = 2,line.ty = 1,
       line.col = "red",...)

Arguments

y a vector for the response variable
family a gamlss.family distribution
freq the frequencies of the data in y if exist. freq is used as weights in the gamlss fit
density  default value is FALSE. Change to TRUE if you would like a non-parametric density plot together with the parametric fitted distribution plot (for continuous variable only)

nbins  The suggested number of bins (argument passed to `truehist()` of package MASS). Either a positive integer, or a character string naming a rule: "Scott" or "Freedman-Diaconis" or "FD". (Case is ignored.)

xlim  the minimum and the maximum x-axis value (if the default values are out of range)

ylim  the minimum and the maximum y-axis value (if the default values are out of range)

main  the main title for the plot

xlab  the label in the x-axis

ylab  the label in the y-axis

data  the data.frame

line.wd  the line width of the fitted distribution

line.ty  the line type of the fitted distribution

line.col  the line color of the fitted distribution

...  for extra arguments to be passed to the `gamlss` function

Details

This function first fits constants for each parameters of a GAMLSS distribution family using the `gamlss` function and them plots the fitted distribution together with the appropriate plot according to whether the y variable is of a continuous or discrete type. Histogram is plotted for continuous and barplot for discrete variables. The function `truehist` of Venables and Ripley’s MASS package is used for the histogram plotting.

Value

returns a plot

Author(s)

Mikis Stasinopoulos

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).
See Also

`gamlss`, `gamlss.family`

Examples

```r
data(abdom)
histDist(y,family="NO", data=abdom)  # use the ylim
histDist(y,family="NO", ylim=c(0,0.005), data=abdom)  # bad fit use PE
histDist(y,family="PE",ymax=0.005, data=abdom, line.col="blue")  # discrete data counts
# Hand at al. p150  Leptinotarsa decemlineata
y <- c(0,1,2,3,4,6,7,8,10,11)
freq <- c(33,12,5,6,5,2,2,2,1,2)
histDist(y, "NBI", freq=freq)  # the same as
histDist(rep(y,freq), "NBI")
```

---

**histSmo**

*Density estimation using the Poisson trick*

Description

This set of functions use the old Poisson trick of discretising the data and then fitting a Poisson error model to the resulting frequencies (Lindsey, 1997). Here the model fitted is a smooth cubic spline curve. The result is a density estimator for the data.

Usage

```r
histSmo(y, lambda = NULL, df = NULL, order = 3, lower = NULL,
upper = NULL, type = c("freq", "prob"),
plot = FALSE, breaks = NULL,
discrete = FALSE, ...)
histSmoC(y, df = 10, lower = NULL, upper = NULL, type = c("freq", "prob"),
plot = FALSE, breaks = NULL,
discrete = FALSE, ...)
histSmoO(y, lambda = 1, order = 3, lower = NULL, upper = NULL,
type = c("freq", "prob"),
plot = FALSE, breaks = NULL,
discrete = FALSE, ...)
histSmoP(y, lambda = NULL, df = NULL, order = 3, lower = NULL,
upper = NULL, type = c("freq", "prob"),
plot = FALSE, breaks = NULL, discrete = FALSE,
...)
```
Arguments

- **y** the variable of interest
- **lambda** the smoothing parameter
- **df** the degrees of freedom
- **order** the order of the P-spline
- **lower** the lower limit of the y-variable
- **upper** the upper limit of the y-variable
- **type** the type of histogram
- **plot** whether to plot the resulting density estimator
- **breaks** the number of break points to be used in the histogram and consequently the number of observations in the Poisson fit
- **discrete** whether to treat the fitting density as a discrete distribution or not
- ... further arguments passed to or from other methods.

Details

Here are the methods used here:

i) The function `histSmoO()` uses Penalised discrete splines (Eilers, 2003). This function is appropriate when the smoothing parameter is fixed.

ii) The function `histSmoC()` uses smooth cubic splines and fits a Poison error model to the frequencies using the cs() additive function of GAMLSS. This function is appropriate if the effective degrees of freedom are fixed in the model.

iii) The function `histSmoP()` uses Penalised cubic splines (Eilers and Marx 1996). It is fitting a Poisson model to the frequencies using the pb() additive function of GAMLSS. This function is appropriate if automatic selection of the smoothing parameter is required.

iv) The function `histSmo()` combines all the above functions in the sense that if lambda is fixed it uses `histSmoO()`, if the df’s are fixed it uses codehistSmoC() and if none of these is specified it uses `histSmoP()`.

Value

Returns a histSmo S3 object. The object has the following components:

- **x** the middle points of the discretise data
- **counts** how many observation are on the discretise intervals
- **density** the density value for each discrete interval
- **hist** the hist object used to discretise the data
- **cdf** The resulting cumulative distribution function useful for calculating probabilities from the estimate density
- **nvCDF** The inverse cumulative distribution function
- **model** The fitted Poisson model only for histSmoP() and histSmoC()
Author(s)

Mikis Stasinopoulos, Paul Eilers, Bob Rigby and Vlasios Voudouris

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

`pb`, `cs`

Examples

```r
# creating data from Pareto 2 distribution
set.seed(153)
Y <- rPARETO2(1000)
## Not run:
# getting the density
histSmo(Y, lower=0, plot=TRUE)
# more breaks a bit slower
histSmo(Y, breaks=200, lower=0, plot=TRUE)
# quick fit using lambda
histSmo(Y, lambda=1, breaks=200, lower=0, plot=TRUE)
# or
histSmo(Y, lambda=1, breaks=200, lower=0, plot=TRUE)
# quick fit using df
histSmo(Y, df=15, breaks=200, lower=0, plot=TRUE)
# or
histSmo(Y, df=15, breaks=200, lower=0)
# saving results
m1<- histSmo(Y, lower=0, plot=T)
plot(m1)
plot(m1, "cdf")
plot(m1, "invcdf")
# using with a histogram
library(MASS)
truehist(Y)
```
lines(m1, col="red")
#-----------------------------
# now generate from SHASH distribution
YY <- rSHASH(1000)
ml<- histSmo(YY)
# calculate Pr(YY>10)
1-ml$cdf(10)
# calculate Pr(-10<YY<10)
1-(1-ml$cdf(10))-ml$cdf(-10)
#-----------------------------
# from discrete distribution
YYY <- rNBI(1000, mu=5, sigma=4)
histSmo(YYY, discrete=TRUE, plot=T)
# YYY <- rPO(1000, mu=5)
histSmo(YYY, discrete=TRUE, plot=T)
# YYY <- rNBI(1000, mu=5, sigma=.1)
histSmo(YYY, discrete=TRUE, plot=T)
# generating from beta distribution
YYY <- rBE(1000, mu=.1, sigma=.3)
histSmo(YYY, lower=0, upper=1, plot=T)
# from truncated data
Y <- with(stylo, rep(word,freq))
histSmo(Y, lower=1, discrete=TRUE, plot=T)
histSmo(Y, lower=1, discrete=TRUE, plot=T, type="prob")
## End(Not run)

IC

_Gives the GAIC for a GAMLSS Object_

**Description**

IC is a function to calculate the Generalised Akaike information criterion (GAIC) for a given penalty $k$ for a fitted GAMLSS object. The function AIC.gamlss is the method associated with a GAMLSS object of the generic function AIC. The function GAIC is a synonymous of the function AIC.gamlss. The function extractAIC is a the method associated a GAMLSS object of the generic function extractAIC and it is mainly used in the stepAIC function. The function Rsq compute a generalisation of the R-squared for not normal models.

**Usage**

IC(object, k = 2)
## S3 method for class 'gamlss'
AIC(object, ..., k = 2, c = FALSE)
GAIC(object, ..., k = 2, c = FALSE)
## S3 method for class 'gamlss'
extractAIC(fit, scale, k = 2, c = FALSE, ...)

Arguments

- object: an gamlss fitted model
- fit: an gamlss fitted model
- ...: allows several GAMLSS object to be compared using a GAIC
- k: the penalty with default k=2.5
- c: whether the corrected AIC, i.e. AICc, should be used, note that it applies only when k=2
- scale: this argument is not used in gamlss

Value

The function IC returns the GAIC for given penalty k of the GAMLSS object. The function AIC returns a matrix contains the df’s and the GAIC’s for given penalty k. The function GAIC returns identical results to AIC. The function extractAIC returns vector of length two with the degrees of freedom and the AIC criterion.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


(see also http://www.gamlss.org/).

See Also

gamlss

Examples

data(abdom)
mod1<-gamlss(y~pb(x),sigma.fo=-pb(x),family=BCT, data=abdom)
IC(mod1)
mod2<-gamlss(y~pb(x),sigma.fo=-x,family=BCT, data=abdom)
AIC(mod1,mod2,k=3)
GAIC(mod1,mod2,k=3)
extractAIC(mod1,k=3)
rm(mod1,mod2)
A function to fit LMS curves for centile estimation

**Description**

This function is designed to help the user easily construct growth curve centile estimation. It is applicable when only "one" explanatory variable is available (usually age).

**Usage**

```r
lms(y, x, families = LMS, data = NULL, k = 2,
    cent = 100 * pnorm((-4:4) * 2/3),
    calibration = TRUE, trans.x = FALSE,
    fix.power = NULL, lim.trans = c(0, 1.5),
    prof = FALSE, step = 0.1, legend = FALSE,
    mu.df = NULL, sigma.df = NULL, nu.df = NULL,
    tau.df = NULL, c.crit = 0.01,
    method.pb = c("ML", "GAIC"), ...)
```

**Arguments**

- `y`: The response variable
- `x`: The unique explanatory variable
- `families`: a list of `gamlss.families` with default `LMS=c("BCG", "BCP", "BTC")`
- `data`: the data frame
- `k`: the penalty to be used in the GAIC
- `cent`: a vector with elements the % centile values for which the centile curves have to be evaluated
- `calibration`: whether calibration is required with default `TRUE`
- `trans.x`: whether to check for transformation in `x` with default `FALSE`
- `fix.power`: if set it fix the power of the transformation for `x`
- `lim.trans`: the limits for the search of the power parameter for `x`
- `prof`: whether to use the profile GAIC of the power transformation
- `step`: if `codeprof=TRUE` is used this determine the step for the profile GAIC
- `legend`: whether a legend is required in the plot with default `FALSE`
- `mu.df`: `mu` effective degrees of freedom if required otherwise are estimated
- `sigma.df`: `sigma` effective degrees of freedom if required otherwise are estimated
- `nu.df`: `nu` effective degrees of freedom if required otherwise are estimated
- `tau.df`: `tau` effective degrees of freedom if required otherwise are estimated
- `c.crit`: the convergence criterion to be pass to `gamlss()`
- `method.pb`: the method used in the `pb()` for estimating the smoothing parameters. The default is local maximum likelihood "ML". "GAIC" is also permitted where `k` is taken from the `k` argument of the function.
- `...`: extra argument which can be passed to `gamlss()`
Details

This function should be used if the construction of the centile curves involves only one explanatory variable.

The model assumes that the response variable has a flexible distribution i.e. \( y \sim D(\mu, \sigma, \nu, \tau) \) where the parameters of the distribution are smooth functions of the explanatory variable i.e. \( g(\mu) = s(x) \), where \( g() \) is a link function and \( s() \) is a smooth function. Occasionally a power transformation in the x-axis helps the construction of the centile curves. That is, in this case the parameters are modelled by \( x^p \) rather than just \( x \), i.e. \( g(\mu) = s(x^p) \). The function lms() uses P-splines (pb()) as a smoother.

If a transformation is needed for \( x \) the function lms() starts by finding an optimum value for \( p \) using the simple model \( NO(\mu = s(x^p)) \). (Note that this value of \( p \) is not the optimum for the final chosen model but it works well in practice.)

After fitting a Normal error model for staring values the function proceeds by fitting several "appropriate" distributions for the response variable. The set of gamlss.family distributions to fit is specified by the argument families. The default families arguments is LMS=c("BCCGo", "BCEGo", "BCTo") that is the LMS class of distributions, Cole and Green (1992). Note that this class is only appropriate when \( y \) is positive (with no zeros). If the response variable contains negative values and zeros then use the argument families=theSHASH where theSHASH <- c("NO", "SHASH0") or add any other list of distributions which you may think is appropriate. Justification of using the specific centile (0.38 2.27 9.12 25.25, 50, 74.75, 90.88, 97.72, 99.62) is given in Cole (1994).

Value

It returns a gamlss fitted object

Note

The function is fitting several models and for large data can be slow

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Vlasios Voudouris <vlasios.voudouris@abm-analytics.com>

References

(see also http://www.gamlss.org/).
See Also

gamlss.centiles.calibration

Examples

```r
## Not run:
data(abdom)
m1 <- lms(y,x, data=abdom, n.cyc=30)
m2 <- lms(y,x, data=abdom, method.pb="GAIC", k=log(610))
# this example takes time
data(db)
m1 <- lms(y=head, x=age, data=db, trans.x=TRUE)

## End(Not run)
```

---

### lo

**Specify a loess fit in a GAMLSS formula**

Description

Allows the user to specify a loess fit within a GAMLSS model. This function is similar to the `lo` function in the `gam` implementation of package `gam` see Chambers and Hastie (1991).

The function `vis.lo()` allows plotting the results.

Usage

```r
lo(formula, control = lo.control(...), ...)
lo.control(span = 0.75, enp.target = NULL,
            degree = 2, parametric = FALSE, drop.square = FALSE,
            normalize = TRUE, family = c("gaussian", "symmetric"),
            method = c("loess", "model.frame"),
            surface = c("interpolate", "direct"),
            statistics = c("approximate", "exact", "none"),
            trace.hat = c("exact", "approximate"),
            cell = 0.2, iterations = 4, iterTrace = FALSE, ...)
vis.lo(obj, se=1, rug = FALSE, partial.resid = FALSE,
       col.term = "darkred", col.shaded = "gray",
       col.res = "lightblue", col.rug = "gray", lwd.term = 1.5,
       cex.res = 1, pch.res = par("pch"),
       type = c("persp", "contour"), col.surface = "gray",
       nlevels = 30, n.grid = 30, image = TRUE, ...)
```

Arguments

- `formula`: a formula specifying the explanatory variables
- `control`: a control to be passed to the loess function
- `...`: extra arguments
<table>
<thead>
<tr>
<th>span</th>
<th>the number of observations in a neighbourhood. This is the smoothing parameter for a loess fit.</th>
</tr>
</thead>
<tbody>
<tr>
<td>enp.target</td>
<td>an alternative way to specify span, as the approximate equivalent number degrees of freedom to be used. See also the help file of the R function loess. For consistency with the older version of lo the effective degrees of freedom df can be also specified instead of span, e.g. df=5</td>
</tr>
<tr>
<td>degree</td>
<td>the degree of local polynomial; can be 1 or 2. See also the help file of loess</td>
</tr>
<tr>
<td>parametric</td>
<td>should any terms be fitted globally rather than locally? See the help file of loess</td>
</tr>
<tr>
<td>drop.square</td>
<td>for fits with more than one predictor and degree=2, should the quadratic term be dropped for particular predictors?. See also help file of loess</td>
</tr>
<tr>
<td>normalize</td>
<td>should the predictors be normalized to a common scale if there is more than one? See the help file of loess</td>
</tr>
<tr>
<td>family</td>
<td>if &quot;gaussian&quot; fitting is by least-squares, and if &quot;symmetric&quot; a re-descending M estimator is used with Tukey's biweight function. See the help file of loess</td>
</tr>
<tr>
<td>method</td>
<td>fit the model or just extract the model frame. See the help file of loess</td>
</tr>
<tr>
<td>surface</td>
<td>should the fitted surface be computed exactly or via interpolation from a kd tree? See also the help file of loess.control</td>
</tr>
<tr>
<td>statistics</td>
<td>should the statistics be computed exactly or approximately? See the help file of loess.control</td>
</tr>
<tr>
<td>trace.hat</td>
<td>should the trace of the smoother matrix be computed exactly or approximately? See the help file of loess.control</td>
</tr>
<tr>
<td>cell</td>
<td>if interpolation is used this controls the accuracy of the approximation via the maximum number of points in a cell in the kd tree. See the help file of loess.control</td>
</tr>
<tr>
<td>iterations</td>
<td>the number of iterations used in robust fitting. See the help file of loess.control</td>
</tr>
<tr>
<td>iterTrace</td>
<td>logical (or integer) determining if tracing information during the robust iterations (iterations&gt;= 2) is produced. See the help file of loess.control</td>
</tr>
<tr>
<td>obj</td>
<td>an loess object fitted within gamlss</td>
</tr>
<tr>
<td>se</td>
<td>if se&gt;0 then stadard erros surfanes are drawn in the 3-dimentional plot. Set se at the required level i.e se=1. 96 will be an approximated 95% CI.</td>
</tr>
<tr>
<td>rug</td>
<td>whether to plot a rug in the plot</td>
</tr>
<tr>
<td>partial.resid</td>
<td>whether to plot the partial residuals</td>
</tr>
<tr>
<td>col.term</td>
<td>the colour of the line of fitted term</td>
</tr>
<tr>
<td>cex.shaded</td>
<td>the shading of standard</td>
</tr>
<tr>
<td>col.shaded</td>
<td>the shading of standard error intervals</td>
</tr>
<tr>
<td>col.res</td>
<td>the colour of partial residuals</td>
</tr>
<tr>
<td>col.rug</td>
<td>the colour of the rug</td>
</tr>
<tr>
<td>lwd.term</td>
<td>the width of the line</td>
</tr>
<tr>
<td>pch.res</td>
<td>The character for the partial residuals</td>
</tr>
<tr>
<td>type</td>
<td>The type of the plot if the x's are two dimensional</td>
</tr>
<tr>
<td>col.surface</td>
<td>the colour of the fitted surface</td>
</tr>
<tr>
<td>nlevels</td>
<td>the number of levels used in contour() plot.</td>
</tr>
<tr>
<td>n.grid</td>
<td>The number of points to evaluate the surface</td>
</tr>
<tr>
<td>image</td>
<td>whether to use image() or just contour</td>
</tr>
</tbody>
</table>
Details

Note that lo itself does no smoothing; it simply sets things up for the function gamlss.lo() which is used by the backfitting function gamlss.add().

Value

A loess object is returned.

Warning

In this version the first argument is a formula NOT a list as in the previous one.

Note

Note that lo itself does no smoothing; it simply sets things up for gamlss.lo() to do the backfitting.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby, (The original lo() function was based on the Trevor Hastie’s S-plus lo() function. See also the documentation of the loess function for the authorship of the function.

References

(see also http://www.gamlss.org/).

See Also

cs, random,

Examples

# fitting a loess curve with span=0.4 plus the a quarterly effect
aids1 <- gamlss(y~lo(~x,span=0.4)+qrt,data=aids,family=PO) #
term.plot(aids1, page=1)
## Not run:
r1 <- gamlss(R~lo(~F1)+lo(~A), data=rent, family=GA)
term.plot(r1, pages=1)
vis.lo(getSmo(r1, which=1), partial=T)
r2 <- gamlss(R~lo(~F1+A), data=rent, family=GA)
term.plot(r2, pages=1)
**Description**

The log-log Survival functions are designed for checking the tails of a single response variable (no explanatory should be involved). There are three different functions:

a) the function `loglogSurv1()` which plots the (left or right) tails of the empirical log-log Survival function against log(y), where y is the variable of interest. The coefficient of a linear fit to the plot can be used as an estimate for Type I tails.

b) the function `loglogSurv2()` which plots the (left or right) tails of the empirical log-log Survival function against log(y). The coefficient of a linear fit to the plot can be used as an estimate for Type II tails.

c) the function `loglogSurv3()` which plots the (left or right) tails of the empirical log-log Survival function against y. The coefficient of a linear fit to the plot can be used as an estimate for Type III tails.

The function `loglogSurv()` combines all the above functions.

The function `logSurv()` is also designed for exploring the tails of a single response variable. It plots the empirical log-survival function against log(y) for specified percentage of the tail and fits a linear, quadratic, and exponential curve to the points of the plot. For distributions defined on the positive real line a good linear fit would indicate a Pareto type tail, a good quadratic fit a log-normal type tail and good exponential fit a Weibull type tail. Note that this function is only appropriate to investigate rather heavy tails and it is not very good to discriminate between different types of tails, as the `loglogSurv()`.

**Usage**

```r
loglogSurv(y, percentage = 10, howmany = NULL, type = c("right", "left"),
           plot = TRUE, print = TRUE, save = FALSE)
loglogSurv1(y, percentage = 10, howmany = NULL, type = c("right", "left"),
            plot = TRUE, print = TRUE, save = FALSE)
loglogSurv2(y, percentage = 10, howmany = NULL, type = c("right", "left"),
            plot = TRUE, print = TRUE, save = FALSE)
loglogSurv3(y, percentage = 10, howmany = NULL, type = c("right", "left"),
            plot = TRUE, print = TRUE, save = FALSE)
logSurv(y, percentage = 10, howmany = NULL, type = c("right", "left"),
         plot = TRUE, print = TRUE, save = FALSE)
```
Arguments

- `y`: a vector, the variable of interest
- `percentage`: what percentage of the tail need to be modelled, default is 10%
- `howmany`: how many observations in the tail needed. This is an alternative to percentage. If it specified it take over from the percentage argument otherwise percentage is used.
- `type`: which tail needs checking the right (default) of the left
- `plot`: whether to plot with default equal TRUE
- `print`: whether to print the coefficients with default equal TRUE
- `save`: whether to save the fitted linear model with default equal FALSE

Details

The functions `loglogSurv1()`, `loglogSurv3()` and `loglogSurv3()` take the upper (or lower) part of an ordered variable create its empirical survival function and plot the log-log of this functions against `log(log(y))`, `log(y)` and `y` respectively. Then they fit a line to the plot. The coefficients of the line can be interpreted as parameters determined the behaviour of the tail. More details can be found in Chapter 6 of "The Distribution Toolbox of GAMLSS" book which can be found in [http://www.gamlss.org/](http://www.gamlss.org/)

Value

A plot

Author(s)

Bob Rigby, Mikis Stasinopoulos and Vlassios Voudouris

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

Examples

data(film90)
F90 <- film90$liborrev1
op<-par(mfrow=c(3,1))
loglogSurv1(F90)
loglogSurv2(F90)
loglogSurv3(F90)
lpred is the GAMLSS specific method which extracts the linear predictor and its (approximate) standard errors for a specified parameter from a GAMLSS object. The lpred can be also used to extract the fitted values (with its approximate standard errors) or specific terms in the model (with its approximate standard errors) in the same way that the predict.lm() and predict.glm() functions can be used for lm or glm objects. The function lp extract only the linear predictor. If prediction is required for new data values then use the function predict.gamlss().

Usage

lpred(obj, what = c("mu", "sigma", "nu", "tau"), parameter = NULL,
      type = c("link", "response", "terms"),
      terms = NULL, se.fit = FALSE, ...)
lp(obj, what = c("mu", "sigma", "nu", "tau"), parameter = NULL, ...)

Arguments

obj a GAMLSS fitted model
what which distribution parameter is required, default what="mu"
parameter equivalent to what
type type="link" (the default) gets the linear predictor for the specified distribution parameter. type="response" gets the fitted values for the parameter while type="terms" gets the fitted terms contribution
terms if type="terms", which terms to be selected (default is all terms)
se.fit if TRUE the approximate standard errors of the appropriate type are extracted
... for extra arguments

Value

If se.fit=FALSE a vector (or a matrix) of the appropriate type is extracted from the GAMLSS object for the given parameter in what. If se.fit=TRUE a list containing the appropriate type, fit, and its (approximate) standard errors, se.fit.

Author(s)

Mikis Stasinopoulos
LR.test

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

`predict.gamlss`

Examples

```r
data(aids)
mod<-.gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
mod.t <- lpred(mod, type = "terms", terms= "qrt")
mod.t
mod.lp <- lp(mod)
mod.lp
rm(mod, mod.t,mod.lp)
```

---

**LR.test**  
Likelihood Ratio test for nested GAMLSS models

Description

The function performs a likelihood ratio test for two nested fitted model.

Usage

```
LR.test(null, alternative, print = TRUE)
```

Arguments

- `null` The null hypothesis (simpler) fitted model
- `alternative` The alternative hypothesis (more complex) fitted model
- `print` whether to print or save the result

Details

Warning: no checking whether the models are nested is performed.
Value

If print=FALSE a list with chi, df and p.val is produced.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


(see also http://www.gamlss.org/).

See Also

gamlss, dropterm

Examples

data(usair)
m0<-gamlss(y~x1+x2, data=usair)
m1<-gamlss(y~x1+x2+x3+x4, data=usair)
LR.test(m0,m1)

model.frame.gamlss Extract a model.frame, a model matrix or terms from a GAMLSS object for a given distributional parameter

Description

model.frame.gamlss, model.matrix.gamlss and terms.gamlss are the gamlss versions of the generic functions model.frame, model.matrix and terms respectively.

Usage

## S3 method for class 'gamlss'
model.frame(formula, what = c("mu", "sigma", "nu", "tau"),
            parameter= NULL, ...)
## S3 method for class 'gamlss'
terms(x, what = c("mu", "sigma", "nu", "tau"),
       parameter= NULL, ...)
## S3 method for class 'gamlss'
model.frame.gamlss

model.matrix(object, what = c("mu", "sigma", "nu", "tau"),
              parameter = NULL, ...)

Arguments

formula: a gamlss object
x: a gamlss object
object: a gamlss object
what: for which parameter to extract the model.frame, terms or model.frame
parameter: equivalent to what
... for extra arguments

Value

a model.frame, a model.matrix or terms

Author(s)

Mikis Stasinopoulos

References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and


Regression and Smoothing: Using GAMLSS in R, Chapman and Hall/CRC.

(see also http://www.gamlss.org/).

See Also

gamlss

Examples

data(aids)
mod<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
model.frame(mod)
model.matrix(mod)
terms(mod, "mu")
rm(mod)
par.plot  

A function to plot parallel plot for repeated measurement data

Description

This function can be used to plot parallel plots for each individual in a repeated measurement study. It is based on the coplot() function of R.

Usage

par.plot(formula = NULL, data = NULL, subjects = NULL, color = TRUE, show.given = TRUE, ...)

Arguments

formula  
a formula describing the form of conditioning plot. A formula of the form y ~ x | a indicates that plots of y versus x should be produced conditional on the variable a. A formula of the form y ~ x| a * b indicates that plots of y versus x should be produced conditional on the two variables a and b.

data  
a data frame containing values for any variables in the formula. This argument is compulsory.

subjects  
a factor which distinguish between the individual participants

color  
whether the parallel plot are shown in colour, color=TRUE (the default) or not

tool.show.given  
logical (possibly of length 2 for 2 conditioning variables): should conditioning plots be shown for the corresponding conditioning variables (default 'TRUE')

...  
for extra arguments

Value

It returns a plot.

Note

Note that similar plot can be fount in the library nlme by Pinheiro and Bates

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>
**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

**See Also**

`gamlss`

**Examples**

```r
library(nlme)
data(Orthodont)
par.plot(distance~age,data=Orthodont,subject=Subject)
par.plot(distance~age|Sex,data=Orthodont,subject=Subject)
par.plot(distance~age|Subject,data=Orthodont,subject=Subject,show.given=FALSE)
```

---

**pcat**

Reduction for the Levels of a Factor.

**Description**

The function is trying to merged similar levels of a given factor. Its based on ideas given by Tutz (2013).

**Usage**

```r
pcat(fac, df = NULL, lambda = NULL, method = c("ML", "GAIC"), start = 0.001, 
Lp = 0, kappa = 1e-05, iter = 100, c.crit = 1e-04, k = 2)
gamlss.pcat(x, y, w, xeval = NULL, ...)
plotDF(y, factor = NULL, formula = NULL, data, along = seq(0, nlevels(factor)), 
kappa = 1e-06, Lp = 0, ...)
plotLambda(y, factor = NULL, formula = NULL, data, along = seq(-2, 2, 0.1), 
kappa = 1e-06, Lp = 0, ...)
```
Arguments

fac, factor       a factor to reduce its levels
df               the effective degrees of freedom df
lambda           the smoothing parameter
method           which method is used for the estimation of the smoothing parameter, "ML" or "GAIC" are allowed.
start            starting value for lambda if it estimated using "ML" or "GAIC"
Lp               The type of penalty required, Lp=0 is the default. Use Lp=1 for lasso type and different values for different required penalty.
kappa            a regulation parameters used for the weights in the penalties.
iter             the number of internal iteration allowed
c.crit           the convergent criterion
k                the penalty if "GAIC" method is used.
x                explanatory factor
y                the response or iterative response variable
w                iterative weights
xeval            indicator whether to predict
formula          A formula
data             A data frame
along            a sequence of values
...              for extra variables

Details

The pcat() is used for the fitting of the factor. The function shrinks the levels of the categorical factor (not towards the overall mean as the function random() is doing) but towards each other. This results to a reduction of the number if levels of the factors. Different norms can be used for the shrinkage by specifying the argument Lp.

Value

The function pcat reruns a vector endowed with a number of attributes. The vector itself is used in the construction of the model matrix, while the attributes are needed for the backfitting algorithms additive.fit(). The backfitting is done in gamlss.pcat.

Note

Note that pcat itself does no smoothing; it simply sets things up for gamlss.pcat() to do the smoothing within the backfitting.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Paul Eilers and Marco Enea
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

random

Examples

```r
# Simulate data
n <- 10  # number of levels
m <- 200 # number of observations
set.seed(2016)
level <- as.factor(floor(runif(m) * n) + 1)
a0 <- rnorm(n)
sigma <- 0.4
mu <- a0[level]
y <- mu + sigma * rnorm(m)
plot(y~level)
points(1:n+1, a0, col="red")
da1 <- data.frame(y, level)
#-----------------
 mn <- gamlss(y~1, data=d1) # null model
 ms <- gamlss(y~level-1, data=d1) # saturated model
 m1 <- gamlss(y~pcat(level), data=d1) # calculating lambda ML
 AIC(mn, ms, m1)
## Not run:
m11 <- gamlss(y~pcat(level), method="GAIC", k=log(200)), data=d1) # GAIC
AIC(mn, ms, m1, m11)
# getting the fitted object -----------------------------------------------
getSmo(m1)
coef(getSmo(m1))
fitted(getSmo(m1))[,1:10]
plot(getSmo(m1)) #
# After the fit a new factor is created this factor has the reduced levels
levels(getSmo(m1)$$factor)
# ---------------------------------------------------------------

## End(Not run)
```

`pdf.plot` *Plots Probability Distribution Functions for GAMLSS Family*
Description

A function to plot probability distribution functions (pdf) belonging to the gamlss family of distributions. This function allows either plotting of the fitted distributions for up to eight observations or plotting specified distributions belonging in the gamlss family.

Usage

```r
pdf.plot(obj = NULL, obs = c(1), family = NO(), mu = NULL,
         sigma = NULL, nu = NULL, tau = NULL, min = NULL,
         max = NULL, step = NULL, allinone = FALSE,
         no.title = FALSE, ...)
```

Arguments

- `obj`: An gamlss object e.g. `obj=model1` where model1 is a fitted gamlss object.
- `obs`: A number or vector of up to length eight indicating the case numbers of the observations for which fitted distributions are to be displayed, e.g. `obs=c(23,58)` will display the fitted distribution for the 23th and 58th observations.
- `family`: This must be a gamlss family i.e. `family=NO`.
- `mu`: The value(s) of the location parameter mu for which the distribution has to be evaluated e.g. `mu=c(3,7)`.
- `sigma`: The value(s) the scale parameter sigma for which the distribution has to be evaluated e.g. `sigma=c(3,7)`.
- `nu`: The value(s) the parameter nu for which the distribution has to be evaluated e.g. `nu=3`.
- `tau`: The value(s) the parameter tau for which the distribution has been evaluated e.g. `tau=5`.
- `min`: Minimum value of the random variable y e.g. `min=0`.
- `max`: Maximum value of y e.g. `max=10`.
- `step`: Steps for the evaluation of y e.g. `step=0.5`.
- `allinone`: This will go.
- `no.title`: Whether you need title in the plot, default is `no.title=FALSE`.
- `...`: for extra arguments.

Details

This function can be used to plot distributions of the GAMLSS family. If the first argument `obj` is specified and it is a GAMLSS fitted object, then the fitted distribution of this model at specified observation values (given by the second argument `obs`) is plotted for a specified y-variable range (arguments `min`, `max`, and `step`).

If the first argument is not given then the `family` argument has to be specified and the pdf is plotted at specified values of the parameters `mu`, `sigma`, `nu`, `tau`. Again the range of the y-variable has to be given.
Value
plot(s) of the required pdf(s) are returned

Warning
The range of some distributions depends on the fitted parameters

Note
The range of the y values given by min, max and step are very important in the plot

Author(s)
Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> and Calliope Akantziliotou

References


(see also http://www.gamlss.org/).

See Also
gamlss

Examples

cpydf.plot(family=BCT, min=1, max=20, step=.05, mu=10, sigma=0.15, nu=-1, tau=c(4,10,20,40) )
# now using an gamlss object
# library(gamlss)
# data(abdom)
#h<-gamlss(y-pb(x), sigma.formula=-pb(x), family=BCT, data=abdom) # fits
#pdf.plot(obj=h , obs=c(23,67), min=50, max=150, step=.5)
Description

This function provides four plots for checking the normalized (randomized for a discrete response distribution) quantile residuals of a fitted GAMLSS object, referred to as residuals below: a plot of residuals against fitted values, a plot of the residuals against an index or a specific explanatory variable, a density plot of the residuals and a normal Q-Q plot of the residuals. If argument ts=TRUE then the first two plots are replaced by the autocorrelation function (ACF) and partial autocorrelation function (PACF) of the residuals.

Usage

```r
## S3 method for class 'gamlss'
plot(x, xvar = NULL, parameters = NULL, ts = FALSE,
     summaries = TRUE, ...)
```

Arguments

- `x`: a GAMLSS fitted object
- `xvar`: an explanatory variable to plot the residuals against
- `parameters`: plotting parameters can be specified here
- `ts`: set this to TRUE if ACF and PACF plots of the residuals are required
- `summarizes`: set this to FALSE if no summary statistics of the residuals are required
- `...`: further arguments passed to or from other methods.

Details

This function provides four plots for checking the normalized (randomized) quantile residuals (called residuals) of a fitted GAMLSS object. Randomization is only performed for discrete response variables. The four plots are

- residuals against the fitted values (or ACF of the residuals if ts=TRUE)
- residuals against an index or specified x-variable (or PACF of the residuals if ts=TRUE)
- kernel density estimate of the residuals
- QQ-normal plot of the residuals

For time series response variables option ts=TRUE can be used to plot the ACF and PACF functions of the residuals.

Value

Returns four plots related to the residuals of the fitted GAMLSS model and prints summary statistics for the residuals if the summary=TRUE.
Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Kalliope Akantziliotou

References


(see also http://www.gamlss.org/).

See Also

gamlss

Examples

data(aids)
a<-gamlss(y~pb(x)+qrt,family=P0,data=aids)
plot(a)
rm(a)

plot.histSmo A Plotting Function for density estimator object histSmo

Description

Plots the estimated density or its c.d.f function or its inverse c.d.f function

Usage

## S3 method for class 'histSmo'
plot(x, type = c("hist", "cdf", "invcdf"), ...)

Arguments

x An histSmo object
type Different plots: a histogram and density estimator, a cdf function or an inverse cdf function.
... for further arguments
Value

returns the relevant plot

Author(s)

Mikis Stasinopoulos, Paul Eilers, Bob Rigby, Vlasios Voudouris and Majid Djennad

References

(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

histSmo

Examples

```r
Y <- rPARETO2(1000)
m1<- histSmo(Y, lower=0, save=TRUE)
plot(m1)
plot(m1, "cdf")
plot(m1, "invcdf")
```

---

**plot2way**

*Function to plot two interaction in a GAMLSS model*

Description

This function is designed to plot a factor to factor interaction in a GAMLSS model.

Usage

```r
plot2way(obj, terms = list(), what = c("mu", "sigma", "nu", "tau"),
        parameter= NULL, show.legend = TRUE, ...)
```
Arguments

- **obj**: A `gamlss` model
- **terms**: this should be a character vector with the names of the two factors to be plotted
- **what**: which parameters? `mu`, `sigma`, `nu`, or `tau`
- **parameter**: equivalent to **what**
- **show.legend**: whether to show the legend in the two way plot
- **...**: Further arguments

Details

This is an experimental function which should be used with prudence since no other check is done on whether this interaction interfere with other terms in the model

Value

The function creates a 2 way interaction plot

Author(s)

Mikis Stasinopoulos

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

term.plot,

Examples

data(aids)
ti <- factor(c(rep(1,18),rep(2,27)))
m1 <- gamlss(y-x+qrt*ti, data=aids, family=NBI)
m2 <- gamlss(y-x+qrt*ti, data=aids, family=NO)
plot2way(m1, c("qrt","ti"))
plot2way(m1, c("ti", "qrt"))
**polyS**

*Auxiliary support for the GAMLSS*

**Description**

These two functions are similar to the `poly` and `polym` in R. Are needed for the `gamlss.lo` function of GAMLSS and should not be used on their own.

**Usage**

```r
polyS(x, ...)  
poly.matrix(m, degree = 1)
```

**Arguments**

- `x`: a variable
- `m`: a variable
- `degree`: the degree of the polynomial
- `...`: for extra arguments

**Value**

Returns a matrix of orthogonal polynomials

**Warning**

Not be use by the user

**Author(s)**

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

**References**


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).


**See Also**

gamlss, gamlss.lo
predict.gamlss  

Retrieve Predictor Values and Standard Errors For New Data In a GAMLSS Model

Description

predict.gamlss is the GAMLSS specific method which produces predictors for a new data set for a specified parameter from a GAMLSS object. The predict.gamlss can be used to extract the linear predictors, fitted values and specific terms in the model at new data values in the same way that the predict.lm() and predict.glm() functions can be used for lm or glm objects. Note that linear predictors, fitted values and specific terms in the model at the current data values can also be extracted using the function lpred() (which is called from predict if new data is NULL).

Usage

## S3 method for class 'gamlss'
predict(object, what = c("mu", "sigma", "nu", "tau"),
        parameter = NULL,
        newdata = NULL, type = c("link", "response", "terms"),
        terms = NULL, se.fit = FALSE, data = NULL, ...)
predictAll(object, newdata = NULL, type = c("response", "link", "terms"),
           terms = NULL, se.fit = FALSE, use.weights = FALSE,
           data = NULL, y.value = "median",
           set.to = .Machine$double.xmin,
           output = c("list", "matrix"), ...)

Arguments

object a GAMLSS fitted model
what which distribution parameter is required, default what = "mu"
parameter equivalent to what
newdata a data frame containing new values for the explanatory variables used in the model
type the default, gets the linear predictor for the specified distribution parameter.
        type = "response" gets the fitted values for the parameter while type = "terms"
        gets the fitted terms contribution
terms if type = "terms", which terms to be selected (default is all terms)
se.fit if TRUE the approximate standard errors of the appropriate type are extracted if exist
use.weights if use.weights = TRUE the old data and the newdata are merged and the model is refitted with weights equal to the prior weights for the old data observations and equal to a very small value (see option set.to) for the newdata values. This trick allows to obtain standard errors for all parameters
data the data frame used in the original fit if not defined in the call
predict.gamlss

y.value how to get the response values for the newdata if they do not exist. The default is taking the median, y.value="median". Other function like "max", "min" are alloed. Also numerical values.

set.to what values the weights for the newdata should take

output whether the output to be a 'list' (default) or a 'matrix'

... for extra arguments

Details

The predict function assumes that the object given in newdata is a data frame containing the right x-variables used in the model. This could possible cause problems if transformed variables are used in the fitting of the original model. For example, let us assume that a transformation of age is needed in the model i.e. `nage<~age^.5`. This could be fitted as `mod<~gamlss(y~cs(age^.5), data=mydata)` or as `nage<~age^.5; mod<~gamlss(y~cs(nage), data=mydata)`. The later could more efficient if the data are in thousands rather in hundreds. In the first case, the code `predict(mod,newdata=data.frame(age=c(34,56))` would produce the right results. In the second case a new data frame has to be created containing the old data plus any new transform data. This data frame has to be declared in the data option. The option newdata should contain a data.frame with the new names and the transformed values in which prediction is required, (see the last example).

Value

A vector or a matrix depending on the options.

Note

This function is under development

Author(s)

Mikis Stasinopoulos

References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

lp, lpred
Examples

data(aids)
  a<-gamlss(y~poly(x,3)+qrt, family=P0, data=aids) #
  newaids<-data.frame(x=c(45,46,47), qrt=c(2,3,4))
  ap <- predict(a, newdata=newaids, type = "response")
  ap
  # now getting all the parameters
  predictAll(a, newdata=newaids)
  rm(a, ap)

data(abdom)
  # transform x
  aa<-gamlss(y~cs(x*.5),data=abdom)
  # predict at old values
  predict(aa)[610]
  # predict at new values
  predict(aa,newdata=data.frame(x=42.43))
  # now transform x first
  nx<-abdom$x*.5
  aaa<-gamlss(y~cs(nx),data=abdom)
  # create a new data frame
  newd<-data.frame( abdom, nx=abdom$x*.5)
  # predict at old values
  predict(aaa)[610]
  # predict at new values
  predict(aaa,newdata=data.frame(nx=42.43*.5), data=newd)

---

**print.gamlss**

*Prints a GAMLSS fitted model*

**Description**

`print.gamlss` is the GAMLSS specific method for the generic function `print` which prints objects returned by modelling functions.

**Usage**

```
## S3 method for class 'gamlss'
print(x, digits = max(3,getOption("digits") - 3), ...)
```

**Arguments**

- `x`  
  a GAMLSS fitted model

- `digits`  
  the number of significant digits to use when printing

- `...`  
  for extra arguments

**Value**

Prints a gamlss object
Author(s)
Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziliotou

References


(see also http://www.gamlss.org/).

See Also
gamlss, deviance.gamlss, fitted.gamlss

Examples
data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids)
print(h) # or just h
rm(h)

prof.dev

Plotting the Profile Deviance for one of the Parameters in a GAMLSS model

Description
This functions plots the profile deviance of one of the (four) parameters in a GAMLSS model. It can be used if one of the parameters mu, sigma, nu or tau is a constant (not a function of explanatory variables) to obtain a profile confidence intervals.

Usage
prof.dev(object, which = NULL, min = NULL, max = NULL, step = NULL, length = 7, startlastfit = TRUE, plot = TRUE, perc = 95, ...)

Arguments

- object: A fitted GAMLSS model
- which: which parameter to get the profile deviance e.g. which="tau"
- min: the minimum value for the parameter e.g. min=1
- max: the maximum value for the parameter e.g. max=20
- step: how often to evaluate the global deviance (defines the step length of the grid for the parameter) e.g. step=1
- length: the length if step is not set, default equal 7
- startlastfit: whether to start fitting from the last fit or not, default value is startlastfit=TRUE
- plot: whether to plot, plot=TRUE or save the results, plot=FALSE
- perc: what % confidence interval is required

... for extra arguments

Details

This function can be use to provide likelihood based confidence intervals for a parameter for which a constant model (i.e. no explanatory model) is fitted and consequently for checking the adequacy of a particular values of the parameter. This can be used to check the adequacy of one distribution (e.g. Box-Cox Cole and Green) nested within another (e.g. Box-Cox power exponential). For example one can test whether a Box-Cox Cole and Green (Box-Cox-normal) distribution or a Box-Cox power exponential is appropriate by plotting the profile of the parameter tau. A profile deviance showing support for tau=2 indicates adequacy of the Box-Cox Cole and Green (i.e. Box-Cox normal) distribution.

Value

Return a profile plot (if the argument plot=TRUE) and an ProfLikelihood.gamlss object if saved. The object contains:

- values: the values at the grid where the parameter was evaluated
- fun: the function which approximates the points using splines
- min: the minimum values in the grid
- max: the maximum values in the grid
- max.value: the value of the parameter maximising the Profile deviance (or GAIC)
- CI: the profile confidence interval (if global deviance is used)
- criterion: which criterion was used

Warning

A dense grid (i.e. small step) evaluation of the global deviance can take a long time, so start with a sparse grid (i.e. large step) and decrease gradually the step length for more accuracy.

Author(s)

Calliope Akantziliotou, Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> and Bob Rigby
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

gamlss, prof.term

Examples

```r
## Not run:
data(abdom)
h<-gamlss(y~pb(x), sigma.formula=~pb(x), family=BCT, data=abdom)
prof.dev(h,"nu",min=-2.000,max=2)
rm(h)
## End(Not run)
```

prof.term

*Plotting the Profile: deviance or information criterion for one of the terms (or hyper-parameters) in a GAMLSS model*

Description

This function plots the profile deviance for a chosen parameter included in the linear predictor of any of the nu,sigma, nu or tau models so profile confidence intervals can be obtained. In can also be used to plot the profile of a specified information criterion for any hyper-parameter when smooth additive terms are used.

Usage

```r
prof.term(model = NULL, criterion = c("GD", "GAIC"), penalty = 2.5, other = NULL, min = NULL, max = NULL, step = NULL, length = 7, xlab = NULL, plot = TRUE, perc = 95, start.prev = TRUE, ...)
```
Arguments

model: this is a GAMLSS model, e.g.
model=gamlss(y~cs(x,df=this), sigma.foc~cs(x,df=3), data=abdom), where this indicates the (hyper)parameter to be profiled

criterion: whether global deviance ("GD") or information criterion ("GAIC") is profiled. The default is global deviance criterion="GD"

penalty: The penalty value if information criterion is used in criterion, default penalty=2.5

other: this can be used to evaluate an expression before the actual fitting of the model (Make sure that those expressions are well define in the global environment)

min: the minimum value for the parameter e.g. min=1

max: the maximum value for the parameter e.g. max=20

step: how often to evaluate the global deviance (defines the step length of the grid for the parameter) e.g. step=1

length: if the step is left NULL then length is considered for evaluating the grid for the parameter. It has a default value of 11

xlabel: if a label for the axis is required

plot: whether to plot, plot=TRUE the resulting profile deviance (or GAIC)

perc: what % confidence interval is required

start.prev: whether to start from the previous fitted model parameters values or not (default is TRUE)

...: for extra arguments

Details

This function can be used to provide likelihood based confidence intervals for a parameter involved in terms in the linear predictor(s). These confidence intervals are more accurate than the ones obtained from the parameters' standard errors. The function can also be used to plot a profile information criterion (with a given penalty) against a hyper-parameter. This can be used to check the uniqueness in hyper-parameter determination using for example find.df.

Value

Return a profile plot (if the argument plot=TRUE) and an ProfLikelihood.gamlss object if saved. The object contains:

values: the values at the grid where the parameter was evaluated

fun: the function which approximates the points using splines

min: the minimum values in the grid

max: the maximum values in the grid

max.value: the value of the parameter maximising the Profile deviance (or GAIC)

CI: the profile confidence interval (if global deviance is used)

criterion: which criterion was used
Warning

A dense grid (i.e. small step) evaluation of the global deviance can take a long time, so start with a sparse grid (i.e. large step) and decrease gradually the step length for more accuracy.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org> and Bob Rigby

References


(see also http://www.gamlss.org/).

See Also

gamlss, prof.dev

Examples

data(aids)
# fitting a linear model
gamlss(y~x+qrt,family=NBI,data=aids)
# testing the linear beta parameter
mod<-.quote(gamlss(y ~ offset(this * x) + qrt, data = aids, family = NBI))
prof.term(mod, min=0.06, max=0.11)
# find the hyper parameter using cubic splines smoothing
mod1<-.quote(gamlss(y ~ cs(x,df=this) + qrt, data = aids, family = NBI))
prof.term(mod1, min=1, max=15, step=1, criterion="GAIC", penalty=log(45))
# find a break point in x
mod2 <-.quote(gamlss(y ~ x+I((x>this)*(x-this))+qrt,family=NBI,data=aids))
prof.term(mod2, min=1, max=45, step=1, criterion="GD")
rm(mod,mod1,mod2)
Description

There are several functions which use P-spline methodology:

a) pbH(), the current version of P-splines which uses SVD in the fitting and therefore is the most reliable
b) pboH() and pbpH(), older versions of P-splines. The first uses a simple matrix algebra in the fits. The second is the last version of pbH() with SVD but uses different method for prediction.
c) pbcH() the new version of cycle P-splines (using SVD)
d) cyH() the older version of cycle P-splines.
e) pbmH() for fitting monotonic P-splines (using SVD)
f) pbzH() for fitting P-splines which allow the fitted curve to shrink to zero degrees of freedom
g) psH() the original P-splines with no facility of estimating the smoothing parameters and
j) pvcH() penalised varying coefficient models.

Theoretical explanation of the above P-splines can be found in Eilers et al. (2016)

The functions take a vector and return it with several attributes. The vector is used in the construction of the design matrix X used in the fitting. The functions do not do the smoothing, but assign the attributes to the vector to aid gamlss in the smoothing. The functions doing the smoothing are gamlss.pbH(), gamlss.pboH(), gamlss.pbcH() gamlss.cyH() gamlss.pvcH(), gamlss.pbmH(),
gamlss.pbz and gamlss.psH() which are used in the backfitting function additive.fit.

The function pbH() is more efficient and faster than the original penalised smoothing function psH(). After December 2014 the pbH() has changed radically to improved performance. The older version of the pbH() function is called now pboH(). pbH() allows the estimation of the smoothing parameters using different local (performance iterations) methods. The method are "ML", "ML-1", "EM", "GAIC" and "GCV".

The function pbmH() fits monotonic smooth functions, that is functions which increase or decrease monotonically depending on the value of the argument mono which takes the values "up" or "down".

The function pbzH() is similar to pbH() with the extra property that when lambda becomes very large the resulting smooth function goes to a constant rather than to a linear function. This is very useful for model selection. The function is based on Maria Durban idea of using a double penalty, one of order 2 and one of order 1. The second penalty only applies if the effective df are close to 2 (that is if a linear is already selected).

The function pbcH() fits a cycle penalised beta regression spline such as the last fitted value of the smoother is equal to the first fitted value. cyH() is the older version.

The function pvcH() fits varying coefficient models see Hastie and Tibshirani(1993) and it is more general and flexible than the old vcH() function which was based on cubic splines.

The function getZmatrix() creates a (random effect) design matrix Z which can be used to fit a P-splines smoother using the reH() function. (The reH() is an interface with the random effect function lme of the package nlme.

Usage

```r
pb(x, df = NULL, lambda = NULL, control = pb.control(...), ...)  
pbo(x, df = NULL, lambda = NULL, control = pbo.control(...), ...)  
pbp(x, df = NULL, lambda = NULL, control = pbp.control(...), ...) 
```
Arguments

x the univariate predictor
df the desired equivalent number of degrees of freedom (trace of the smoother matrix minus two for the constant and linear fit)
lambda the smoothing parameter
control setting the control parameters
by a factor, for fitting different smoothing curves to each level of the factor or a continuous explanatory variable in which case the coefficients of the by variable change smoothly according to x i.e. beta(x)*z where z is the by variable.

... for extra arguments
inter the no of break points (knots) in the x-axis
degree the degree of the piecewise polynomial
order the required difference in the vector of coefficients
start the lambda starting value if the local methods are used, see below
quantiles if TRUE the quantile values of x are use to determine the knots
ts if TRUE assumes that it is a seasonal factor
method The method used in the (local) performance iterations. Available methods are "ML", "ML-1", "EM", "GAIC" and "GCV"
the penalty used in "GAIC" and "GCV"
for monotonic P-splines whether going "up" or "down"
the smoothing hyper-parameter for the monotonic part of smoothing
the no of break points in the x-axis
minimum value for creating the B-spline
maximum value for creating the B-spline
whether to use the sin penalty or not
at which level the second penalty of order 1 should start

Details

The \texttt{ps()} function is based on Brian Marx function which can be found in his website. The \texttt{pb()}, \texttt{cy()}, \texttt{pvc()} and \texttt{pbm()} functions are based on Paul Eilers's original R functions. Note that \texttt{ps()} and \texttt{pb()} functions behave differently at their default values if \texttt{df} and \texttt{lambda} are not specified. \texttt{ps(x)} by default uses 3 extra degrees of freedom for smoothing \texttt{x}. \texttt{pb(x)} by default estimates \texttt{lambda} (and therefore the degrees of freedom) automatically using a "local" method. The local (or performance iterations) methods available are: (i) local Maximum Likelihood, "ML", (ii) local Generalized Akaike information criterion, "GAIC", (iii) local Generalized Cross validation "GCV" (iv) local EM-algorithm, "EM" (which is very slow) and (v) a modified version of the ML, "ML-1" which produce identical results with "EM" but faster.

The function \texttt{pb()} fits a P-spline smoother.

The function \texttt{pbm()} fits a monotonic (going up or down) P-spline smoother.

The function \texttt{pbc()} fits a P-spline smoother where the beginning and end are the same.

The \texttt{pvc()} fits a varying coefficient model.

Note that the local (or performance iterations) methods can occasionally make the convergence of \texttt{gamlss} less stable compared to models where the degrees of freedom are fixed.

Value

the vector \texttt{x} is returned, endowed with a number of attributes. The vector itself is used in the construction of the model matrix, while the attributes are needed for the backfitting algorithms \texttt{additive.fit()}.

Warning

There are occasions where the automatic local methods do not work. One accusation which came to our attention is when the range of the response variable values is very large. Scaling the response variable will solve the problem.

Author(s)

Mikis Stasinopoulos \texttt{<mikis.stasinopoulos@gamlss.org>}, Bob Rigby and Paul Eilers
References


(see also http://www.gamlss.org/).

See Also
gamlss, gamlss.ps, cs

Examples

#-------------------------------
# pb() and ps() functions
data(aids)
# fitting a smoothing cubic spline with 7 degrees of freedom
# plus the a quarterly effect
aids1<-gamlss(y~ps(x,df=7)+qrt,data=aids,family=PO) # fix df's
aids2<-gamlss(y~pb(x,df=7)+qrt,data=aids,family=PO) # fix df's
aids3<-gamlss(y~pb(x)+qrt,data=aids,family=PO) # estimate lambda
with(aids, plot(x,y))
with(aids, lines(x,fitted(aids1),col="red"))
with(aids, lines(x,fitted(aids2),col="green"))
with(aids, lines(x,fitted(aids3),col="yellow"))
rm(aids1, aids2, aids3)
#-------------------------------
# Not run:
# pbc()
# simulate data
set.seed(555)
x = seq(0, 1, length = 100)
y = sign(cos(1 * x * 2 * pi + pi / 4)) + rnorm(length(x)) * 0.2
plot(y~x)
m1<-gamlss(y~pbc(x))
lines(fitted(m1)-x)
rm(y,x,m1)
#-------------------------------
# the pvc() function
# function to generate data
genData <- function(n=200) {
  f1 <- function(x) -60 + 1.5 * x - 0.1 * x^2
  f2 <- function(x) -120 + 10 * x + 0.08 * x^2
  set.seed(1441)
  x1 <- runif(n/2, min=0, max=55)
  x2 <- runif(n/2, min=0, max=55)
  y1 <- f1(x1) + rNO(n=n/2, mu=0, sigma=20)
  y2 <- f2(x2) + rNO(n=n/2, mu=0, sigma=30)
  y <- c(y1, y2)
  x <- c(x1, x2)
  f <- gl(2, n/2)
  da <- data.frame(y, x, f)
}
daa <- genData(500)
plot(y ~ x, data = da, pch = 21, bg = c("gray", "yellow3") [unclass(f)])
  # fitting models
  # smoothing x
  m1 <- gamlss(y ~ pb(x), data = da)
  # parallel smoothing lines
  m2 <- gamlss(y ~ pb(x)+f, data = da)
  # linear interaction
  m3 <- gamlss(y ~ pb(x)+f*x, data = da)
  # varying coefficient model
  m4 <- gamlss(y ~ pvc(x, by = f), data = da)
  GAIC(m1, m2, m3, m4)
  # plotting the fit
  lines(fitted(m4)[da$f==1][order(da$x[da$f==1])]-da$x[da$f==1]
        [order(da$x[da$f==1])], col = "blue", lwd = 2)
  lines(fitted(m4)[da$f==2][order(da$x[da$f==2])]-da$x[da$f==2]
        [order(da$x[da$f==2])], col = "red", lwd = 2)
rm(da, m1, m2, m3, m4)

# the rent data
# first with a factor
data(rent)
plot(R ~ Fl, data = rent, pch = 21, bg = c("gray", "blue") [unclass(rent$B)])
  r1 <- gamlss(R ~ pb(Fl), data = rent)
  # identical to model
  r11 <- gamlss(R ~ pvc(Fl), data = rent)
  # now with the factor
  r2 <- gamlss(R ~ pvc(Fl, by = B), data = rent)
  lines(fitted(r2)[rent$B==1][order(rent$Fl[rent$B==1])]-rent$Fl[rent$B==1]
        [order(rent$Fl[rent$B==1])], col = "blue", lwd = 2)
  lines(fitted(r2)[rent$B==0][order(rent$Fl[rent$B==0])]-rent$Fl[rent$B==0]
        [order(rent$Fl[rent$B==0])], col = "red", lwd = 2)
  # probably not very sensible model
rm(r1, r11, r2)
  #-------
  # now with a continuous variable
  # additive model
  h1 <- gamlss(R ~ pb(Fl) + pb(A), data = rent)
# varying-coefficient model
h2 <- gamlss(R~pb(Fl)+pb(A)+pvc(A,by=Fl), data=rent)
AIC(h1,h2)
rm(h1,h2)

# monotone function
set.seed(1334)
x = seq(0, 1, length = 100)
p = 0.4
y = sin(2 * pi * p * x) + rnorm(100) * 0.1
plot(y~x)
m1 <- gamlss(y~pbm(x))
points(fitted(m1)-x, col="red")

yy <- -y
plot(yy~x)
m2 <- gamlss(yy~pbm(x, mono="down"))
points(fitted(m2)-x, col="red")

# the pbz() function
# creating uncorrelated data
set.seed(123)
y=rNO(100)
x<-1:100
plot(y~x)

# ML estimation
m1 <- gamlss(y~pbz(x))
m2 <- gamlss(y~pbz(x))
AIC(m1,m2)
op <- par( mfrow=c(1,2))
term.plot(m1, partial=T)
term.plot(m2, partial=T)
par(op)

# GAIC estimation
m11 <- gamlss(y~pbz(x, method="GAIC", k=2))
m21 <- gamlss(y~pbz(x, method="GAIC", k=2))
AIC(m11,m21)
op <- par( mfrow=c(1,2))
term.plot(m11, partial=T)
term.plot(m21, partial=T)
par(op)

# GCV estimation
m12 <- gamlss(y~pbz(x, method="GCV"))
m22 <- gamlss(y~pbz(x, method="GCV"))
AIC(m12,m22)
op <- par( mfrow=c(1,2))
term.plot(m12, partial=T)
term.plot(m22, partial=T)
par(op)

# fixing df is more trycky since df are the extra df
m13 <- gamlss(y~pbz(x, df=0))
m23 <- gamlss(y~pbz(x, df=0))
AIC(m13,m23)
Q.stats

# here the second penalty is not take effect therefore identical results
m14 <- gamlss(y~pbz(x, df=1))
m24 <- gamlss(y~pbz(x, df=1))
AIC(m14,m24)

# fixing lambda
m15 <- gamlss(y~pbz(x, lambda=1000))
m25 <- gamlss(y~pbz(x, lambda=1000))
AIC(m15,m25)

# prediction
m1 <- gamlss(y~pbz(x), data=data.frame(y,x))
m2 <- gamlss(y~pbz(x), data=data.frame(y,x))
AIC(m1,m2)
predict(m1, newdata=data.frame(x=c(80, 90, 100, 110)))
predict(m2, newdata=data.frame(x=c(80, 90, 100, 110)))

## End(Not run)

---

**Q.stats**

*A function to calculate the Q-statistics*

---

**Description**

This function calculates and prints the Q-statistics (or Z-statistics) which are useful to test normality of the residuals within a range of an independent variable, for example age in centile estimation, see Royston and Wright (2000).

**Usage**

```r
Q.stats(obj = NULL, xvar = NULL, resid = NULL, xcut.points = NULL, n.inter = 10,
         zvals = TRUE, save = TRUE, plot = TRUE, digits.xvar = getOption("digits"),
         ...)
```

**Arguments**

- **obj**: a GAMLSS object
- **xvar**: a unique explanatory variable
- **resid**: quantile or standardised residuals can be given here instead of a GAMLSS object in obj. In this case the function behaves differently (see details below)
- **xcut.points**: the x-axis cut off points e.g. c(20, 30). If xcut.points=NULL then the n.inter argument is activated
- **n.inter**: if xcut.points=NULL this argument gives the number of intervals in which the x-variable will be split, with default 10
- **zvals**: if TRUE the output matrix contains the individual Z-statistics rather than the Q statistics
save whether to save the Q-statistics or not with default equal to TRUE. In this case the functions produce a matrix giving individual Q (or z) statistics and the final aggregate Q’s.
plot whether to plot a visual version of the Q statistics (default is TRUE)
digits.xvar to control the number of digits of the xvar in the plot
... for extra arguments

Details

Note that the function Q.stats behaves differently depending whether the obj or the resid argument is set. The obj argument produces the Q-statistics (or Z-statistics) table appropriate for centile estimation (therefore it expect a reasonable large number of observations). The argument resid allows any model residuals, (not necessary GAMLSS), suitable standardised and is appropriate for any size of data. The resulting table contains only the individuals Z-statistics.

Value

A table containing the Q-statistics or Z-statistics. If plot=TRUE it produces also an graphical representation of the table.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby with contributions from Elaine Borghie

References

(see also http://www.gamlss.org/).

See Also
gamlss, centiles.split, wp

Examples

data(abdom)
hh<-gamlss(y~pb(x), sigma.formula=-pb(x), family=BCT, data=abdom)
Q.stats(h,xvar=abdom$x,n.inter=8)
Q.stats(h,xvar=abdom$x,n.inter=8,zvals=FALSE)
Description

The quantile sheets function `quantsheets()` is based on the work of Sabine Schnabe and Paul Eiler (see references below). The estimation of the quantile curves is done simultaneously by also smoothing in the direction of y as well as x. This avoids (but do not eliminate completely) the problem of crossing quantiles.

Usage

```r
quantsheets(y, x, x.lambda = 1, p.lambda = 1, data = NULL,
    cent = 100 * pnorm((-4:4) * 2/3),
    control = quantsheets.control(...), print = TRUE, ...
)
```

```r
quantsheets.control(x.inter = 10, p.inter = 10, degree = 3, logit = FALSE,
    order = 2, kappa = 0, n.cyc = 100, c.crit = 1e-05, plot = TRUE,
    power = NULL, ...
)
```

```r
findPower(y, x, data = NULL, lim.trans = c(0, 1.5), prof = FALSE,
    k = 2, c.crit = 0.01, step = 0.1)
```

```r
z.scoresQS(object, y, x, plot = FALSE, tol = NULL)
```

Arguments

- `y` the y variable
- `x` the x variable
- `x.lambda` smoothing parameter in the direction of x
- `p.lambda` smoothing parameter in the direction of y (probabilities)
- `data` the data frame
- `cent` the centile values where the quantile sheets is evaluated
- `control` for the parameters controlling the algorithm
- `print` whether to print the sample percentages
- `x.inter` number of intervals in the x direction for the B-splines
- `p.inter` number of intervals in the probabilities (y-direction) for the B-splines
- `degree` the degree for the B-splines
- `logit` whether to use logit(p) instead of p (probabilities) for the y-axis
- `order` the order of the penalty
kappa is a ridge parameter set to zero (for no ridge effect)
n.cyc number of cycles of the algorithm
c.crit convergence criterion of the algorithm
plot whether to plot the resulting quantile sheets
power The value of the power transformation in the x axis if needed
lim.trans the limits for looking for the power transformation parameter using findPower()
prof whether to use the profile GAIC or optim() to the parameter the power transformation
k the GAIC penalty
step the steps for the profile GAIC if the argument prof of findPower() is TRUE
object a fitted quantsheets object
tol how far out from the range of the y variable should go for estimating the distribution of y using the flexDist() function

Details

The advantage of quantile sheets is that they estimates simultaneously all the quantiles. This almost eliminates the problem of crossing quantiles. The method is very fast and useful for exploratory tool. The function needs two smoothing parameters. Those two parameters have to specified by the user. They are not estimated automatically. They can be selected by visual inspection.

The disadvantages of quantile sheets comes from the fact that like all non-parametric techniques do not have a goodness of fit measure to change how good is the models and the residuals based diagnostics are not existence since it is difficult to define residuals in this set up.

In this implementation we do provide residuals by using the flexDist() function from package gamlss.dist. This is based on the idea that by knowing the quantiles of the distribution we can reconstruct non parametrically the distribution itself and this is what flexDist() is doing. As a word of caution, such a construct is based on several assumptions and depends on several smoothing parameters. Treat those residuals with caution. The same caution should apply to the function z.scoresQS().

Value

Using the function quantsheets() a quantsheets object is returned having the following methods: print(), fitted(), predict() and resid().

Using findPower() a single values of the power parameter is returned.

Using z.scoresQS a vector of z-scores is returned.

Author(s)

Mikis Stasinopoulos based on function provided by Paul Eiler and Sabine Schnabe
References


(see also [http://www.gamlss.org/](http://www.gamlss.org/)).

See Also

*lm*: for a parametric equivalent results.

Examples

data(abdom)
m1 <- quantSheets(y,x, data=abdom)
head(fitted(m1))
p1 <- predict(m1, newdata=c(20,30,40))
matpoints(c(20,30,40), p1)
z.scoresQS(m1,y=c(150, 300),x=c(20, 30) )
# If we needed a power transformation not appropriate for this data
findPower(y,x, data=abdom)

---

**random**  
Specify a random intercept model in a GAMLSS formula

**Description**

They are two functions for fitting random effects within a GAMLSS model, `random()` and `re()`.

The function `random()` is based on the original `random()` function of Trevor Hastie in the package `gam`. In our version the function has been modified to allow a "local" maximum likelihood estimation of the smoothing parameter $\lambda$. This method is equivalent to the PQL method of Breslow and Clayton (1993) applied at the local iterations of the algorithm. In fact for a GLM model and a simple random effect it is equivalent to the `glmmPQL()` function in the package `MASS` see Venables and Ripley (2002). Venables and Ripley (2002) claimed that this iterative method was first introduced by Schall (1991). Note that in order for the "local" maximum likelihood estimation procedure to operate both argument `df` and `lambda` has to be `NULL`.

The function `re()` is an interface for calling the `lme()` function of the package `nlme`. This gives the user the ability to fit complicated random effect models while the assumption of the normal distribution for the response variable is relaxed. The theoretical justification comes again from the fact that this is a PQL method, Breslow and Clayton (1993).
Usage

random(x, df = NULL, lambda = NULL, start=10)

re(fixed = ~1, random = NULL, correlation = NULL, method = "ML", ...)

Arguments

x    a factor
df   the target degrees of freedom
lambda  the smoothing parameter lambda which can be viewed as a shrinkage parameter.
start starting value for lambda if local Maximul likelihood is used.
fixed a formula specify the fixed effects of the lme() model. This, in most cases can be also included in the gamlss parameter formula
random a formula or list specufying the random effect part of the model as in lme() function
correlation the correlation structure of the lme() model
method which method, "ML" (the default), or "REML"
... this can be used to pass arguments for lmeControl()

Details

The function random() can be seen as a smoother for use with factors in gamlss(). It allows the fitted values for a factor predictor to be shrunk towards the overall mean, where the amount of shrinking depends either on lambda, or on the equivalent degrees of freedom or on the estimated sigma parameter (default). Similar in spirit to smoothing splines, this fitting method can be justified on Bayesian grounds or by a random effects model. Note that the behavior of the function is different from the original Hastie function. Here the function behaves as follows: i) if both df and lambda are NULL then the PQL method is used ii) if lambda is not NULL, lambda is used for fitting iii) if lambda is NULL and df is not NULL then df is used for fitting.

Since factors are coded by model.matrix() into a set of contrasts, care has been taken to add an appropriate "contrast" attribute to the output of random(). This zero contrast results in a column of zeros in the model matrix, which is aliased with any column and is hence ignored.

The use of the function re() requires knowledge of the use of the function lme() of the package nlme for the specification of the appropriate random effect model. Some care should betaken whether the data set is

Value

x is returned with class "smooth", with an attribute named "call" which is to be evaluated in the backfitting additive.fit() called by gamlss()

Author(s)

For re() Mikis Stasinopoulos and Marco Enea and for random() Trevor Hastie (amended by Mikis Stasinopoulos),
References


See Also

`gamlss`, `gamlss.random`

Examples

```r
#------------- Example 1 from Pinheiro and Bates (2000) page 15----------
# bring nlme
library(nlme)
data(ergoStool)
# lme model
l1<-lme(effort~Type, data=ergoStool, random=~1|Subject, method="ML")
# use random()
t1<-gamlss(effort~Type+random(Subject), data=ergoStool )
# use re() with fixed effect within re()
t2<-gamlss(effort+re(fixed~Type, random=~1|Subject), data=ergoStool )
# use re() with fixed effect in gamlss formula
t3<-gamlss(effort~Type+re(random=~1|Subject), data=ergoStool )
# compare lme fitted values with random
plot(fitted(l1), fitted(t1))
# compare lme fitted values with random
plot(fitted(l1), fitted(t2))
lines(fitted(l1), fitted(t3), col=2)
# getting the fitted coefficients
getSmof(t2)
#---------------------------------'
## Not run:
#-------------Example 2 Hodges data-----------------------------
data(hodges)
plot(prind~state, data=hodges)
ml<- gamlss(prind~random(state), sigma.fo=~random(state), nu.fo=~random(state),
```
tau.fo=random(state), family=BCT, data=hodges)
m2<- gamlss(prind=re(random=-1|state), sigma.fo=re(random=-1|state),
nu.fo=re(random=-1|state), tau.fo=re(random=-1|state), family=BCT,
data=hodges)

# comparing the fitted effective degrees of freedom
m1$mu.df
m2$mu.df
m1$sigma.df
m2$sigma.df
m1$nu.df
m2$nu.df
m1$tau.df
m2$tau.df

# random effect for tau is not needed
m3<- gamlss(prind=random(state), sigma.fo=random(state), nu.fo=random(state),
family=BCT, data=hodges, start.from=m1)
plot(m3)

# term plots work for random but not at the moment for re()
op <- par(mfrow=c(2,2))
term.plot(m3, se=TRUE)
term.plot(m3, se=TRUE, what="sigma")
term.plot(m3, se=TRUE, what="nu")
par(op)

# getting information from a fitted lme object
coef(getSmo(m2))
ranef(getSmo(m2))
VarCorr(getSmo(m2))
summary(getSmo(m2))
intervals(getSmo(m2))
fitted(getSmo(m2))

# plotting
plot(getSmo(m2))
qqnorm(getSmo(m2))

# example 3 from Pinheiro and Bates (2000) page 42
data(Pixel)
l1 <- lme(pixel~ day*I(day^2), data=Pixel, random=list(Dog=~day, Side=~1),
method="ML")

# this will fail
#t1<-gamlss(pixel-re(fixed=-day+I(day^2), random=list(Dog=~day, Side=~1)),
# data=Pixel)
# but this is working

# checking the model
refit

Refit a GAMLSS model

```r
plot(t1)
wpt(t1, ylim.all=2)
# two observation fat try LO
t2<-gamlss(distance~I(age-11)+re(random=-I(age-11)|Subject, opt="optim", numIter=100), data=Orthodont, family=L0)
plot(t2)
wpt(t2, ylim.all=2)
# a bit better but not satisfactory Note that 3 parameters distributions fail
library(MASS)
data(bacteria)
summary(glmPQL(y ~ trt + I(week > 2), random = ~1 | ID,
family = binomial, data = bacteria))
s1 <- gamlss(y ~ trt + I(week > 2)+random(ID), family = BI, data = bacteria)
s2 <- gamlss(y ~ trt + I(week > 2)+re(random=-1|ID), family = BI,
data = bacteria)
s3 <- gamlss(y ~ trt + I(week > 2)+re(random=-1|ID, method="REML"), family = BI,
data = bacteria)
# the estimate of the random effect sd sigma_b
sqrt(getSmo(s1)$tau2)
getSmo(s2)
getSmo(s3)
#------Example 5 from Venable and Ripley (2002)-----------------------
data(ovary)
# AR1
l1 <- lme(follicles~sin(2*pi*Time)+cos(2*pi*Time), data=ovary,
random=pdDiag(~sin(2*pi*Time)), correlation=corAR1())
# ARMA
l2 <- lme(follicles~sin(2*pi*Time)+cos(2*pi*Time), data=ovary,
random=pdDiag(~sin(2*pi*Time)), correlation=corARMA(q=2))
# now gamlss
# AR1
t1 <- gamlss(follicles~re(fixed=-sin(2*pi*Time)+cos(2*pi*Time),
random=pdDiag(~sin(2*pi*Time)),
correlation=corAR1()), data=ovary)
plot(fitted(l1)-fitted(t1))
# ARMA
t2 <- gamlss(follicles~re(fixed=-sin(2*pi*Time)+cos(2*pi*Time),
random=pdDiag(~sin(2*pi*Time)),
correlation=corARMA(q=2), data=ovary)
plot(fitted(l2)-fitted(t2))
AIC(t1, t2)
wpt(t2, ylim.all=1)
#-----------------------------------------------

## End(Not run)
```
Description

This function refits a GAMLSS model. It is useful when the algorithm has not converged after 20 outer iteration (the default value)

Usage

refit(object, ...)

Arguments

object a GAMLSS fitted model which has not converged
...
for extra arguments

Details

This function is useful when the iterations have reach the maximum value set by the code(n.cyc) of the gamlss.control function and the model has not converged yet

Value

Returns a GAMLSS fitted model

Note

The function update does a very similar job

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

References


(see also http://www.gamlss.org/).

See Also

gamlss, update.gamlss
residuals.gamlss

Examples

data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
refit(h)
rm(h)

residuals.gamlss  Extract Residuals from GAMLSS model

Description

residuals.gamlss is the GAMLSS specific method for the generic function residuals which extracts the residuals for a fitted model. The abbreviated form resid is an alias for residuals.

Usage

## S3 method for class 'gamlss'
residuals(object, what = c("z-scores", "mu", "sigma", "nu", "tau"),
          type = c("simple", "weighted", "partial"),
          terms=NULL, ...)

Arguments

object  a GAMLSS fitted model
what    specify whether the standardized residuals are required, called here the "z-scores",
        or residuals for a specific parameter
type    the type of residual if residuals for a parameter are required
terms   if type is "partial" this specifies which term is required
        ...
        for extra arguments

Details

The "z-scores" residuals saved in a GAMLSS object are the normalized (randomized) quantile residuals (see Dunn and Smyth, 1996). Randomization is only needed for the discrete family distributions, see also rqres.plot. Residuals for a specific parameter can be "simple" = (working variable - linear predictor),"weighted"= sqrt(working weights)*(working variable - linear predictor) or "partial"= (working variable - linear predictor)+contribution of specific terms.

Value

a vector or a matrix of the appropriate residuals of a GAMLSS model. Note that when weights are used in the fitting the length of the residuals can be different from N the length of the fitted values. Observations with weights equal to zero are not appearing in the residuals. Also observations with frequencies as weights will appear more than once according to their frequencies.
Note

The "weighted" residuals of a specified parameter can be zero and one if the square of first derivative have been used in the fitting of this parameter.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

References


(see also http://www.gamlss.org/).

See Also

print.gamlss, summary.gamlss, fitted.gamlss, coef.gamlss, residuals.gamlss, update.gamlss, plot.gamlss, deviance.gamlss, formula.gamlss

Examples

data(aids)
h <- gamlss(y=poly(x,3)+qrt, family=NB1, data=aids) #
plot(aids$x,resid(h))
plot(aids$x,resid(h,"sigma") )
rm(h)

ri

Specify ridge or lasso Regression within a GAMLSS Formula

Description

The function ri() allow the user to fit a ridge regression within GAMLSS. It allows the coefficients of a set of explanatory variables to be shrunk towards zero. The amount of shrinking depends either on lambda, or on the equivalent degrees of freedom (df). The type of shrinking depends on the argument Lp see example.

Usage

ri(X, df = NULL, lambda = NULL, method = c("ML", "GAIC"), order = 0, start = 10, Lp = 2, kappa = 1e-05, iter = 100, c.crit = 1e-06, k = 2)
Arguments

A matrix of explanatory variables X which is standardised (mean=0, sd=1) automatically

the effective degrees of freedom df

the smoothing parameter lambda

which method is used for the estimation of the smoothing parameter, ‘ML’ or ‘GAIC’ are allowed.

the order of the difference applied to the coefficients with default zero. (Do not change this unless there is some ordering in the explanatory variables.)

starting value for lambda if it estimated using ‘ML’ or ‘GAIC’

The type of penalty required, Lp=2 a proper ridge regression is the default. Use codeLp=1 for lasso and different values for different penalties.

a regulation parameters used for the weights in the penalties.

the number of internal iteration allowed see details.

c.crit is the convergent criterion

k is the penalty if ‘GAIC’ method is used.

Details

This implementation of ridge and related regressions is based on an idea of Paul Eilers which used weights in the penalty matrix. The type of weights are defined by the argument Lp. Lp=2 is the standard ridge regression, Lp=1 fits a lasso regression while Lp=0 allows a "best subset" regression see Hastie et al (2009) page 71.

Value

x is returned with class "smooth", with an attribute named "call" which is to be evaluated in the backfitting additive.fit() called by gamlss()

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Paul Eilers

References


(see also http://www.gamlss.org/).
Description

This function plots worm plots, van Buuren and Fredriks M. (2001), or QQ-plots of the normalized randomized quantile residuals (Dunn and Smyth, 1996) for a model using a discrete GAMLSS family distribution.

Usage

rqres.plot(obj = NULL, howmany = 6, plot.type = c("few", "all"),
           type = c("wp", "QQ"), xlim = NULL, ylim = NULL, ...)
get.rqres(obj = NULL, howmany = 10, order = FALSE)

Arguments

obj a fitted GAMLSS model object from a "discrete" type of family
howmany The number randomise quantile residuals required i.e. howmany=6
plot.type whether to plot few of the randomised quantile residual realisations, "few" in a separate plots (there must be less than 8) or all "all" in one plot (with their median)
type whether to plot worm plots "wp"or QQ plots "QQ" with default worm plots
xlim setting manually the xlim of the graph
ylim               setting manually the ylim of the graph
order              whether to order the realization of randomised quantile residuals
...                for extra arguments to be passed to wp()

Details

For discrete family distributions, the \texttt{gamlss()} function saves on exit one realization of randomized quantile residuals which can be plotted using the generic function \texttt{plot} which calls the \texttt{plot.gamlss}. Looking at only one realization can be misleading, so the current function creates QQ-plots for several realizations. The function allows up to 10 QQ-plots to be plotted. Occasionally one wishes to create a lot of realizations and then take a median of them (separately for each ordered value) to create a single median realization. The option all in combinations with the option howmany creates a QQ-plot of the medians of the normalized randomized quantile residuals. These ‘median’ randomized quantile residuals can be saved using the option (save=TRUE).

Value

If save is TRUE then the vector of the median residuals is saved.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>

References


See Also

\texttt{plot.gamlss}, \texttt{gamlss}

Examples

data(aids) # fitting a model from a discrete distribution
h<-gamlss(y~pb(x)+qrt, family=NBI, data=aids) #
plot(h)
# plot qq- plots from 6 realization of the randomized quantile residuals
**Rsq**

*Generalised (Pseudo) R-squared for GAMLSS models*

**Description**

This function gives the generalised R-squared of Nagelkerke (1991) for a GAMLSS model.

**Usage**

```r
Rsq(object, type = c("Cox Snell", "Cragg Uhler", "both"))
```

**Arguments**

- **object**: a GAMLSS object
- **type**: which definition of R squared. Can be the "Cox Snell" or the Nagelkerke, "Cragg Uhler" or "both".

**Details**

The `Rsq()` function uses the definition for R-squared:

\[
R^2 = 1 - \left( \frac{L(0)}{L(\hat{\theta})} \right)^{2/n}
\]

where \(L(0)\) is the null model (only a constant is fitted to all parameters) and \(L(\hat{\theta})\) is the current fitted model. This definition sometimes is referred to as the Cox & Snell R-squared. The Nagelkerke /Cragg & Uhler’s definition divides the above with

\[
1 - L(0)^{2/n}
\]

**Value**

The `Rsq()` produces a single value if type="Cox Snell" or "Cragg Uhler" and a list if type="both".

**Note**

The null model is fitted using the function `gamlssML()` which can create warning messages

**Author(s)**

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>
rvcov

References


(see also http://www.gamlss.org/).

See Also

GAIC

Examples

data(aids)
m1 <- gamlss(y-x+qrt, data=aids, family=NBI)
Rsq(m1)
Rsq(m1, type="both")
rm(m1)

rvcov

Robust Variance-Covariance matrix of the parameters from a fitted GAMLSS model

Description

The function rvcov() is designed for providing robust standard errors for the parameters estimates of a GAMLSS fitted model. The same result can be obtained by using vcov(fitted_model, robust=TRUE). The function get() gets the K matrix (see details below).

Usage

rvcov(object, type = c("vcov", "cor", "se", "coef", "all"),
hessian.fun = c("R", "PB") )
get.K(object, what = c("K", "Deriv"))

Arguments

object a GAMLSS fitted object
type this argument for rvcov() function whether variance-covariance matrix, correlation matrix, standard errors or all of them
what this an argument for the function get.K() allowing to get either K or the first derivative of the likelihood with respect to the parameters (the β’s in the GAMLSS notation).
hessian.fun How to obtain numerically the Hessian i) using optimHess(), option "R" ii) using a function by Pinheiro and Bates taken from package nlme, option "PB".
Details

The robust standard errors are calculated for the robust sandwich estimator of the variance-covariance given by \( S = V K V \) where \( V \) is the standard variance-covariance matrix (the inverse of the information matrix) and \( K \) is an estimate of the variance of the first derivatives of the likelihood. The function \( \text{getNkHI} \) is used to get the required \( K \) matrix.

Value

A variance covariance matrix or other relevant output

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Vlasios Voudouris

References


(see also http://www.gamlss.org/).

See Also

\( \text{vcov}, \ldots \)

Examples

\begin{verbatim}
# generate from a gamma distribution
Y <- rGA(200, mu=1, sigma=2)
hist(Y)
# fitting the wrong model i.e. sigma=1
m1 <- gamlss(Y~1, family=EXP)
# the conventional se is too precise
vcov(m1, type="se")
# the sandwich se is wider
rvcov(m1, type="se")
# fitting the correct model
m2 <- gamlss(Y~1, family=GA)
vcov(m2, type="se")
rvcov(m2, type="se")
# similar standard errors
# also obtained using
vcov(m2, type="se", robust=TRUE)
\end{verbatim}
The function `stepGAIC()` performs stepwise model selection using a Generalized Akaike Information Criterion (GAIC). It is based on the function `stepAIC()` given in the library MASS of Venables and Ripley (2002). The function has been changed recently to allow parallel computation. The parallel computations are similar to the ones performed in the function `boot()` of the `boot` package.

Note that since version 4.3-5 of `gamlss` the `stepGAIC()` do not have the option of using the function `stepGAIC.CH()` through the argument `additive`.

Note that `stepGAIC()` is relying to the `dropterm()` and `addterm()` methods applied to `gamlss` objects. `drop1()` and `add1()` are equivalent methods to the `dropterm()` and `addterm()` respectively but with different default arguments (see the examples).

The function `stepGAIC.VR()` is the old version of `stepGAIC()` with no parallel computations.

The function `stepGAIC.CH()` is based on the S function `step.gam()` (see Chambers and Hastie (1991)) and it is more suited for model with smoothing additive terms when the degrees of freedom for smoothing are fixed in advance. This is something which rarely used these days, as most of the smoothing functions allow the calculations of the smoothing parameter, see for example the additive function `pb()`.

The functions `stepGAIC.VR()` and `stepGAIC.CH()` have been adapted to work with `gamlss` objects and the main difference is the `scope` argument, see below.

While the functions `stepGAIC()` is used to build models for individual parameters of the distribution of the response variable, the functions `stepGAICA11.A()` and `stepGAICA11.A()` are building models for all the parameters.

The functions `stepGAICA11.A()` and `stepGAICA11.B()` are based on the `stepGAIC()` function but use different strategies for selecting an appropriate final model.

`stepGAICA11.A()` has the following strategy:

**Strategy A:**

i) build a model for `mu` using a forward approach.

ii) given the model for `mu` build a model for `sigma` (forward)

iii) given the models for `mu` and `sigma` build a model for `nu` (forward)

iv) given the models for `mu`, `sigma` and `nu` build a model for `tau` (forward)

v) given the models for `mu`, `sigma`, `nu` and `tau` check whether the terms for `nu` are needed using backward elimination.

vi) given the models for `mu`, `sigma`, `nu` and `tau` check whether the terms for `sigma` are needed (backward).

vii) given the models for `mu`, `sigma`, `nu` and `tau` check whether the terms for `mu` are needed (backward).

Note for this strategy to work the `scope` argument should be set appropriately.
stepGAICall.B() uses the same procedure as the function stepGAIC() but each term in the scope is fitted to all the parameters of the distribution, rather than the one specified by the argument what of stepGAIC(). The stepGAICall.B() relies on the addAll() and dropAll() functions for the selection of variables.

Usage

stepGAIC(object, scope, direction = c("both", "backward", "forward"),
          trace = T, keep = NULL, steps = 1000, scale = 0,
          what = c("mu", "sigma", "nu", "tau"),
          parameter = NULL, k = 2,
          parallel = c("no", "multicore", "snow"),
          ncpus = 1L, cl = NULL, ...)

stepGAIC.VR(object, scope, direction = c("both", "backward", "forward"),
             trace = T, keep = NULL, steps = 1000, scale = 0,
             what = c("mu", "sigma", "nu", "tau"),
             parameter = NULL, k = 2,
             parallel = c("no", "multicore", "snow"),
             ncpus = 1L, cl = NULL, ...)

stepGAIC.CH(object, scope = gamlss.scope(model.frame(object)),
             direction = c("both", "backward", "forward"),
             trace = T,
             keep = NULL, steps = 1000,
             what = c("mu", "sigma", "nu", "tau"),
             parameter = NULL, k = 2,
             parallel = c("no", "multicore", "snow"),
             ncpus = 1L, cl = NULL, ...)

stepGAICall.A(object, scope = NULL, sigma.scope = NULL, nu.scope = NULL,
               tau.scope = NULL, mu.try = TRUE, sigma.try = TRUE,
               nu.try = TRUE, tau.try = TRUE,
               parallel = c("no", "multicore", "snow"),
               ncpus = 1L, cl = NULL, ...)

stepGAICall.B(object, scope, direction = c("both", "backward", "forward"),
               trace = T, keep = NULL, steps = 1000, scale = 0, k = 2,
               parallel = c("no", "multicore", "snow"),
               ncpus = 1L, cl = NULL, ...)

dropAll(object, scope, test = c("Chisq", "none"), k = 2, sorted = FALSE,
        trace = FALSE, parallel = c("no", "multicore", "snow"),
        ncpus = 1L, cl = NULL, ...)

addAll(object, scope, test = c("Chisq", "none"), k = 2, sorted = FALSE,
       trace = FALSE, parallel = c("no", "multicore", "snow"),
       ncpus = 1L, cl = NULL, ...)

Arguments

object

an gamlss object. This is used as the initial model in the stepwise search.
scope defines the range of models examined in the stepwise search. For the function `stepAIC()` this should be either a single formula, or a list containing components upper and lower, both formulae. See the details for how to specify the formulae and how they are used. For the function `stepGAIC` the scope defines the range of models examined in the step-wise search. It is a list of formulae, with each formula corresponding to a term in the model. A 1 in the formula allows the additional option of leaving the term out of the model entirely. +

direction the mode of stepwise search, can be one of both, backward, or forward, with a default of both. If the scope argument is missing the default for direction is backward.

trace if positive, information is printed during the running of `stepAIC`. Larger values may give more information on the fitting process.

keep a filter function whose input is a fitted model object and the associated 'AIC' statistic, and whose output is arbitrary. Typically 'keep' will select a subset of the components of the object and return them. The default is not to keep anything.

steps the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.

scale scale is not used in `gamlss`

what which distribution parameter is required, default what="mu"

parameter equivalent to what

k the multiple of the number of degrees of freedom used for the penalty. Only 'k = 2' gives the genuine AIC: 'k = log(n)' is sometimes referred to as BIC or SBC.

parallel The type of parallel operation to be used (if any). If missing, the default is "no".

ncpus integer: number of processes to be used in parallel operation: typically one would chose this to the number of available CPUs.

cl An optional parallel or snow cluster for use if `parallel = "snow"`. If not supplied, a cluster on the local machine is created for the duration of the call.

sigma.scope scope for sigma if different to scope in stepGAICall.A()

nu.scope scope for nu if different to scope in stepGAICall.A()

tau.scope scope for tau if different to scope in stepGAICall.A()

mu.try The default value is is TRUE, set to FALSE if no model for mu is needed

sigma.try The default value is TRUE, set to FALSE if no model for sigma is needed

nu.try The default value is TRUE, set to FALSE if no model for nu is needed

tau.try The default value is TRUE, set to FALSE if no model for tau is needed

test whether to print the chi-square test or not

sorted whether to sort the results

... any additional arguments to 'extractAIC'. (None are currently used.)
Details

The set of models searched is determined by the scope argument.

For the function `stepGAIC.VR()` the right-hand-side of its lower component is always included in the model, and right-hand-side of the model is included in the upper component. If scope is a single formula, it specifies the upper component, and the lower model is empty. If scope is missing, the initial model is used as the upper model.

Models specified by scope can be templates to update object as used by `update.formula`.

For the function `stepGAIC.CH()` each of the formulas in scope specifies a "regimen" of candidate forms in which the particular term may enter the model. For example, a term formula might be

\[- x1 + \log(x1) + cs(x1, df=3)\]

This means that \(x1\) could either appear linearly, linearly in its logarithm, or as a smooth function estimated non-parametrically. Every term in the model is described by such a term formula, and the final model is built up by selecting a component from each formula.

The function `gamlss.scope` similar to the S `gam.scope()` in Chambers and Hastie (1991) can be used to create automatically term formulae from specified data or model frames.

The supplied model object is used as the starting model, and hence there is the requirement that one term from each of the term formulas of the parameters be present in the formula of the distribution parameter. This also implies that any terms in formula of the distribution parameter not contained in any of the term formulas will be forced to be present in every model considered.

When the smoother used in `gamlss` modelling belongs to the new generation of smoothers allowing the determination of the smoothing parameters automatically (i.e. \(pb()\), \(cy()\)) then the function `stepGAIC.VR()` can be used for model selection (see example below).

Value

the stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the 'keep=' argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood.

The function `stepGAICALL.A()` returns with a component "anovaAll" containing all the different anova tables used in the process.

Author(s)

Mikis Stasinopoulos based on functions in MASS library and in Statistical Models in S

References


See Also

gamlss.scope

Examples

```r
## Not run:
data(usair)
#
# null model
mod0 <- gamlss(y~1, data = usair, family = GA)
# all the explanatory variables x1:x6 fitted linearly
mod1 <- gamlss(y - ., data = usair, family = GA)

# dropping terms
dropterm(mod1)
# with chi-square information
drop1(mod1)
# for parallel computations use something like
defectCores()
drop1(mod1, parallel = "snow", ncpus = nC)
drop1(mod1, parallel = "multicore", ncpus = nC)

# adding terms
addterm(mod0, scope = as.formula(paste("-", paste(names(usair[-1]),
collapse = "+"), sep = "")))
# with chi-square information
add1(mod0, scope = as.formula(paste("-", paste(names(usair[-1]),
collapse = "+"), sep = "")))
# for parallel computations
defectCores()
add1(mod0, scope = as.formula(paste("-", paste(names(usair[-1]),
collapse = "+"), sep = "")), parallel = "snow", ncpus = nC)

# stepGAIC
# find the best subset for the mu
mod2 <- stepGAIC(mod1)
mod2$anova
# for parallel computations
mod2$ <- stepGAIC(mod1, parallel = "snow", ncpus = nC)
# find the best subset for sigma
mod3 <- stepGAIC(mod2, what = "sigma", scope = ~x1+x2+x3+x4+x5+x6)
mod3$anova
```
# find the best model using pb() smoother
only three variables are used here for simplicity

mod20<-stepGAIC(mod0, scope=list(lower=-1, upper=-pb(x1)+pb(x2)+pb(x5)))
edf(mod20)

# note that x1 and x2 enter linearly

# the stepGAIC.CH function (no parallel here)
# creating a scope from the usair model frame
gs<-gamlss.scope(model.frame(y=x1*x2+x3*x4+x5+x6, data=usair))
gs
mod5<-stepGAIC.CH(mod0, gs)
mod5$anova

# now stepGAICAll.A
mod7<-stepGAICAll.A(mod0, scope=list(lower=-1, upper=-x1*x2+x3*x4+x5*x6))

# now stepGAICAll.B
drop1All(mod1, parallel="snow", ncpus=nC)
add1All(mod0, scope=as.formula(paste("~", paste(names(usair[-1]),
collapse="+"))), parallel="snow", ncpus=nC)
mod8<-stepGAICAll.B(mod0, scope=list(lower=-1, upper=-x1*x2+x3*x4+x5*x6))

## End(Not run)

---

**summary.gamlss**

*Summarizes a GAMLSS fitted model*

**Description**

`summary.gamlss` is the GAMLSS specific method for the generic function `summary` which summarize objects returned by modelling functions.

**Usage**

```r
## S3 method for class 'gamlss'
summary(object, type = c("vcov", "qr"),
  robust=FALSE, save = FALSE,
  hessian.fun = c("R", "PB"),
  digits = max(3,getOption("digits") - 3),...)
```

**Arguments**

- **object**: a GAMLSS fitted model
type

the default value vcov uses the vcov() method for gamlss to get the variance-covariance matrix of the estimated beta coefficients, see details below. The alternative qr is the original method used in gamlss to estimated the standard errors but it is not reliable since it do not take into the account the inter-correlation between the distributional parameters mu, sigma, nu and tau.

robust
whether robust (sandwich) standard errors are required

save
whether to save the environment of the function so to have access to its values

hessian.fun
whether when calculate the Hessian should use the "R" function optimHess() or a function based on Pinheiro and Bates nlme package, "PB".

digits
the number of digits in the output

... for extra arguments

Details

Using the default value type="vcov", the vcov() method for gamlss is used to get the variance-covariance matrix (and consequently the standard errors) of the beta parameters. The variance covariance matrix is calculated using the inverse of the numerical second derivatives of the observed information matrix. This is a more reliable method since it take into the account the inter-correlation between the all the parameters. The type="qr" assumes that the parameters are fixed at the estimated values. Note that both methods are not appropriate and should be used with caution if smoothing terms are used in the fitting.

Value

Print summary of a GAMLSS object

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby and Calliope Akantziliotou

References


(see also http://www.gamlss.org/).

See Also

gamlss, deviance.gamlss, fitted.gamlss
Examples

```r
data(aids)
h<-gamlss(y~poly(x,3)+qrt, family=PO, data=aids) #
summary(h)
rm(h)
```

---

**term.plot**

*Plot regression terms for a specified parameter of a fitted GAMLSS object*

---

Description

Plots regression terms against their predictors, optionally with standard errors and partial residuals added. It is based on the R function `termplot` but is suitably changed to apply to GAMLSS objects.

Usage

```r
term.plot(object, what = c("mu", "sigma", "nu", "tau"),
          parameter = NULL, data = NULL,
          envir = environment(formula(object)), partial.resid = FALSE,
          rug = FALSE, terms = NULL, se = TRUE, ylim = c("common", "free"),
          scheme = c("shaded", "lines"), xlabs = NULL, ylabs = NULL,
          main = NULL, pages = 0, col.term = "darkred",
          col.se = "orange", col.shaded = "gray", col.res = "lightblue",
          col.rug = "gray", lwd.term = 1.5, lty.se = 2, lwd.se = 1,
          cex.res = 1, pch.res = par("pch"),
          ask = interactive() & & nb.fig < n.tms & & .Device != "postscript",
          use.factor.levels = TRUE, surface.gam = FALSE,
          polys = NULL, polys.scheme = "topo", ...)
```

Arguments

- **object**: a fitted GAMLSS object
- **what**: the required parameter of the GAMLSS distribution i.e. "mu"
- **parameter**: equivalent to what
- **data**: data frame in which variables in object can be found
- **envir**: environment in which variables in object can be found
- **partial.resid**: logical; should partial residuals be plotted or not
- **rug**: add rug plots (jitter 1-d histograms) to the axes?
- **terms**: which terms to be plotted (default 'NULL' means all terms)
- **se**: plot point-wise standard errors?
there are two options here a) "common" and b) "free". The "common" option plots all figures with the same ylim range and therefore allows the viewer to check the relative contribution of each terms compate to the rest. In the 'free' option the limits are computed for each plot separately.

whether the se’s should appear shaded or as lines

vector of labels for the x axes

vector of labels for the y axes

logical, or vector of main titles; if 'TRUE', the model’s call is taken as main title, 'NULL' or 'FALSE' mean no titles.
in how many pages the plot should appear. The default is 0 which allows differnt page for each plot
the colour of the term line
the colour of the se’s lines
the colour of the shaded area
the colour of the partial residuals
the colour of the rug
line width of the fitted terms
line type for standard errors
line width for the standard errors
plotting character expansion for the partial residuals
characters for points in the partial residuals
logical; if 'TRUE', the user is asked before each plot, see 'par(ask=.)'.

Should x-axis ticks use factor levels or numbers for factor terms?
whether to use surface plot if a ga() term is fitted
The polygone nformation filr for MRF models
Color scheme for polygones for RMF models
other graphical parameters

The function uses the lpred function of GAMLSS. The 'data' argument should rarely be needed, but in some cases 'termplot' may be unable to reconstruct the original data frame. Using 'na.action=na.exclude' makes these problems less likely. Nothing sensible happens for interaction terms.

a plot of fitted terms.

Mikis Stasinopoulos based on the existing termplot() function
References

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and

online.org/v23/i07.

Regression and Smoothing: Using GAMLSS in R, Chapman and Hall/CRC.
(see also http://www.gamlss.org/).

See Also
termplot

Examples

data(aids)
a<-gamlss(y~pb(x)+qrt,data=aids,family=NBI)
term.plot(a, pages=1)
rm(a)

update.gamlss  
Update and Re-fit a GAMLSS Model

Description

update.gamlss is the GAMLSS specific method for the generic function update which updates
and (by default) refits a GAMLSS model.

Usage

## S3 method for class 'gamlss'
update(object, formula, ..., 
what = c("mu", "sigma", "nu", "tau", "All"),
parameter= NULL, evaluate = TRUE)

Arguments

object  a GAMLSS fitted model
formula.  the formula to update
...  for updating argument in gamlss()
what  the parameter in which the formula needs updating for example "mu", "sigma", "nu" "tau" or "All". If "All" all the formulae are updated. Note that the what argument has an effect only if only if the argument formula. is set
parameter  equivalent to what
evaluate  whether to evaluate the call or not
Value

Returns a GAMLSS call or fitted object.

Author(s)

Mikis Stasinopoulos <mikis.stasinopoulos@gamlss.org>, Bob Rigby

References


(see also http://www.gamlss.org/).

See Also

print.gamlss, summary.gamlss, fitted.gamlss, coef.gamlss, residuals.gamlss, plot.gamlss, deviance.gamlss, formula.gamlss

Examples

data(aids)
# fit a poisson model
h.po <-gamlss(y~pb(x)+qrt, family=P0, data=aids)
# update with a negative binomial
h.nb <-update(h.po, family=NBI)
# update the smoothing
h.nb1 <-update(h.nb,~cs(x,8)+qrt)
# remove qrt
h.nb2 <-update(h.nb1,~-qrt)
# put back qrt take log of y and fit a normal distribution
h.nb3 <-update(h.nb1,log(.)+qrt, family=NQ)
# verify that it is the same
h.no<-gamlss(log(y)~-cs(x,8)+qrt,data=aids )

VC.test          Vuong and Clarke tests

Description

The Vuong and Clarke tests for GAMLSS fitted models.
Usage

VC.test(obj1, obj2, sig.lev = 0.05)

Arguments

obj1 The first fitted gamlss object
obj2 The second fitted gamlss object
sig.lev Significance level used for testing.

Details

The Vuong (1989) and Clarke (2007) tests are likelihood-ratio-based tests for model selection that use the Kullback-Leibler information criterion. The implemented tests can be used for choosing between two bivariate models which are non necessary nested.

In the Vuong test, the null hypothesis is that the two models are equally close to the actual model, whereas the alternative is that one model is closer. The test follows asymptotically a standard normal distribution under the null. Assume that the critical region is ($-c, c$), where $c$ is typically set to 1.96. If the value of the test is greater than $c$ then we reject the null hypothesis that the models are equivalent in favour of the model in obj1. Vice-versa if the value is smaller than $-c$ we reject the null hypothesis that the models are equivalent in favour of the model in obj2. If the value falls within $(-c, c)$ then we cannot discriminate between the two competing models given the data.

In the Clarke test, if the two models are statistically equivalent then the log-likelihood ratios of the observations should be evenly distributed around zero and around half of the ratios should be larger than zero. The test follows asymptotically a binomial distribution with parameters $n$ and 0.5. Critical values can be obtained as shown in Clarke (2007). Intuitively, the model in obj1 is preferred over that in obj2 if the value of the test is significantly larger than its expected value under the null hypothesis (‘coden/2), and vice versa. If the value is not significantly different from $n/2$ then obj1 can be thought of as equivalent to obj2.

Value

For the Vuong test it returns its value and the decision and for the Clarke test returns the value the p-value and the decision. Decisions criteria are as discussed above.

Author(s)

Mikis Stasinopoulos and Giampierro Marra

References


See Also

LR.test
Examples

library(gamlss)
# fitting different models
m0 <- gamlss(y~x+qrt, data=aids, family=PO)
m1 <- gamlss(y~pb(x)+qrt, data=aids, family=PO)
m2 <- gamlss(y~pb(x)+qrt, data=aids, family=NBI)
# comparison of the models
VC.test(m0,m2)
VC.test(m0,m1)
VC.test(m1,m2)

Worm plot

Description

Provides a single plot or multiple worm plots for a GAMLSS fitted or more general for any fitted models where the method resid() exist and the residuals are defined sensibly. The worm plot (a de-trended QQ-plot), van Buuren and Fredriks M. (2001), is a diagnostic tool for checking the residuals within different ranges (by default not overlapping) of the explanatory variable(s).

Usage

wp(object = NULL, xvar = NULL, resid = NULL, n.inter = 4,
    xcut.points = NULL, overlap = 0, xlim.all = 4,
    xlim.worm = 3.5, show.given = TRUE, line = TRUE,
    ylim.all = 12 * sqrt(1/length(resid)),
    ylim.worm = 12 * sqrt(n.inter/length(resid)),
    cex = 1, cex.lab = 1, pch = 21, ...
)

Arguments

object a GAMLSS fitted object or any other fitted model where the resid() method works (preferably it should be standardised or quantile residuals)
xvar the explanatory variable(s) against which the worm plots will be plotted. If only one variable is involved use xvar=x1 if two variables are involved use xvar=x1*x2. See also note below for use of formula if the data argument is not found in the fitted model
resid if object is missing this argument can be used to specify the residual vector (again it should a quantile residuals or it be assumed to come from a normal distribution)
n.inter the number of intervals in which the explanatory variable xvar will be cut
xcut.points the x-axis cut off points e.g. c(20, 30). If xcut.points=NULL then the n.inter argument is activated
overlap how much overlapping in the xvar intervals. Default value is overlap=0 for non overlapping intervals
xlim.all  for the single plot, this value is the x-variable limit, default is xlim.all=4
xlim.worm  for multiple plots, this value is the x-variable limit, default is xlim.worm=3.5
show.given whether to show the x-variable intervals in the top of the graph, default is show.given=TRUE
line whether to plot the polynomial line in the worm plot, default value is line=TRUE
ylim.all  for the single plot, this value is the y-variable limit, default value is ylim.all=12*sqrt(1/length(fitted))
ylim.worm for multiple plots, this values is the y-variable limit, default value is ylim.worm=12*sqrt(n.inter/length(fitted))
cex the cex plotting parameter for changing the side of worm with default cex=1
cex.lab the cex plotting parameter for changing the size of the axis labels
pch the pch plotting parameter with default pch=21
... for extra arguments

Details
If the xvar argument is not specified then a single worm plot is used. In this case a worm plot is a de-trended normal QQ-plot so departure from normality is highlighted.

If a single xvar is specified (with or without the use of a formula) i.e. xvar=x1 or xvar=~x1) then we have as many worm plot as n.iter. In this case the x-variable is cut into n.iter intervals with an equal number observations and de-trended normal QQ (i.e. worm) plots for each interval are plotted. This is a way of highlighting failures of the model within different ranges of the the single explanatory variable. The fitted coefficients from fitting cubic polynomials to the residuals (within each x-variable interval) can be obtain by e.g. coeffs<-wp(model1,xvar=x,n.iter=9). van Buren and Fredriks M. (2001) used these residuals to identify regions (intervals) of the explanatory variable within which the model does not fit adequately the data (called “model violation”)

Two variables can be displayed with the use of a formula, i.e. xvar=~x1*x2. In this case the n.iter can be a vector with two values.

Value
For multiple plots the xvar intervals and the coefficients of the fitted cubic polynomials to the residuals (within each xvar interval) are returned.

Note
Note that the wp() function, if the argument object is used, is looking for the data argument of the object. If the argument data exists it uses its environment to find xvar (whether it is a formula or not). As a result if data exists within object xvar=~x*f can be used (assuming that x and f are in the data) otherwise the variable should be explicitly defined i.e. xvar=~data$x*data$f.

Author(s)
Mikis Stasinopoulos and Bob Rigby
References


See Also
gamlss, plot.gamlss

Examples

data(abdom)
# with data
a<-gamlss(y~pb(x),sigma.fo=-pb(x,1),family=LO, data=abdom)
wp(a)
coeff1<-wp(a,xvar=x)
coeff1
## Not run:
# no data argument
b <- gamlss(abdom$y~pb(abdom$x),sigma.fo=-pb(abdom$x),family=LO)
wp(b)
wp(b, xvar=abdom$x)# not wp(b, xvar=x)
# using the argument resid
# this will work
wp(resid=resid(a), xvar=abdom$x)
# not this
# wp(resid=resid(a), xvar=x)
# this example uses the rent data
ml <- gamlss(R~pb(Fl)+pb(A)+loc, sigma.fo=-pb(Fl)+pb(A), data=rent, family=GA)
# a single worm plot
wp(ml, ylim.all=0.5)
# a single continuous x variable
wp(ml, xvar=Fl, ylim.worm=.8)
# a single x variable changing the default number of intervals
wp(ml, xvar=Fl, ylim.worm=1.5, n.inter=9)
# different x variable changing the default number of intervals
B1<-wp(ml, xvar=A, ylim.worm=1.2, n.inter=9)
B1
# the number five plot has intervals
# [5,] 1957.5 1957.5
# rather disappointing
# try formula for xvar
wp(ml, xvar=-A, ylim.worm=1.2, n.inter=9)
z.scores

Z-scores for lms objects

Description
This creates z-scores for new values of y and x given a fitted lms object.

Usage
z.scores(object, y, x)

Arguments

object a lms fitted object
y new y values
x new x values

Details
This is simply a job that can be also done by centiles.pred().

Value
the required z-scores

Author(s)
Mikis Stasinopoulos
z.scores

References

Cole, T. J. and Green, P. J. (1992) Smoothing reference centile curves: the LMS method and penal-
ized likelihood, Statist. Med. 11, 1305–1319
Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and
Flexible Regression and Smoothing: Using GAMLSS in R, Chapman and Hall/CRC.
(see also http://www.gamlss.org/).

See Also
centiles.pred

Examples

## Not run:
IND<-sample.int(7040, 1000, replace=FALSE)
db1 <- db[IND,]
plot(head~age, data=db1)
m0 <- lms(head, age, data=db1,trans.x=TRUE )
z.scores(m0, x=c(2,15,30,40),y=c(45,50,56,63))
## End(Not run)
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