

Package ‘gamlss.ggplots’

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Title Plotting Functions for Generalized Additive Model for Location
Scale and Shape

Version 2.1-12

Date 2024-04-21

Description Functions for plotting Generalized Additive Models for Loca-
tion Scale and Shape from the 'gamlss' package, Stasinopou-
los and Rigby (2007) <[doi:10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07)>, using the graphical methods from 'ggplot2'.

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URL <https://www.gamlss.com/>

BugReports <https://github.com/gamlss-dev/gamlss.ggplots/issues>

Depends R (>= 3.5.0), gamlss.dist, gamlss (>= 4.3.3), gamlss.foreach

Imports methods, ggridges, ellipse, gamlss.inf, foreach, mgcv,
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Suggests glmnet, reshape2, igraph, networkD3, grid, gridExtra

LazyLoad yes

NeedsCompilation no

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gamlss.ggplots-package

Plotting Functions for Generalized Additive Model for Location Scale and Shape

Description

Functions for plotting Generalized Additive Models for Location Scale and Shape from the 'gamlss' package, Stasinopoulos and Rigby (2007) <doi:10.18637/jss.v023.i07>, using the graphical methods from 'ggplot2'.

Details

The DESCRIPTION file:

Package:	gamlss.ggplots
Title:	Plotting Functions for Generalized Additive Model for Location Scale and Shape
Version:	2.1-12
Date:	2024-04-21
Authors@R:	c(person("Mikis", "Stasinopoulos", role = c("aut", "cre", "cph"), email = "d.stasinopoulos@gre.ac.uk", comment = NA), NA)

Description: Functions for plotting Generalized Additive Models for Location Scale and Shape from the 'gamlss' package,
 License: GPL-2 | GPL-3
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 Depends: R (>= 3.5.0), gamlss.dist, gamlss (>= 4.3.3), gamlss.foreach
 Imports: methods, ggridges, ellipse, gamlss.inf, foreach, mgcv, ggplot2, yaImpute
 Suggests: glmnet, reshape2, igraph, networkD3, grid, gridExtra
 LazyLoad: yes
 Author: Mikis Stasinopoulos [aut, cre, cph] (<<https://orcid.org/0000-0003-2407-5704>>), Robert Rigby [aut] (<<https://orcid.org/0000-0002-1166-004X>>)
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Index of help topics:

ACE	Alternating Conditional Expectations
boot_coef	Plotting Bootstrap Coefficients
centile_bucket	Centile bucket plot
family_pdf	Plotting Probabilities Density Functions (pdf's) for GAMLSS
fit_PB	P-spline smoother
fitted_cdf	Plotting Cumulative Distribution Functions (cdf's) for GAMLSS,
fitted_centiles	Plotting centile (growth) curves
fitted_devianceIncr	Plotting the deviance increment of GAMLSS
fitted_leverage	Plot of the linear leverage of a GAMLSS model
fitted_terms	Plotting fitted additive terms
gamlss.ggplots-package	Plotting Functions for Generalized Additive Model for Location Scale and Shape
histSmo_plot	Supporting histSmo()
model_GAIC	Plotting GAIC for GAMLSS models
model_pca	Plotting residuals using PCA
moment_bucket	Moment bucket plot
moment_gray_half	Functions to create the background for the bucket plots
pcr_coef_path	Plotting the fitted path of a PCR model.
pe_param	Partial Effect of a term on the parameters and predictors
pe_pdf	Partial Effect of a term on the response distribution
prof_term	Plotting the profile deviance of one fitted term
resid_density	Density of the residuals in a GAMLSS model
resid_dtop	Detrended Transformed Owen's Plot and ECDF for the residuals
resid_index	A residual plots
resid_qqplot	QQ-plot of the residuals of a GAMLSS model
resid_symmetry	Symmetry plots

```

resid_wp           Worm plot using ggplot2
resp_mu            Plotting the response against quantities of the
                   fitted model
y_hist             Histogram and density plot.

```

The following convention has been used to name the functions:

`fitted_NAME`: plots concerning fitted values from a single fitted model

`resid_NAME`: plots concerning residuals from a single fitted model

`predict_NAME`: plots concerning prediction values from a single fitted model usually having `newdata` option.

`model_NAME`: plots concerning different fitted models

where NAME refer to different characteristics.

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Maintainer: Mikis Stasinopoulos <d.stasinopoulos@gre.ac.uk>

References

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

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, [doi:10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.

Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, [doi:10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. [doi:10.1201/b21973](https://doi.org/10.1201/b21973)

Stasinopoulos, M. D., Rigby, R. A., and De Bastiani F., (2018) GAMLSS: a distributional regression approach, *Statistical Modelling*, Vol. **18**, pp, 248-273, SAGE Publications Sage India: New Delhi, India.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[gamlss](#), [gamlss.family](#)

Examples

```
library(gamlss)
m1 <- gamlss(y~pb(x), data=abdom)
resid_index(m1)
```

ACE

Alternating Conditional Expectations

Description

The function ACE() uses the alternating conditional expectations algorithm to find a transformations of y and x that maximise the proportion of variation in y explained by x. It is a less general function than the ace() function of the package ‘acepack’ in that it takes only one explanatory variable. The function ACE() is used by the function mcor() to calculate the maximal correlation between x and y.

Usage

```
ACE(x, y, weights, data = NULL, con_crit = 0.001,
    fit.method = c("loess", "P-splines"), nseg = 10,
    max.df = 6, ...)

mcor(x, y, data = NULL, fit.method = c("loess", "P-splines"),
    nseg = 10, max.df = 6, ...)
```

Arguments

x	the unique x-variables
y	the y-variable
weights	prior weights
data	a data frame for y, x and weights
con_crit	the convergence criterio of the algorithm
fit.method	the method use to fit the smooth functions \$t_1()\$ and \$t_2()\$
nseg	the number of knots
max.df	the maximum od df allowed
...	arguments to pass to the fitted functions fir_PB or loess()

Details

The function ACE is a simplified version of the function ace() of the package **acepack**.

Value

A fitted ACE model with methods print.ACE() and plot.ACE()

Author(s)

Mikis Stasinopoulos

References

- Eilers, P. H. C. and Marx, B. D. (1996). Flexible smoothing with B-splines and penalties (with comments and rejoinder). *Statist. Sci.*, **11**, 89-121.
- Rigby, R. A. and Stasinopoulos D. M.(2005). Generalized additive models for location, scale and shape, (with discussion),*Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

`fit_PB`

Examples

```
data(rent)
ACE(F1, R, data=rent)
pp <- ACE(F1, R, data=rent)
pp
plot(pp)
mcov(F1, R, data=rent)
```

`boot_coef`

Plotting Bootstrap Coefficients

Description

The function `boot_coef()` plots in one or multiple pages the results from a bootstrap generated by the function `BayesianBoot()`, `NonParametricBoot` or `nonpar_boot()`.

The function `boot_coef_one()` plots a single parameter.

Usage

```
boot_coef(x, terms = NULL, hist.col = "black",
          hist.fill = "white", dens.fill = "#FF6666",
          alpha = 0.2, nrow = NULL, ncol = NULL,
          plots.per.page = 9, one.by.one = FALSE, title, ...)

boot_coef_one(x, par = 1, rug = TRUE, alpha = 0.2, hist.col = "black",
               hist.fill = "white", line.col = "gray",
               dens.fill = "#FF6666", title, ...)
```

Arguments

x	a Bayesian.boot or NonParametric.boot object
terms	which terms to plot (default NULL means all terms)
par	which parameter to plot
hist.col	colour of the border histogram
hist.fill	the colour of the histogram
dens.fill	the colour of the density estimate
alpha	transparency constant
nrow	how many rows
ncol	how many columns
plots.per.page	the maximum plots per page
one.by.one	whether single plots
rug	whether rug is required for boot_coef_one()
line.col	the vertical line colour for boot_coef_one()
title	the title
...	for more argument

Details

The function plots in one or multiple pages the results from a bootstrap simulation

Value

Creates a ggplot object

Author(s)

Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

[term.plot](#)

Examples

```
data(aids)
a <- gamlss(y ~ pb(x) + qrt, data = aids, family = NBI)
registerDoParallel(cores = 2)
B1 <- BayesianBoot(a, B=100)
stopImplicitCluster()
boot_coef(B1)
```

centile_bucket

Centile bucket plot

Description

A bucket plot is a graphical way to check the skewness and kurtosis of a continuous variable or the residuals of a fitted GAMLSS model. It plots the centile skewness (tail or central) and transformed centile kurtosis of the variable (or residuals) together with a cloud of points obtained using a non-parametric bootstrap from the original variable (or residuals). It also provides a graphical way of performing a Monte Carlo simulation test on whether the centile skewness and transformed centile kurtosis of the variable of interest are simultaneously equal to zero.

There are two function here:

- i) `cenlile_bucket()` for a single bucket plot. Note that `model_cent_bucket()` and `centile_bucket()` are synonymous.
- ii) `centile_bucket_wrap()` for multiple bucket plots cut according to terms in the model.

Usage

```
centile_bucket(x, ..., type = c("tail", "central"), weights = NULL,
  no_bootstrap = 99, col_bootstrap = hcl.colors(length.obj,
  palette = "Set 2"), alpha_bootstrap = 1, text_to_show = NULL,
  cex_text = 5, col_text = "black", colour_bucket = FALSE,
  line_width = 0.5, sim_test = FALSE, no_sim_test = 1000,
  col_sim_test = gray(0.7), alpha_sim_test = 0.1, seed_test = 1234)

model_cent_bucket(x, ..., type = c("tail", "central"), weights = NULL,
  no_bootstrap = 99, col_bootstrap = hcl.colors(length.obj,
  palette = "Set 2"), alpha_bootstrap = 1, text_to_show = NULL,
  cex_text = 5, col_text = "black", colour_bucket = FALSE,
  line_width = 0.5, sim_test = FALSE, no_sim_test = 1000,
  col_sim_test = gray(0.7), alpha_sim_test = 0.1, seed_test = 1234)

centile_bucket_wrap(x, ..., type = c("tail", "central"), weights = NULL,
  xvar = NULL, n_inter = 4, no_bootstrap = 99,
  col_bootstrap = hcl.colors(length.obj, palette = "Set 2"),
  alpha_bootstrap = 1, text_to_show = NULL, check_overlap_text = FALSE,
  cex_text = 5, col_text = "black", colour_bucket = FALSE,
  line_width = 0.5, sim_test = FALSE, no_sim_test = 1000,
  col_sim_test = gray(0.7), alpha_sim_test = 0.1, seed_test = 1234)
```

Arguments

x	x should be a continuous vector of a GAMLSS fitted model.
...	for more than one continuous vectors or fitted models
type	whether "tail" or "central" skewness and kurtosis
weights	if priors weights are needed
no_bootstrap	the number of bootstrap samples for the cloud around the point of skewness and kurtosis.
col_bootstrap	The colour of the bootstrap samples
alpha_bootstrap	The transparency parameter of the bootstrap samples.
text_to_show	what text to show in the plots, default the names of vectors or models
cex_text	the character size of the text
col_text	the colour of the text
colour_bucket	whether colour or gray lines in the bucket
line_width	the line width
sim_test	whether to Monde Carlo simulation is needed to check the null hypothesis that there is no centile skewness and transformed centile kurtosis in the sample.
no_sim_test	The number of simulation for the test

col_sim_test	the colour used for displaying the Monde Carlo test values
alpha_sim_test	The transparency parameter of the Monde Carlo samples.
seed_test	A seed value for the Monde Carlo simulation.
xvar	the x term
n_inter	how many intervals needed
check_overlap_text	whether to check overlapping text

Details

More details about centile bucket plots is given in De Bastiani *et al.* (2022)

Value

A plot displaying the centile skewness and transformed centile kurtosis of the sample or residual of a model.

Note

The bucket plot provides an additional residual diagnostic tool that can be used for fitted model checking, alongside other diagnostic tools, for example worm plots, and Q (and Z) statistics.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- De Bastiani, F., Stasinopoulos, D. M., Rigby, R. A., Heller, G. Z., and Lucas A. (2022) Bucket Plot: A Visual Tool for Skewness and Kurtosis Comparisons. To be published.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:[10.1201/9780429298547](https://doi.org/10.1201/9780429298547) An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi:[10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:[10.1201/b21973](https://doi.org/10.1201/b21973)
- Stasinopoulos, M. D., Rigby, R. A., and De Bastiani F., (2018) GAMLSS: a distributional regression approach, *Statistical Modelling*, Vol. **18**, pp. 248-273, SAGE Publications Sage India: New Delhi, India.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

[wp](#), [Q.stats](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A), data=rent, family=GA)
centile_bucket(m1)

centile_bucket_wrap(m1, xvar=rent$A)
```

family_pdf

*Plotting Probabilities Density Functions (pdf's) for GAMLSS***Description**

The function `family_pdf()` takes a GAMLSS family distribution and plots different pdf's according to the specified parameters.

The function `fitted_pdf()` takes a `gamlss` fitted object and plots the fitted distributions for specified observations.

The function `fitted_pdf_data()` it does the same as `fitted_pdf()` but it adds also the observation values as grey vertical lines.

The function `predict_pdf()` takes a fitted object and test data and plots the predictive pdf's.

Usage

```
family_pdf(family = NO(), mu = NULL, sigma = NULL, nu = NULL, tau = NULL,
           title, from = 0, to = 10, no.points = 201,
           alpha = 0.4, col.fill = hcl.colors(lobs, palette = "viridis"),
           size.seqment = 1.5, plot.point = TRUE, size.point = 1,
           plot.line = TRUE, size.line = 0.2, ...)

fitted_pdf(model, obs, title, from = 0, to = 10, no.points = 201, alpha = 0.4,
           col.fill = hcl.colors(lobs, palette = "viridis"),
           size.seqment = 1.5, plot.point = TRUE, size.point = 1, plot.line = TRUE,
           size.line = 0.2, ...)

fitted_pdf_data(model, obs, from, to, ...)

predict_pdf(model, newdata, title, from = 0, to = 10, no.points = 201,
            alpha = 0.4, col.fill = hcl.colors(lobs, palette = "viridis"),
            size.seqment = 1.5, plot.point = TRUE, size.point = 1,
            plot.line = TRUE, size.line = 0.2, ...)
```

Arguments

<code>family</code>	A GAMLSS family
<code>model</code>	A GAMLSS fitted model
<code>obs</code>	observations to plot fitted distributions
<code>newdata</code>	for test data
<code>mu</code>	the <code>mu</code> parameter value(s)
<code>sigma</code>	the <code>sigma</code> parameter value(s)
<code>nu</code>	the <code>nu</code> parameter value(s)
<code>tau</code>	the <code>tau</code> parameter value(s)
<code>title</code>	a different title for the default
<code>from</code>	minimum value for the response
<code>to</code>	maximum value for the response
<code>no.points</code>	number of points (relevant for continuous responses)
<code>alpha</code>	transparency factor
<code>col.fill</code>	the colour palette default is <code>hcl.colors(lobj, palette="viridis")</code>
<code>size.segment</code>	for discrete responses the size of the bars
<code>plot.point</code>	for discrete responses whether to put points on the top of the bars
<code>size.point</code>	for discrete responses
<code>plot.line</code>	for discrete responses whether to joint the bars with lines
<code>size.line</code>	for discrete responses the size of the joining lines
<code>...</code>	for extra arguments

Details

The functions `family_pdf()` and `fitted_pdf()` are ggplot version of the function `pdf.plot()` used to plot fitted distributions of GAMLSS family at specified observation values. Note that the range of the response has to be specified using the argument `from` to.

For discrete fitted distributions maybe increase the value of `alpha` for clearer plot.

For binomial type of data (discrete response with upper limit) the function `family_pdf()` takes the argument `to` as the binomial denominator, For fitted model with binomial type responses the function `fitted_pdf()` takes the binomial denominator from the fitted model and set the argument `to` to the maximum of those binomial denominators.

Value

Creates a plot

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. 23, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.
- (see also <https://www.gamlss.com/>).

See Also

[gamlss](#), [resid_density](#)

Examples

```
#####
# function fitted_pdf
# continuous variabe
a1 <- gamlss(y~pb(x),sigma.fo=~pb(x), data=abdom, family=LO)
fitted_pdf(a1, obs=c(10,15,20), from=30, to=100)
# count data
p1 <- gamlss(y~pb(x)+qrt, data=aids, family=NBI)
fitted_pdf(p1, obs=c(10:15), from=25, to=130, alpha=.9)
# binomial type
h<-gamlss(y~ward+loglos+year, sigma.formula=~year+ward, family=BB, data=aep)
fitted_pdf(h, obs=c(10:15), alpha=.9)
#####
# function predict_pdf
predict_pdf(a1, newdata=abdom[10:20, ], from=30, to=100)
# count data
predict_pdf(p1, newdata=aids[10:15, ], from=30, to=150)
# binomial
predict_pdf(h, newdata=aep[10:15, ], from=0, to=20)
#####
# function family_pdf
# continuous
family_pdf(from=-5,to=5, mu=0, sigma=c(.5,1,2))
# count data
family_pdf(NBI, to=15, mu=1, sigma=c(.5,1,2), alpha=.9, size.segment = 3)
# binomial type
family_pdf(BB, to=15, mu=.5, sigma=c(.5,1,2), alpha=.9, , size.segment = 3)
```

fitted_cdf*Plotting Cumulative Distribution Functions (cdf's) for GAMLSS,*

Description

The function `family_cdf()` takes a GAMLSS family distribution and plots different pdf's according to the specified parameters.

The function `fitted_cdf()` takes a `gamlss` fitted object and plots the fitted distributions for specified observations.

The function `fitted_cdf_data()` is similar to `fitted_cdf()` but also adds the data points as gray vertical lines.

The function `predict_pdf()` (NOT IMPLEMENTED YET) takes a fitted object and test data and plots the predictive cdf's.

Usage

```
fitted_cdf(model, obs, title, from = 0, to = 10, no.points = 201,
            alpha = 1, size.line = 1.2,
            col.fill = hcl.colors(lobs, palette = "viridis"),
            size.seqment = 1.5, size.point = 1,
            plot.line = TRUE, size.line.disc = 0.2, lower.tail = TRUE, ...)

fitted_cdf_data(model, obs, from, to, ...)

predict_cdf(model, newdata, title, from = 0, to = 10, no.points = 201,
            alpha = 0.4, size.line = 1.2,
            col.fill = hcl.colors(lobs, palette = "viridis"),
            size.seqment = 1.5, plot.point = TRUE, size.point = 1,
            plot.line = TRUE, size.line.disc = 0.2, lower.tail = TRUE, ...)

family_cdf(family = NO(), mu = NULL, sigma = NULL, nu = NULL,
            tau = NULL, title, from = 0, to = 10, no.points = 201,
            alpha = 0.4, size.line = 1.2, col.fill = hcl.colors(lobs,
            palette = "viridis"), size.seqment = 1.5, plot.point = TRUE,
            size.point = 1, plot.line = TRUE, lower.tail = TRUE, ...)
```

Arguments

<code>family</code>	A GAMLSS family
<code>model</code>	A GAMLSS fitted model
<code>obs</code>	observations to plot fitted distributions
<code>newdata</code>	for test data
<code>mu</code>	the <code>mu</code> parameter value(s)

sigma	the sigma parameter value(s)
nu	the nu parameter value(s)
tau	the tau parameter value(s)
title	a different title for the default
from	minimum value for the response
to	maximum value for the response
no.points	number of points (relevant for continuous responses)
alpha	transparency factor
col.fill	the colour palette default is hcl.colors(lobes, palette="viridis")
size.segment	for discrete responses the size of the bars
plot.point	for discrete responses whether to put points on the top of the bars
size.point	for discrete responses
plot.line	for discrete responses whether to joint the bars with lines
size.line.disc	for discrete responses the size of the joining lines
size.line	The size of the lines
lower.tail	if TRUE cdf is plotted if FALSE the survival function
...	for extra arguments

Details

The functions `family_cdf()`, `fitted_cdf()`, and `predict_cdf()` are function to plot cdf's for a `gamlss.family`, `fitted_gamlss` model or predictive `gamlss` model, respectively.

For discrete fitted distributions maybe increase the value of `alpha` for clearer plot.

For binomial type of data (discrete response with upper limit) the function `family_cdf()` takes the argument `to` as the binomial denominator, For fitted model with binomial type responses the function `fitted_cdf()` takes the binomial denominator from the fitted model and set the argument `to` to the maximum of those binomial denominators.

Value

Creates a plot

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[gamlss](#)

Examples

```
# function fitted_cdf
# continuous variabe
a1 <- gamlss(y~pb(x),sigma.fo=~pb(x), data=abdom, family=LO)
fitted_cdf(a1, obs=c(10,15,20), from=30, to=100)
fitted_cdf(a1, obs=c(10,15,20), from=30, to=100, lower.tail=FALSE)
# count data
p1 <- gamlss(y~pb(x)+qrt, data=aids, family=NBI)
fitted_cdf(p1, obs=c(10:15), from=10, to=130, alpha=.9)
fitted_cdf(p1, obs=c(10:15), from=10, to=130, alpha=.9, lower.tail=FALSE)
# binomial type
h<-gamlss(y~ward+loglos+year, sigma.formula=~year+ward, family=BB, data=aep)
fitted_cdf(h, obs=c(10:15), alpha=.9)
fitted_cdf(h, obs=c(10:15), alpha=.9, lower.tail=FALSE)
#####
# function predict_pdf
predict_cdf(a1, newdata=abdom[c(10,15,20), ], from=30, to=100)
predict_cdf(a1, newdata=abdom[10:20, ], from=30, to=100, lower.tail=FALSE)
# count data
predict_cdf(p1, newdata=aids[10:15, ], from=10, to=150)
predict_cdf(p1, newdata=aids[10:15, ], from=10, to=150, lower.tail=FALSE)
# binomial
predict_cdf(h, newdata=aep[10:15, ], from=0, to=20)
predict_cdf(h, newdata=aep[10:15, ], from=0, to=20, lower.tail=FALSE)
#####
# function family_cdf
# continuous
family_cdf(from=-5,to=5, mu=0, sigma=c(.5,1,2))
family_cdf(from=-5,to=5, mu=0, sigma=c(.5,1,2), lower.tail=FALSE)
# count data
family_cdf(NBI, to=15, mu=1, sigma=c(.5,1,2), alpha=.9, size.seqment = 3)
family_cdf(NBI, to=15, mu=1, sigma=c(.5,1,2), alpha=.9, size.seqment = 3, lower.tail=FALSE)
# binomial type
family_cdf(BB, to=15, mu=.5, sigma=c(.5,1,2), alpha=.9, , size.seqment = 3)
family_cdf(BB, to=15, mu=.5, sigma=c(.5,1,2), alpha=.9, , size.seqment = 3, lower.tail=FALSE)
```

<code>fitted_centiles</code>	<i>Plotting centile (growth) curves</i>
------------------------------	---

Description

The function `fitted_centiles()` plots centiles curves for distributions belonging to the GAMLSS family of distributions. The plot is equivalent to the standard plot of `gamlss:::centiles()` without a legend.

The function `fitted_centiles_legend()` plots centiles curves for distributions belonging to the GAMLSS family of distributions and it is equivalent to the standard plot of `gamlss:::centiles()` with a legend. The function is slower than `fitted_centiles()` since in order to plot the legend the data have to expanded.

The function `model_centiles()` plots centile curves for more than one model. There is no equivalent plot in the original GAMLSS centile plots but it perform the same function as `gamlss:::centiles.com()` which compares centiles from different models.

Usage

```
fitted_centiles(obj, xvar,
                cent = c(99.4, 98, 90, 75, 50, 25, 10, 2, 0.4),
                points = TRUE, point.col = "gray",
                point.size = 1, line.size = 0.8,
                line.col = hcl.colors(lc, palette = "Dark 2"),
                line.type = rep(1, length(cent)),
                xlab = NULL, ylab = NULL, title, ...)

fitted_centiles_legend(obj, xvar,
                       cent = c(99.4, 98, 90, 75, 50, 25, 10, 2, 0.4),
                       points = TRUE, point.col = "gray", point.size = 1,
                       line.size = 0.8, line.col = hcl.colors(ncent,
                       palette = "Dark 2"), line.type = rep(1, length(cent)),
                       show.legend = TRUE, save.data = FALSE, title,
                       xlab = NULL, ylab = NULL, ...)

model_centiles(obj, ..., cent = c(97, 90, 75, 50, 25, 10, 3),
               xvar, xlab = "age", points = TRUE,
               point.col = gray(0.8),
               point.size = 0.05, line.size = 0.7,
               line.col = hcl.colors(ncent, palette = "Dark 2"),
               ncol = 2, nrow = ceiling(nnames/ncol), in.one = FALSE,
               title)
```

Arguments

<code>obj</code>	a fitted <code>gamlss</code> object
<code>xvar</code>	the (unique) explanatory variable

<code>cent</code>	a vector with elements the % centile values for which the centile curves have to be evaluated (note that the order is from the highest to the lowest so legend and the plots are matching)
<code>points</code>	whether to plot the points (TRUE) of the data or not (FALSE)
<code>point.col</code>	the colour of the points
<code>point.size</code>	the size of the points
<code>line.size</code>	the size of the centile lines
<code>line.col</code>	the colour of the centile lines
<code>line.type</code>	the type of line (different types of lines for each centile are working with <code>fitted_centiles_legend()</code>)
<code>xlab</code>	the label of the x-axis variable
<code>ylab</code>	the label of the response variable
<code>in.one</code>	whether the <code>model_centile</code> plot should be one or multiple
<code>title</code>	the title if need it otherwise a default title is printed
<code>show.legend</code>	whether to show the legend
<code>save.data</code>	whether to save the data.frame of the plot
<code>nrow</code>	the number of rows in the <code>model_centiles()</code> plot
<code>ncol</code>	the number of columns in the <code>model_centiles()</code> plot
<code>...</code>	for extra arguments for <code>fitted_centiles()</code> , and <code>fitted_centiles.legend()</code> and extra models for <code>model_centiles()</code>

Details

Centiles are calculated using the fitted values in `obj` and `xvar` must correspond exactly to the predictor in `obj` to plot correctly.

Value

A plot is created

Warning

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

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda de Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[centiles](#)

Examples

```
data(abdom)
h<-gamlss(y~pb(x), sigma.formula=~pb(x), family=BCTo, data=abdom)
h1 <- gamlss(y~pb(x), sigma.formula=~pb(x), family=L0, data=abdom)
fitted_centiles(h)
fitted_centiles_legend(h)
model_centiles(h, h1)
```

fitted_devianceIncr *Plotting the deviance increment of GAMLSS*

Description

There are two plotting function here:

- i) `fitted_devianceIncr()` plots the fitted model deviance components. This is useful for identifying observations with unusual y-values (given the current fitted distribution).
- iii) `model_devianceIncr_diff` plots the difference of deviance increments from two fitted GAMLSS model. This function is useful if the GAIC and the residuals contradict each other. For example the GAIC is better for model 1 but the residuals look lot better for model 2. This can happens if the two distributions are better suited to fit different parts of the response distribution i.e. one model fits the center better but the other fits the tail better.

Usage

```
fitted_devianceIncr(obj, plot = TRUE, title, quan.val = 0.99,
                     annotate = TRUE, line.col = "steelblue4",
                     point.col = "darkblue", annot.col = "white",
                     newdata = NULL)
```

```
model_devianceIncr_diff(model1, model2, against = "index",
                        tol = 20, data, newdata)
```

Arguments

obj	a GAMLSS fitted object
plot	whether to create just the plot or save also the values with high deviance increment
title	a title if needed it.
quan.val	The quantile values of the deviance increment from which the observation should be identify
annotate	whether to plot the quantile values above in the plot.
line.col	the colour of the line
point.col	the colour of the points
annot.col	the colour of the annotation for the deviance increment plot
model1	The first fitted GAMLSS model
model2	The second fitted GAMLSS model
against	you can plot the deviance increment an index, the response or an x-variable
tol	if the absolute value of deviance increment exceeds the tol the number of the observation is plotted
data	The data if can not be found from model1
newdata	evaluates the function in new data

Details

The functions are diagnostic tools to check unusual observations in the response.

Value

return a plot

Author(s)

Mikis Stasinopoulos, Rober Rigby and Fernanda de Bastiani

References

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

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[gamlss](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A)+H+loc, data=rent, family=GA )
m2 <- gamlss(R~pb(F1)+pb(A)+H+loc, data=rent, family=NO )
fitted_devianceIncr(m1)
model_devianceIncr_diff(m1,m2, against="F1")
```

fitted_leverage

Plot of the linear leverage of a GAMLSS model

Description

This is plot of the "linear" leverage of a GAMLSS fitted model. By linear we mean the leverage (hat-values) we would have obtain in all the explanatory variables for all distribution parameters where put together and used to fit a linear model to the response. The "linear" leverage is them the hat-values obtained by fitting this simple linear model. Hopefully the "linear" leverage can indicate observations with extreme values in the x's. Note that observations with hight linear leverage may not be influential in the GAMLSS fitting especially if the x-variables are fitted using smoothers.

Usage

```
fitted_leverage(obj, plot = TRUE, title, quan.val = 0.99,
                annotate = TRUE, line.col = "steelblue4",
                point.col = "steelblue4", annot.col = "darkred")
```

Arguments

obj	A GAMLSS fitted model
plot	whether to plot ot not
title	for different title than the default
quan.val	which quantile value of the leverage should be taked to indicate the observation values

annotate	whether to annotate the extreme leverages
line.col	the colour of the lines
point.col	the colout of the points
annot.col	the colour used for annotation

Value

Returns a plot of the linear leverage against index.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

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

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[gamlss](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A)+loc+H, data=rent, family=GA)
fitted_leverage(m1)
```

<code>fitted_terms</code>	<i>Plotting fitted additive terms</i>
---------------------------	---------------------------------------

Description

The function `fitted_terms()` is doing what the function `term.plot()` is doing for GAMLSS models but it uses `ggplot2` package. The function `pe_terms()` is synonymous to `fitted_terms()` in the package `gamlss`.

Usage

```
fitted_terms(object,
             what = c("mu", "sigma", "nu", "tau"),
             parameter = NULL, data = NULL, terms = NULL,
             envir = environment(formula(object)),
             partial = FALSE, rug = FALSE, rug.sides = "b",
             rug.col = "gray", alpha = 0.2,
             ylim = c("common", "free"), xlabs = NULL,
             ylabs = NULL, main = NULL, term.col = "darkred",
             resid.col = "lightblue", resid.alpha = 0.8,
             resid.size = 1, nrow = NULL, ncol = NULL,
             plots.per.page = 9, one.by.one = FALSE,
             surface.gam = FALSE, polys = NULL,
             polys.scheme = "topo", col.ribbon = "darksalmon",
             col.shaded = "gray", ...)

pe_terms(object,
         what = c("mu", "sigma", "nu", "tau"),
         parameter = NULL, data = NULL, terms = NULL,
         envir = environment(formula(object)),
         partial = FALSE, rug = FALSE, rug.sides = "b",
         rug.col = "gray", alpha = 0.2,
         ylim = c("common", "free"), xlabs = NULL,
         ylabs = NULL, main = NULL, term.col = "darkred",
         resid.col = "lightblue", resid.alpha = 0.8,
         resid.size = 1, nrow = NULL, ncol = NULL,
         plots.per.page = 9, one.by.one = FALSE,
         surface.gam = FALSE, polys = NULL,
         polys.scheme = "topo", col.ribbon = "darksalmon",
         col.shaded = "gray", ...)
```

Arguments

<code>object</code>	a <code>gamlss</code> fitted model
<code>what</code>	which distribution parameters, i.e. "mu"

parameter	which distribution parameters (equivalent to what)
data	data frame in which variables in object can be found
terms	which terms to plot (default NULL means all terms); a vector passed to lpred(..., type = "terms", terms =*)
envir	environment in which variables in object can be found
partial	logical; should partial residuals be plotted?
rug	add rug plots to the axes
rug.sides	which side the rug "b"=bottom
rug.col	the colour for the rug
alpha	the alpha for the shade
ylim	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 seperatly.
xlabs	the x label
ylabs	the y label
main	title NOT WORKING
term.col	the colour of the line for term
resid.col	the colour of the partial residuals
resid.alpha	The alpha for the partial residuals
resid.size	the size of the partial residuals
nrow	the number or rows in a mupliple plot
ncol	the number of rows in a mupliple plot
plots.per.page	the number of plots per page in multiple plots
one.by.one	whether to plot the terms one by one
surface.gam	whether to use surface plot if a ga() term is fitted
polys	for GRMF models
polys.scheme	The polygone information file for MRF models
col.ribbon	he colour of the ribbon
col.shaded	he colour of the shaded area
...	for extra argument

Value

A multiple plot

Author(s)

Mikis Stasinopoulos

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
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- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
- (see also <https://www.gamlss.com/>).

See Also

[term.plot](#)

Examples

```
data(aids)
a <- gamlss(y ~ pb(x) + qrt, data = aids, family = NBI)
fitted_terms(a, pages = 1)
```

fit_PB

P-spline smoother

Description

The function `fit_PB()` fits a P-spline univariate smoother [Eilers and Marx (1996)] to `y` against the `x` with prior weights `weights`.

Usage

```
fit_PB(x, y, weights, data, xmin, xmax, nseg = 20,
       lambda = 10, order = 2, degree = 3, max.df = 20,
       ylim, plot = TRUE, col.ribbon = "pink")
```

Arguments

x	the explanatory variable
y	the response
weights	possible prior weights (set to one by default)
data	the data frame where x, y and weights are coming from
xmin	the x minimum if different from min(x)
xmax	the x maximum if different from max(x)
nseg	the number of knots
lambda	the smotthing parameter
order	the ordr of the difference
degree	the degree of the piewise polynomial
max.df	the maximum allowed degress of freedom
ylim	the ylim in the plot
plot	whether to plot the results
col.ribbon	the color in the se of the fitted values

Value

A object Psplines is produced with methods `print()`, `coef()` `deviance()`, `fitted()`, `predict()` and `resid()`.

Note

The function `fit_PB()` is an engine for getting the maximal correlation between two continuous variables. It can be also used on its own as a smoother.

Author(s)

Mikis Stasinopoulos

References

- Eilers, P. H. C. and Marx, B. D. (1996). Flexible smoothing with B-splines and penalties (with comments and rejoinder). *Statist. Sci.*, **11**, 89-121.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:[10.1201/9780429298547](https://doi.org/10.1201/9780429298547).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:[10.1201/b21973](https://doi.org/10.1201/b21973)
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
- (see also <https://www.gamlss.com/>).

See Also

ACE

Examples

```
data(abdom)
m1 <- fit_PB(x,y, data=abdom)
```

histSmo_plot *Supporting histSmo()*

Description

This function helps to plot density estimates created by the `histSmo()` function.

Usage

```
histSmo_plot(x, col_fill_bar = gray(0.5), col_bar = "pink",
              col_line = "darkblue", width_line = 1, title, xlabel)
```

Arguments

<code>x</code>	a <code>histSmo</code> object
<code>col_fill_bar</code>	The fill colour of the bars
<code>col_bar</code>	the colour of the border of the bars
<code>col_line</code>	the colour of the lines
<code>width_line</code>	the width of the lines
<code>title</code>	title if needed
<code>xlabel</code>	x axis label if needed.

Details

This function supports `histSmo()`.

Value

A plot

Author(s)

Mikis Stasinopoulos, Rober Rigby and Fernanda de Bastiani

References

- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. 23, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

[histSmo](#)

Examples

```
a1 <- histSmo(abdom$y)
gg1 <- histSmo_plot(a1)
gg1
```

model_GAIC

Plotting GAIC for GAMLSS models

Description

The function `model_GAIC()` is similar to the function `GAIC.scaled()` of the package **gamlss**. It produces, [for a given set of different fitted models or for a table produced by `chooseDist()`], the scaled Akaike values (see Burnham and Anderson (2002) section 2.9 for a similar concept of the GAIC weights. The plot of the GAIC's should not be interpreted as posterior probabilities of models given the data but can be used for model selection purpose since they produce a scaled ranking of the model using their relative importance i.e. from the worst to the best model.

The function `model_GAIC_lollipop()` is almost identical to `model_GAIC()` but the result is a lollipop plot.

Usage

```
model_GAIC(object, ..., k = 2, c = FALSE, plot = TRUE,
           which = 1, diff.dev = 1000, text.to.show = NULL,
           col = "rosybrown", width = 0.9, horiz = TRUE,
           scale = c("[0,1]", "[max,min]"), title)
```

```
model_GAIC_lollipop(object, ..., k = 2, c = FALSE, plot = TRUE,
                      which = 1, diff.dev = 1000, text.to.show = NULL,
                      col = "skyblue", col.point = "blue", pch.point = 19,
                      width = 0.9, horiz = TRUE,
                      scale = c("[0,1]", "[max,min]"), order.val = TRUE, title)
```

Arguments

object	a set of gamlss fitted model(s) or a matrix table produced by chooseDist().
...	it allows several GAMLSS object to be compared using a GAIC
k	the penalty with default k=2
c	whether the corrected AIC, i.e. AICc, should be used, note that it applies only when k=2
plot	whether to plot with default equal TRUE
which	which column of GAIC table to plot
diff.dev	this argument applies only a matrix table produced by chooseDist() and prevents models with a difference in deviance greater than diff.dev from the 'best' model to be considered (or plotted).
text.to.show	if NULL, model_GAIC() shows the model names otherwise the character in this list (the length of which should be equal to the length of models)
col	The colour of the bars (or lines. in the lollipop)
col.point	The colour of the points in the lollipop
pch.point	The points character in the lollipop
width	the width of the bars
horiz	whether to plot the bars horizontally (default) or vertically
scale	the scale of the plot, "[0,1]" plots the AIC's from the worst to the best models in a scale from [0,1]. "[max,min]" plots the AIC's from the worst model to the best model but in the original scale of the AIC's
title	if different title is needed
order.val	whether to order the models from the best to the worst

Details

The option allow the AIC to be plotted from worst to best on a [0,1] scale using the formula i.e. $(AIC_w - AIC_m)/(AIC_w - AIC_b)$ where the AIC_w and AIC_b are the worst and best AIC, respectively, and AIC_m is the AIC of the current model. If the option scale is set to [max,min] the difference $(AIC_w - AIC_m)$ is plotted.

Value

It returns a bar plot using package **ggplot2**.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Burnham K. P. and Anderson D. R (2002). *Model Selection and Multimodel Inference A Practical Information-Theoretic Approach*, Second Edition, Springer-Verlag New York, Inc.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
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- (see also <https://www.gamlss.com/>).

See Also

[GAIC.scaled](#)

Examples

```
data(abdom)
m1 <- gamlss(y~x, family=NO, data=abdom)
m2 <- gamlss(y~x, sigma.fo=~x, family=NO, data=abdom)
m3 <- gamlss(y~pb(x), sigma.fo=~x, family=NO, data=abdom)
m4 <- gamlss(y~pb(x), sigma.fo=~pb(x), family=NO, data=abdom)

model_GAIC(m1,m2, m3, m4)

MT <- chooseDist(m3)
model_GAIC(MT)
model_GAIC(MT, which=2)
model_GAIC_lollipop(m1,m2, m3, m4)
```

model_pca

Plotting residuals using PCA

Description

The function `model_pca()` plots several GAMLSS residuals using Principal Component Analysis.

Usage

```
model_pca(obj, ..., scale = TRUE, arrow_size = 1.5)
```

Arguments

obj	A gamlss object
...	for extra GAMLSS models
scale	whether to scale the residuals
arrow_size	the arrow size in the biplot

Details

The function `model_pca()` plot a `biplot()` plot of the residuals from different models. It uses Principal Component Analysis in the residuals of different models and plots the results.

Value

A biplot of the first two components is plotted.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. 23, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
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- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

`gamlss`, `resid_index`

Examples

```
m1 <- gamlss(y~x, data=abdom)
m2 <- gamlss(y~pb(x), data=abdom)
m3 <- gamlss(y~pb(x), sigma.fo=~pb(x), data=abdom)
model_pca(m1,m2,m3)
```

moment_bucket	<i>Moment bucket plot</i>
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Description

A bucket plot is a graphical way to check the skewness and kurtosis of a continuous variable or the residuals of a fitted GAMLSS model. It plots the transformed moment skewness and transformed moment kurtosis of the variable (or residuals) together with a cloud of points obtained using a non-parametric bootstrap from the original variable (or residuals). It also provides a graphical way of performing the Jarque-Bera test (JarqueandBera,1980).

There are two function here:

- i) `moment_bucket()` for a single bucket plot. Note that `model_mom_bucket()` and `moment_bucket()` are synonymous.
- ii) `moment_bucket_wrap()` for multiple bucket plots cut according to terms in the model.

Usage

```
moment_bucket(x, ..., weights = NULL, no_bootstrap = 99,
              col_bootstrap = hcl.colors(length.obj, palette = "Set 2"),
              alpha_bootstrap = 1, text_to_show = NULL,
              cex_text = 5, col_text = "black", colour_bucket = FALSE,
              line_width = 0.5, col_JB_test = gray(.7), alpha_JB_test = .1)

model_mom_bucket(x, ..., weights = NULL, no_bootstrap = 99,
                  col_bootstrap = hcl.colors(length.obj, palette = "Set 2"),
                  alpha_bootstrap = 1, text_to_show = NULL,
                  cex_text = 5, col_text = "black", colour_bucket = FALSE,
                  line_width = 0.5, col_JB_test = gray(.7), alpha_JB_test = .1)

moment_bucket_wrap(x, ..., weights = NULL, xvar = NULL, n_inter = 4,
                    no_bootstrap = 99,
                    col_bootstrap = hcl.colors(length.obj, palette = "Set 2"),
                    alpha_bootstrap = 1, text_to_show = NULL,
                    check_overlap_text = FALSE, cex_text = 5,
                    col_text = "black", colour_bucket = FALSE,
                    col_JB_test = gray(.7), alpha_JB_test = .1)
```

Arguments

<code>x</code>	<code>x</code> should be a continuous vector of a GAMLSS fitted model.
<code>...</code>	this for more than one continuous vectors or fitted models
<code>weights</code>	if priors weights are needed
<code>no_bootstrap</code>	the number of bootstrap samples for the cloud around the point of skewness and kurtosis.

col_bootstrap	The colour of the bootstrap samples
alpha_bootstrap	The transparency parameter of the bootstrap samples.
text_to_show	what text to show in the plots, default the names of vectors or models
cex_text	the character size of the text
col_text	the colour of the text
colour_bucket	whether colour or gray lines in the bucket
line_width	the line width
xvar	the x term
n_inter	how many intervals needed
check_overlap_text	whether to check overlapping text
col_JB_test	the colour for the Jarque-Bera test
alpha_JB_test	the transparency constant for the Jarque-Bera test

Value

A plot displaying the transformed moment skewness and transformed moment kurtosis of the sample or residual of a model.

Note

The bucket plot provides an additional residual diagnostic tool that can be used for fitted model checking, alongside other diagnostic tools, for example worm plots, and Q (and Z) statistics.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- De Bastiani, F., Stasinopoulos, D. M., Rigby, R. A., Heller, G. Z., and Lucas A. (2022) Bucket Plot: A Visual Tool for Skewness and Kurtosis Comparisons. To be published.
- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/9780429298547 An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi:10.18637/jss.v023.i07.
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- Stasinopoulos, M. D., Rigby, R. A., and De Bastiani F., (2018) GAMLSS: a distributional regression approach, *Statistical Modelling*, Vol. **18**, pp. 248-273, SAGE Publications Sage India: New Delhi, India.

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 (see also <https://www.gamlss.com/>).

See Also

[wp](#), [Q.stats](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A), data=rent, family=GA)
moment_bucket(m1)
moment_bucket_wrap(m1, xvar=rent$A)
```

moment_gray_half *Functions to create the background for the bucket plots*

Description

The functions plot the moment transformed skewness and moment transformed kurtosis of five important 4-parameter distributions in GAMLSS.

Usage

```
moment_gray_half(legend = FALSE)

moment_gray_both(line_width = 1)

moment_colour_half(legend = TRUE)

moment_colour_both(legend = TRUE, line_width = 1)

centile_colour_half(type = c("tail", "central"), legend = TRUE,
                     line_width = 1)

centile_colour_both(type = c("tail", "central"), legend = TRUE,
                     line_width = 1)

centile_gray_both(type = c("tail", "central"), legend = TRUE,
                  line_width = 0.5)
```

Arguments

legend	whether legend is required
line_width	line width
type	whether to plot ‘tail’ or ‘central’ skewness and kurtosis.

Details

The functions are described in Rigby *et al* (2019)

Value

A plot is created.

Note

The functions are used by the bucket plot function `model_mom_bucket()` to create the background of the bucket plots.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda de Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. doi:10.1201/9780429298547 An older version can be found in <https://www.gamlss.com/>.
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- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

[momentSK](#), [centileSK](#)

Examples

```
moment_gray_half()  
moment_gray_both()  
moment_colour_half()  
moment_colour_both()  
  
centile_colour_both()  
centile_gray_both()  
centile_colour_half()
```

<code>pcr_coef_path</code>	<i>Plotting the fitted path of a PCR model.</i>
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Description

This function is similar to the function `plot.PCR()` which is used to plot the path of a fitted principal component regression model, fitted using the function `fitPCR()` of the package **gamlss.foreach**.

Usage

```
pcr_coef_path(x, legend=FALSE, plot=TRUE)

pcr_path(x, parameter = c("mu", "sigma", "nu", "tau"),
          legend = FALSE, plot = TRUE)
```

Arguments

<code>x</code>	a fitted PCR object (or a fitted GAMLSS object for function <code>pcr_path()</code>)
<code>legend</code>	whether legend is needed
<code>plot</code>	whether to plot the path
<code>parameter</code>	which GAMLSS parameter, between "mu", "sigma", "nu", "tau"

Value

A gg-plot.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also[plot.PCR](#)**Examples**

```
library(gamlss.foreach)
library(glmnet)
library(ggplot2)
data(QuickStartExample)
attach(QuickStartExample)
hist(y, main="(a)")
if (is.null(rownames(x)))
  colnames(x) <- paste0("X", seq(1:dim(x)[2]))
# fitting
MM<- fitPCR(x,y, k=log(100))
pp<-pcr_coef_path(MM)
pp+ ggplot2::geom_vline(xintercept = MM$pc, colour = "gray")
# using gamlss
m1 <- gamm(y~pcr(x=x))
pcr_path(m1)
```

pe_param

*Partial Effect of a term on the parameters and predictors***Description**

The function `pe_param()` is similar to the function `getPEF()` of the **gamlss** package. It plot the partial effect that a particular term has one of the parameters of the distribution or its predictor eta. The function `pe2_param()` is build for partial effects from two terms and it is suitable to display first order interactions.

Usage

```
pe_param(obj = NULL, term = NULL, data = NULL, n.points = 100,
         parameter = c("mu", "sigma", "nu", "tau"),
         type = c("parameter", "eta"), scenario = list(),
         how = c("median", "last", "fixed"),
         col = "darkblue", size = 1.3, name.obj = NULL,
         rug.plot = TRUE, rug.col = "gray", rug.size = 0.5,
         data.plot = FALSE, data.col = "lightblue",
         data.size = 0.1, factor.size = 15,
         data.alpha = 0.9, bins = 30,
         filled = FALSE, ylim = NULL,
         title)

pe_1_param(obj = NULL, term = NULL, data = NULL, n.points = 100,
```

```

parameter = c("mu", "sigma", "nu", "tau"),
type = c("parameter", "eta"),
how = c("median", "last", "fixed"),
scale.from = c("mean", "median", "none"),
scenario = list(), col = "darkblue", size = 1.3,
name.obj = NULL, data.plot = FALSE,
data.col = "lightblue", data.size = 0.1,
data.alpha = 0.9, rug.plot = TRUE, rug.col = "gray",
rug.size = 0.5, factor.size = 15,
ylim = NULL, title)

pe_2_param(obj = NULL, terms = NULL, data = NULL, n.points = 100,
parameter = c("mu", "sigma", "nu", "tau"),
type = c("parameter", "eta"),
how = c("median", "last", "fixed"),
scenario = list(), col = "darkblue",
size = 1.3, data.plot = TRUE,
data.col = "lightblue", data.size = 0.1,
data.alpha = 0.9, bins = 30,
filled = FALSE, name.obj = NULL, title)

pe_param_grid(model, terms, maxcol = 2, maxrow = 3, ylim=NULL, ...)

```

Arguments

<code>obj</code>	a GAMLSS fitted object
<code>model</code>	a GAMLSS fitted model
<code>term</code>	the model term we want to investigate can be one i.e. "Fl" or two c("Fl", "A")
<code>terms</code>	a list of model terms for example list(c("Fl", "A"), "H", "loc"))
<code>data</code>	the data frame used otherwise it takes it from the fitted model
<code>n.points</code>	the number of points for the evaluation of the term
<code>parameter</code>	the distribution parameter in which the term is fitted
<code>type</code>	here you specify or the distribution parameter i.e "parameter" or its prediction, "eta"
<code>how</code>	how to set all the other terms in the model
<code>scenario</code>	this can be a list of values for the rest of the terms in the model for the distribution parameter
<code>plot</code>	whether to plot the result
<code>col</code>	the colour of the partial effect of the term
<code>size</code>	the size of the line of partial effect of the term
<code>bins</code>	the number of binds for the contour plot
<code>filled</code>	whether to display the values in the contour
<code>title</code>	the title if different from the default
<code>name.obj</code>	this is a way to pass the name of the object

maxcol	the maximum columns in the grid plot
maxrow	the maximum rowss in the grid plot
data.plot	whether to plot the data
rug.plot	whether to print the rug bellow the figure
rug.size	the size of the rug
rug.col	the colour of the rug
data.col	the color of the data points
data.size	the size of the data points
data.alpha	the trnsparance constant of the data points
factor.size	the size of the symbol if a factor is plotted
ylim	if a common y limit is required
scale.from	whethet to substact from the mean the median or from zero
...	for passing argument from the function pe_param_grid to the function pe_param

Details

The functions `pe_param()` and `pe_param_grid()` can be used to help the use the interpretation of a GAMLSS model. The functions `pe_param()` provides the partial effect of one or two terms of a specified parameter of the distribution while the rest of the terms in the model are set on specific values or scenarios. The function `pe_param()` calls `pe_1param()` if the argument terms is one i.e. "Fl" or the function `pe_2param()` if the terms are two i.e. `c("Fl","A")`. The `pe_param_grid()` plots multiple plots specified by the list used in the `term` argument.

Similar functions are `pe_quantile()` and `pe_moment()`.

Value

It is plotting the partial effect or is producing the resulting function

Author(s)

Mikis Stasinopoulos, Rober Rigby and Fernanda de Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.
 (see also <https://www.gamlss.com/>).

See Also

[getPEF](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A)+loc+H, data=rent, gamily=GA)
pe_param(m1, "A")
pe_param(m1, c("F1","A"), filled=TRUE)
pe_param_grid(m1, list(c("F1","A"), c("H","loc")), filled=TRUE)
# the terms are additive no interaction
```

pe_pdf

Partial Effect of a term on the response distribution

Description

The function `pe_pdf()` plots the partial effect that a specified term has on the distribution of the response.

The function `pe_pdf_grid()` plot multiple plots on the same page.

Usage

```
pe_pdf(obj = NULL, term = NULL, from = NULL, to = NULL,
       y.grid.points = 100, x.grid.points = 10, x.values,
       data = NULL, scale = NULL, how = c("median", "last"),
       scenario = list(), size = 0.1, horizontal = TRUE,
       col.fill = hcl.colors(lqq, palette = "viridis"),
       alpha = 0.6, xlim = NULL, title)

pe_pdf_grid(model, terms, maxcol = 2, maxrow = 3, ...)
```

Arguments

<code>obj, model</code>	A GAMLSS object
<code>term</code>	The model term
<code>terms</code>	The model terms, more than one for <code>pe_pdf_grid()</code> .
<code>from</code>	start from
<code>to</code>	end to
<code>y.grid.points</code>	in how many points the pdf should be evaluates

x.grid.points	in how many points the terms should be plotted
x.values	possible x values
data	The data used for modelling
scale	This is a very important value for plotting correctly the fitted distributions. If the default values it is not working please try different values
how	How to fix the rest of the variables. For continuous it takes the median for factor the level with the highest frequency.
scenario	Alternatively scenario for fixing the values.
size	the size of the pdf line
horizontal	whether to plot the partial pdf on the x-axis and the x on the y-axis or opposite
col.fill	how to fill the pdf body
alpha	the transparency factor
xlim	the limits for plotting x-axis
title	whether to use a different title from the default one
maxcol	maximum of columns in the grid for pe_pdf_grid()
maxrow	maximum of rows on the grid for pe_pdf_grid()
...	extra argument to be passed from pe_pdf() to pe_pdf_grid()

Details

The function `pe_pdf()` is one of the functions designed to help the user to interpret the GAMLSS model. Provides the partial effect that one of the continuous terms has on distribution of the response while the rest of the variables in the model are set to specific values or scenarios. Other similar functions are `pe_param()`, `pe_moment()` and `pe_quantile()`.

Value

A plot of the conditional distribution given the term

Author(s)

Mikis Stasinopoulos, Robert Rigby and Fernanda de Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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 (see also <https://www.gamlss.com/>).

See Also

[pe_param](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A)+loc+H, data=rent, gamily=GA)
pe_pdf(m1, "A")
pe_pdf(m1, "A")
pe_pdf(m1, "A", horizontal=FALSE)
pe_pdf_grid(m1, c("F1", "A", "H", "loc"))
```

prof_term

Plotting the profile deviance of one fitted term

Description

Plotting the profile deviance of a fitted term in GAMLSS

Usage

```
prof_term(model = NULL, criterion = c("GD", "GAIC"),
          penalty = 2.5, from = NULL, to = NULL,
          step = NULL, length = 7, xlabel = NULL, plot = TRUE,
          perc = 95, start.prev = TRUE, line.col = "darkgreen",
          dash.line.type = 3, dash.line.size = 0.8, text.size = 5, title)
```

Arguments

model	a GAMLSS fitted model
criterion	whether Global deviance or GAIC
penalty	the penalty k for GAIC
from	start from
to	finish at
step	using step
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 x label is required
plot	whether to plot the function
perc	what percentage confidence interval is required

start.prev	whether to start from the previous fitted model parameters values or not (default is TRUE)
line.col	the colour of the plotting line
dash.line.type	the type of vertical dash line for CI's
dash.line.size	The size of the dash lines
text.size	the size of text
title	the title

Details

This function is the ggplot2 version of the original prof.term() function.

Value

creates a plot

Author(s)

Mikis Stasinopoulos

References

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

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[prof.term](#)

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, from = .06, to=0.13)
```

resid_density	<i>Density of the residuals in a GAMLSS model</i>
---------------	---

Description

The function `resid_density()` plots an histogram and a density estimator of the normalised quantile residuals from a fitted GAMLSS model. The function `model_density()` plots density estimators of the normalised quantile residuals from more than one fitted GAMLSS models.

Usage

```
resid_density(obj, resid, hist.col = "black", hist.fill = "white",
              dens.fill = "#FF6666", title)
model_density(obj, ..., title)
```

Arguments

<code>obj</code>	The function needs a GAMLSS fitted model or
<code>resid</code>	any standarised residual
<code>hist.col</code>	The colour of the border of the histogram
<code>hist.fill</code>	The colout of the hisogram
<code>dens.fill</code>	the colour of the desnsity
<code>title</code>	A title if needed
<code>...</code>	extra GAMLSS models

Details

This function `resid_density()` is a denity plot (similar to of the four plots produced when the plotting function `plot.gamlss()` is used within the `gamlss` package. I uses plotting function from the `ggplot2` package.

Value

A density plot of the residuals is produced.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, <https://www.jstatsoft.org/v23/i07/>.
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
- (see also <https://www.gamlss.com/>).

See Also

[plot.gamlss](#)

Examples

```
data(abdom)
a<-gamlss(y~pb(x),family=L0,data=abdom)
b<-gamlss(y~pb(x),family=N0,data=abdom)
resid_density(a)
model_density(a,b)
```

resid_dtop

Detrended Transformed Owen's Plot and ECDF for the residuals

Description

The function `resid_dtop()` provides single de-trended transformed Owen's plot, Owen (1995), for a GAMLSS fitted objects or any other residual vector (suitable standardised). 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.

The function `resid_ecdf()` provides the empirical cumulative distribution function of the residuals.

The function `y_ecdf()` provides the empirical cumulative distribution function of any numerical vector `y`.

Usage

```
resid_dtop(obj, resid, type = c("Owen", "JW"), conf.level = c("95", "99"),
           value = 2, points.col = "steelblue4",
           check_overlap = TRUE, title, ylim, ...)

resid_ecdf(obj, resid, type = c("Owen", "JW"), conf.level = c("95", "99"),
           value = 2, points.col = "steelblue4",
           check_overlap = TRUE, show.outliers = TRUE, title, ...)

y_ecdf(y, type = c("Owen", "JW"), conf.level = c("95", "99"), value = 2,
       points.col = "steelblue4", check_overlap = TRUE,
       show.outliers = FALSE, from, to, title, ...)
```

Arguments

<code>obj</code>	A GAMLSS fitted model
<code>resid</code>	if the object is not specified the residual vector can be given here
<code>y</code>	a numeric vector
<code>type</code>	whether to use Owen (1995) or Jager and Wellner (2004) approximate formula
<code>conf.level</code>	95% (default) or 99% percent confidence interval for the plots
<code>value</code>	cut off point for large residuals
<code>points.col</code>	the colour of the points in the plot
<code>check_overlap</code>	to check for overlap when plotting the observation numbers
<code>title</code>	required title
<code>show.outliers</code>	whether to show the number of an outlier observation
<code>ylim</code>	if the y limit should be different from the default <code>max(y)+1</code>
<code>from</code>	where to start the ecdf
<code>to</code>	where to finish the ecdf
<code>...</code>	further arguments

Value

A ggplot is generated

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda de Bastiani

References

- Jager, L. and Wellner, J. A (2004) A new goodness of fit test: the reversed Berk-Jones statistic, University of Washington, Department of Statistics, Technical report 443.
- Owen A. B. (1995) Nonparametric Confidence Bands for a Distribution Function. Journal of the American Statistical Association Vol. 90, No 430, pp. 516-521.

Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, 54, part 3, 1-38.

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[resid_wp](#)

Examples

```
library(ggplot2)
data(abdom)
a<-gamlss(y~pb(x),sigma.fo=~pb(x,1),family=L0,data=abdom)
resid_dtop(a)
resid_ecdf(a)+ stat_function(fun = pN0, args=list(mu=0, sigma=1))
# create a gamma distributed random variable
y <- rGA(1000, mu=3, sigma=1)
gp<- y_ecdf(y)
gp + stat_function(fun = pGA, args=list(mu=3, sigma=1))
```

resid_index

A residual plots

Description

The function `resid_index()` is plotting the residuals of a GAMLSS fitted model (or any other suitable standardised residual) against the observation number index.

The function `resid_mu()` plots the residuals against fitted values for `mu`.

The function `resid_median()` plots the residuals against fitted median values.

The function `resid_param()` plots the residuals against any of the GAMLSS fitted parameters, `mu`, `sigma`, `nu`, or `tau`.

The function `resid_quantile()` plots the residuals against any fitted quantile.

The function `resid_xvar()` plots the residuals against an explanatory term.

The function `resid_plots()` produces a plot similar to the one that the function `plot()` produce for a GAMLSS model in package **gamlss**. This is, four plots: a) `resid_index()`(b) `resid_mu()`, (c) `resid_density()` and (d) `resid_qqplot()`.

Residuals above (or below) certain specified value are identified.

Usage

```
resid_index(obj, resid, plot = TRUE, value = 2, title, annotate = TRUE,
            no.lines = FALSE)

resid_mu(obj, resid, plot = TRUE, value = 2, title, annotate = TRUE)

resid_median(obj, resid, plot = TRUE, value = 3, title,
             annotate = TRUE)

resid_param(obj, param = c("mu", "sigma", "nu", "tau"), title,
            line.col = "darkred", point.col = "steelblue4",
            point.shape = 20)

resid_quantile(obj, quantile = 0.5, title, newdata,
                line.col = "darkred", point.col = "steelblue4",
                point.shape = 20)

resid_plots(obj, theme = c("original", "ts", "new", "ecdf"), value = 3)

resid_xvar(obj, xvar, plot = TRUE, value = 2, title, annotate = TRUE)
```

Arguments

<code>obj</code>	a GAMLSS object
<code>resid</code>	or any other suitable standardised residual vector.
<code>xvar</code>	a continuous explanatory variable
<code>plot</code>	whether to plot the result
<code>param</code>	which GAMLSS parameter <code>mu</code> , <code>sigma</code> , <code>nu</code> , or <code>tau</code>
<code>value</code>	the cut off value for the identification of very large or very small residuals
<code>annotate</code>	whether the threshold annotation should appear or not
<code>line.col</code>	the colour of the line
<code>point.col</code>	the colour of the points
<code>point.shape</code>	the shape of the points
<code>title</code>	a title of the plot if needed
<code>theme</code>	what type of plots should <code>resid_plots()</code> used : "original" is like using <code>plot.gamlss()</code> , "ts" is like using <code>plot.gamlss(ts="TRUE")</code> (not implemented yet), "new" it uses (a) <code>resid_index()</code> , (b) <code>resid_density()</code> , (c) <code>resid_wp()</code> and (d) <code>resid_dtop()</code> .

no.lines	this option allows to hide the horizontal lines so the resulting gg-plot can be used later with say <code>facet_wrap()</code> see example
newdata	whether the evaluation should be in newdata or the old data points
quantile	which quantile? default the median (0.50).

Value

A plot of the residuals is returned.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape.(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC, doi:[10.1201/9780429298547](https://doi.org/10.1201/9780429298547). An older version can be found in <https://www.gamlss.com/>.
- Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, doi:[10.18637/jss.v023.i07](https://doi.org/10.18637/jss.v023.i07).
- Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC. doi:[10.1201/b21973](https://doi.org/10.1201/b21973)
- Stasinopoulos, M. D., Rigby, R. A., and De Bastiani F., (2018) GAMLSS: a distributional regression approach, *Statistical Modelling*, Vol. **18**, pp. 248-273, SAGE Publications Sage India: New Delhi, India.
- Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.
(see also <https://www.gamlss.com/>).

See Also

[gamlss](#), [plot.gamlss](#)

Examples

```
library(ggplot2)
data(rent)
r1<-gamlss(R~pb(F1)+pb(A)+H+loc,family=GA,data=rent)
resid_index(r1)
resid_mu(r1)
resid_median(r1)
resid_param(r1)
resid_quantile(r1)
resid_xvar(r1, A)
resid_plots(r1)
resid_index(r1, no.lines=TRUE)+facet_wrap(~ cut_number(rent$A, 6))
```

resid_qqplot*QQ-plot of the residuals of a GAMLSS model*

Description

The function `resid_qqplot()` produces a single QQ-plot of the residuals from a fitted GAMLSS model or any other model with suitable standardised residuals.

The function `add_resid_qqplot()` takes a QQ-plot created by `resid_qqplot()` and adds another QQ-plot from a different fitted model.

The function `model_resid_qqplots()` takes different fitted models and creates QQ-plots for all fitted models.

Usage

```
resid_qqplot(obj, resid, value = 3, points.col = "steelblue4",
             line.col = "darkgray", check_overlap = TRUE, title)

add_resid_qqplot(gg, obj, value = 3, points.col = "sienna",
                  line.col = "darkgray", check_overlap = TRUE, title)

model_qqplot(obj, ..., line.col = "steelblue4", title)
```

Arguments

<code>obj</code>	A GAMLSS fitted model or
<code>resid</code>	any other residual suitable standardised.
<code>gg</code>	a ggplot
<code>value</code>	A cut off value to identify large or small residuals
<code>points.col</code>	the colour of the points in the plot
<code>line.col</code>	the colour of the line in the plot
<code>check_overlap</code>	if observations are identified this reduces the cluttering
<code>title</code>	a title if needed it
<code>...</code>	extra GAMLSS models

Details

This is a standard QQ-plot but with the advantage of being able to identify large or small residuals.

Value

A QQ-plot is created

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[plot.gamlss](#)

Examples

```
data(abdom)
a<-gamlss(y~pb(x),family=L0,data=abdom)
b<-gamlss(y~pb(x),family=N0,data=abdom)
gg <- resid_qqplot(a)
add_resid_qqplot(gg, b)
model_qqplot(a,b)
```

resid_symmetry

Symmetry plots

Description

The functions `resid_symmetry()` and `y_symmetry()` plot symmetry plots for residuals and single variable, respectively.

Usage

```
resid_symmetry(model, title)

y_symmetry(y, title)
```

Arguments

<code>model</code>	A model which allows the function <code>resid()</code>
<code>y</code>	a single variable
<code>title</code>	A title for the plot if needed

Details

The function orders the data (or residuals) and takes the median minus the lower half and plot it against the upper half minus the median.

Value

The symmetry plot is produced.

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. 56). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[resid_index](#)

Examples

```
y <- rBCT(1000, mu=3, sigma=.1, nu=-1, tau=5)
y_hist(y)
gg <- y_symmetry(y)
```

<code>resid_wp</code>	<i>Worm plot using ggplot2</i>
-----------------------	--------------------------------

Description

The function produces worm plot of the residuals of a fitted model. A worm plot is a de-trended normal QQ-plot so departure from normality is highlighted.

The function `plot_wp()` it is similar to the **gamlss** package function `wp()` when the argument `xvar` is not used.

Usage

```
resid_wp(obj, resid, value = 3, points_col = "steelblue4",
         poly_col = "darkred",
         check_overlap = TRUE, title, ylim)

model_wp(obj, ..., title)

resid_wp_wrap(obj, resid, value = 3, xvar = NULL, n_inter = 4,
              points_col = "steelblue4", poly_col = "darkred",
              alpha_bound = 0.1, check_overlap = TRUE, title, ylim)

model_wp_wrap(obj, ..., xvar = NULL, value = 3, n_inter = 4,
              points_col = "steelblue4", alpha_bound = 0.1,
              check_overlap = TRUE, ylim, title)
```

Arguments

<code>obj</code>	a GAMLSS fitted object or any other fitted model where the <code>resid()</code> method works (preferably the residuals should be standardised or better normalised quantile residuals. Note for <code>model_wp</code> only <code>gamlss</code> object are accepted.)
<code>resid</code>	if object is missing this argument can be used to specify the residual vector (again it should a normalised quantile residual vector)
<code>value</code>	A cut off point to indicate large residuals, default is <code>value=3</code>
<code>xvar</code>	the x term for which the worm plot will be plotted against
<code>n_inter</code>	the number of intervals for continuous x-term
<code>points_col</code>	the color of the points in the plot
<code>poly_col</code>	the colour of the fitted polynomial in the plot
<code>check_overlap</code>	to check for overlap when plotting the observation numbers
<code>alpha_bound</code>	the transparency parameter for the confidence bound
<code>title</code>	required title
<code>ylim</code>	if the y limit should be different from the default <code>max(y)+1</code>
...	extra GAMLSS models

Value

A worm plot is produced

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

van Buuren and Fredriks M. (2001) Worm plot: simple diagnostic device for modelling growth reference curves. *Statistics in Medicine*, **20**, 1259–1277

Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.

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

Stasinopoulos D. M., Rigby R.A., Heller G., Voudouris V., and De Bastiani F., (2017) *Flexible Regression and Smoothing: Using GAMLSS in R*, Chapman and Hall/CRC.

Stasinopoulos, M.D., Kneib, T., Klein, N., Mayr, A. and Heller, G.Z., (2024). *Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications* (Vol. **56**). Cambridge University Press.

(see also <https://www.gamlss.com/>).

See Also

[wp](#)

Examples

```
data(abdom)
# with data
a<-gamlss(y~pb(x),sigma.fo=~pb(x,1),family=L0,data=abdom)
resid_wp(a)
resid_wp(resid=resid(a))
```

Description

All plots are of the response variable against fitted values of interest.

The function `resp_mu()` is the ‘original’ one plotting the response against the parameter `mu`. The function reports the Pearson’s correlation coefficient and plot a lines (45% degrees) through the graph.

The function `resp_param()` plots the response against any fitted parameter `mu`, `sigma`, `nu` or `tau`. The function also plots a smooth curve going through the data and gives the Pearson’s correlation coefficient.

The function `resp_quantile()` plots the response against any fitted quantile, with default the median (0.50). The function also plots a smooth curve going through the data and gives the Pearson’s correlation coefficient.

The function `quantile_gamlss()` is used by the function `resp_quantile()` to calculate the quantiles of the fitted distribution .

Usage

```
resp_mu(obj, title, line.col = "darkred",
        point.col = "steelblue4",
        point.shape = 20)

resp_param(obj, param = c("mu", "sigma", "nu", "tau"),
           title, line.col = "darkred", point.col = "steelblue4",
           point.shape = 20)

resp_quantile(obj, quantile = 0.5, title, newdata,
              line.col = "darkred", point.col = "steelblue4",
              point.shape = 20)

quantile_gamlss(obj, quantile = 0.5, newdata)
```

Arguments

<code>obj</code>	a GAMLSS fitted object
<code>param</code>	which parameters? <code>mu</code> , <code>sigma</code> , <code>nu</code> or <code>tau</code> , [only for <code>resp_param()</code>].
<code>quantile</code>	which quantile? default the median (0.50), [only for <code>resp_quantile()</code> and <code>quantile_gamlss()</code>].
<code>title</code>	a title if needed it, by default for the function <code>fitted_resp</code> it print the correlation coefficients between the two variable.
<code>line.col</code>	the colour of the line
<code>point.col</code>	the colour of the points
<code>point.shape</code>	the shape of the points
<code>newdata</code>	whether the evaluation should be in <code>newdata</code> or the old data points [only for functions <code>resp_quantile()</code> and <code>quantile_gamlss()</code>]

Details

This is standard plot in regression where the fitted values are plotted against the response. In GAMLSS model is done by plotting the response against the fitted values of the *mu* model which is most case is a location parameter.

Value

A plot is returned

Note

Do not use this plot if *mu* is not a location parameter.

Author(s)

Mikis Stasinopoulos, Rober Rigby and Fernanda de Bastiani

References

- Rigby, R. A. and Stasinopoulos D. M. (2005). Generalized additive models for location, scale and shape,(with discussion), *Appl. Statist.*, **54**, part 3, pp 507-554.
- Rigby, R. A., Stasinopoulos, D. M., Heller, G. Z., and De Bastiani, F. (2019) *Distributions for modeling location, scale, and shape: Using GAMLSS in R*, Chapman and Hall/CRC. An older version can be found in <https://www.gamlss.com/>.
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(see also <https://www.gamlss.com/>).

See Also

[resid_plots](#)

Examples

```
m1 <- gamlss(R~pb(F1)+pb(A)+H+loc, data=rent, family=GA )
resp_mu(m1)
resp_param(m1)
resp_quantile(m1)
```

<code>y_hist</code>	<i>Histogram and density plot.</i>
---------------------	------------------------------------

Description

The function `y_hist()` creates a histogram and a density plot for a continuous variable.

The functions `y_acf()` and `y_pacf()` plot the autocorrelation and partial autocorrelation functions for `y`.

The function `y_dots()` is design for long tail right skewed variables. It is a plot emphasising the right tail of the distribution for such variables.

Usage

```

y_hist(y, data, with.density = TRUE, hist.col = "black",
       hist.fill = "white", dens.fill = "#FF6666",
       binwidth = (max(y)-min(y))/20, from, to, title)

y_acf(x, data, title)

y_pacf(x, data, title)

y_dots(y, data, value=3, point.size = 2, point.col = "gray",
       quantile = c(.10, .50, .90),
       line.col = c("black", "red", "black"),
       line.type = c("dotted", "solid", "dotted"),
       line.size = c(1,1,1), x.axis.col = "black",
       x.axis.line.type = "solid", seed = 123, from, to, title)

```

Arguments

<code>y, x</code>	a continuous variable
<code>data</code>	where to find argument <code>y</code>
<code>value</code>	value to identify outliers i.e. for upper tail an outliers is if it is greater than $Q_3 + value * IQ$
<code>with.density</code>	whether a density is required, default is TRUE
<code>hist.col</code>	the colour of lines of the histogram
<code>hist.fill</code>	the colour of the histogram
<code>dens.fill</code>	the color of the density plot
<code>binwidth</code>	the binwidth for the histogram
<code>from</code>	where to start the histogram (you may have to change <code>binwidth</code>)
<code>to</code>	where to finish the histogram (you may have to change <code>binwidth</code>)
<code>point.size</code>	the size of the points in <code>y_dots</code>

point.col	the colour of the points in y_dots
quantile	the quantile values to plot in y_dots, the default is 0.10, .50 and .90
line.col	the color of the vertical lines indicating the 0.10, .50 and .90 quantiles in y_dots
line.type	the type of the vertical lines indicationg the 0.10, .50 and .90 quantiles in y_dots
line.size	the size of the vertical lines indication the 0.10, .50 and .90 quantiles in y_dots
x.axis.col	the colour of the x-axis
x.axis.line.type	the type of the x-axis
seed	the seed to jitter the y
title	use this for a different title

Value

A ggplot is returned

Author(s)

Mikis Stasinopoulos, Bob Rigby and Fernanda De Bastiani

References

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(see also <https://www.gamlss.com/>).

See Also

[plot.ecdf](#)

Examples

```
library(ggplot2)
y <- rBCT(1000, mu=3, sigma=.1, nu=-1, tau=5)
y_hist(y)
gg <- y_hist(y, with.dens=FALSE)
gg + stat_function(fun = dBCT, args=list(mu=3, sigma=.1, nu=-1, tau=5),
                   colour = "black")
gg + stat_function(fun = dBCT, args=list(mu=3, sigma=.1, nu=-1, tau=5),
```

```
geom = "area", alpha=0.5, fill="pink", color="black", n=301)  
y_acf(diff(EuStockMarkets[,1]))  
y_dots(rent$R)
```

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