Package ‘gamlss.mx’

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Type Package

Title Fitting Mixture Distributions with GAMLSS

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LazyLoad yes

Depends R (>= 2.2.1), gamlss.dist, gamlss, nnet, stats, graphics

Suggests MASS

Description The main purpose of this package is to allow fitting of mixture distributions with generalised additive models for location scale and shape models see Chapter 7 of Stasinopoulos et al. (2017) <doi:10.1201/b21973-4>.

License GPL-2 | GPL-3

URL https://www.gamlss.com/

NeedsCompilation no

Repository CRAN

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R topics documented:

`gamlss.mx-package` *The GAMLSS add on package for mixture distributions*

Description

The main purpose of this package is to allow the user of the GAMLSS models to fit mixture distributions.

Details

Package:	gamlss.mx
Type:	Package
Version:	0.0
Date:	2005-08-3
License:	GPL (version 2 or later)

This package has two main function the `gamlssMX()` which is loosely based on the package `flexmix` of R and the function `gamlssNP()` which is based on the `npmlreg` package of Jochen Einbeck, Ross Darnell and John Hinde (2006) which in turns is based on several GLIM4 macros originally written by Murray Aitkin and Brian Francis. It also contains the function `gqz()` which is written by Nick Sofroniou and the function `gauss.quad()` written by Gordon Smyth.

Author(s)

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References

Jochen Einbeck, Ross Darnell and John Hinde (2006) npmlreg: Nonparametric maximum likelihood estimation for random effect models, R package version 0.34

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

See Also

gamlss,gamlss.family

Examples

```
data(enzyme)
mmNO <- gamlssMX(act~1, family=NO, K=2, data=enzyme)
mmNO

# also to make sure that it reaches the maximum
mmNOs <- gamlssMXfits(n=10, act~1, family=NO, K=2, data=enzyme)
fyNO<-dMX(y=seq(0,3,.01), mu=list(1.253, 0.1876), sigma=list(exp(-0.6665 ), exp(-2.573 )),
                  pi=list(0.4079609, 0.5920391 ), family=list("NO","NO") )
hist(enzyme$act,freq=FALSE,ylim=c(0,3.5),xlim=c(0,3),br=21)
lines(seq(0,3,.01),fyNO, col="red")
# equivalent model using gamlssNP
mmNP <- gamlssNP(act~1, data=enzyme, random=~1,sigma.fo=~MASS,family=NO, K=2)
```

---

dMX *Evaluate the d (pdf) and p (cdf) functions from GAMLSS mixtures*

Description

The functions dMX() and pMX() can be used to evaluated the pdf (p function) and the cdf (p function) receptively from a gamlss.family mixture. The functions getpdfMX() and getpdfNP() can be used to evaluate the fitted d function at a specified observation and therefore for plotting the fitted distribution of a fitted model at this observation.

Usage

```
dMX(y, mu = list(mu1 = 1, mu2 = 5), sigma = list(sigma1 = 1, sigma2 = 1),
       nu = list(nu1 = 1, nu2 = 1), tau = list(tau1 = 1, tau2 = 1),
      pi = list(pi1 = 0.2, pi2 = 0.8), family = list(fam1 = "NO", fam2 = "NO"),
       log = FALSE, ...)
pMX(q, mu = list(mu1 = 1, mu2 = 5), sigma = list(sigma1 = 1, sigma2 = 1),
       nu = list(nu1 = 1, nu2 = 1), tau = list(tau1 = 1, tau2 = 1),
      pi = list(pi1 = 0.2, pi2 = 0.8), family = list(fam1 = "NO", fam2 = "NO"),
       log = FALSE, ...)
getpdfMX(object = NULL, observation = 1)
getpdfNP(object = NULL, observation = 1)
```

Arguments

`y,q`	vector of quantiles
`mu`	a vector of `mu`'s
`sigma`	a vector of `sigma`'s
`nu`	a vector of `nu`'s
`tau`	a vector of `tau`'s
`pi`	a vector of `pi`'s
`family`	a vector of GAMLSS `family`'s
`log`	whether the `log` of the function or not
`object`	a fitted `gamlssMX` object
`observation`	the observation number in which we want to plot the fitted mixture
`...`	for extra arguments

Value

Returns values or pdf or cdf.

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

(see also `https://www.gamlss.com/`).

Examples

```
fyNO<-dMX(y=seq(0,3,.01), mu=list(1.253, 0.1876), sigma=list(exp(-0.6665 ), exp(-2.573 )),
                pi=list(0.4079609, 0.5920391 ), family=list("NO","NO") )
plot(fyNO~seq(0,3,.01), type="l")
FyNO<-pMX(q=seq(0,3,.01), mu=list(1.253, 0.1876), sigma=list(exp(-0.6665 ), exp(-2.573 )),
                pi=list(0.4079609, 0.5920391 ), family=list("NO","NO") )
plot(FyNO~seq(0,3,.01), type="l")
```

`enzyme` *Data used in gamlss.mx*

Description

enzyme : The data comprise independent measurement of enzyme activity in the blood of 245 individuals. The data were analysed by Bechker *at al.* (1993).

brains : the brain size, `brain`, and body weight, `body`, for 28 differnt animals.

Usage

```
data(enzyme)
data(brains)
```

Format

enzyme : data frame with 245 observations on the following variable `act`.

brains : data frame with 28 observations on the following variables. `body`, `brain`

`act` a numeric vector showing enzyme activity in the blood of 245 individuals.

`body` a numeric vector showing the body weight of 28 differnt animals

`brain` a numeric vector showing the brain size of 28 differnt animals

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

Examples

```
data(enzyme)
hist(enzyme$act)
data(brains)
brains$lbrain<-log(brains$brain)
brains$lbody<-log(brains$body)
with(brains, plot(lbrain~lbody))
```

`gamlssMX` *Function to fit finite mixture of gamlss family distributions*

Description

The function `gamlssMX` is design for fitting a K fold non parametric mixture of gamlss family distributions.

Usage

```
gamlssMX(formula = formula(data), pi.formula = ~1,
         family = "NO", weights, K = 2, prob = NULL,
         data, control = MX.control(...),
         g.control = gamlss.control(trace = FALSE, ...),
         zero.component = FALSE,   ...)
gamlssMXfits(n = 5, formula = formula(data), pi.formula = ~1,
         family = "NO", weights, K = 2, prob = NULL,
         data, control = MX.control(),
         g.control = gamlss.control(trace = FALSE),
         zero.component = FALSE, ... )
```

Arguments

`formula`	This argument it should be a formula (or a list of formulea of length K) for modelling the `mu` parameter of the model. Note that modelling the rest of the distributional parameters it can be done by using the usual ... which passes the arguments to `gamlss()`
`pi.formula`	This should be a formula for modelling the prior probabilities as a function of explanatory variables. Note that no smoothing of other additive terms are allowed here only the usual linear terms. The modelling here is done using the `multinom()` function from package `nnet`
`family`	This should be a `gamlss.family` distribution (or a list of distributions). Note that if different distributions are used here their parameters should be comparable for ease of interpretation.
`weights`	prior weights if needed
`K`	the number of finite mixtures with default `K=2`
`prob`	prior probabilities if required for starting values

`data`	the data frame nedded for the fit. Note that this is compulsory if `pi.formula` is used.
`control`	This argument sets the control parameters for the EM iterations algorithm. The default setting are given in the `MX.control` function
`g.control`	This argument can be used to pass to `gamlss()` control parameters, as in `gamlss.control`
`n`	the number of fits required in `gamlssMXfits()`
`zero.component`	whether zero component models exist, default is `FALSE`
`...`	for extra arguments

Author(s)

Mikis Stasinopoulos and Bob Rigby

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

See Also

`gamlss`, `gamlss.family`

Examples

```
library(MASS)
data(geyser)
# fitting 2 finite normal mixtures
m1<-gamlssMX(waiting~1,data=geyser,family=NO, K=2)

#fitting 2 finite gamma mixtures
m2<-gamlssMX(waiting~1,data=geyser,family=GA, K=2)
# fitting a model for pi
# first create a data frame
geyser1<-matrix(0,ncol=2, nrow=298)
geyser1[,1] <-geyser$waiting[-1]
```

```
geyser1[,2] <-geyser$duration[-299]
colnames(geyser1)<- c("waiting", "duration")
geyser1 <-data.frame(geyser1)
# get the best of 5 fits
m3<-gamlssMXfits(n=5, waiting~1, pi.formula=~duration, data=geyser1,family=NO, K=2)
m3
```

---

gamlssNP *A function to fit finite mixtures using the gamlss family of distributions*

Description

This function will fit a finite (or normal) mixture distribution where the kernel distribution can belong to any gamlss family of distributions using the EM algorithm. The function is based on functions `alldist()` and `allvc` of the `npmlreg` package of Jochen Einbeck, John Hinde and Ross Darnell.

Usage

```
gamlssNP(formula, random = ~1, family = NO(), data = NULL, K = 4,
          mixture = c("np", "gq"),
          tol = 0.5, weights, pluginz, control = NP.control(...),
          g.control = gamlss.control(trace = FALSE, ...), ...)
```

Arguments

`formula`	a formula defining the response and the fixed effects for the `mu` parameters
`random`	a formula defining the random part of the model
`family`	a gamlss family object
`data`	the data frame which for this function is mandatory even if it the data are attached
`K`	the number of mass points/integretion points (supported values are 1:10,20)
`mixture`	the mixing distribution, "np" for non-parametric or "gq" for Gaussian Quadrature
`tol`	the toletance scalar ussualy between zero and one
`weights`	prior weights
`pluginz`	optional
`control`	this sets the control parameters for the EM iterations algorithm. The default setting is the `NP.control` function
`g.control`	the gamlss control function, `gamlss.control`, passed to the gamlss fit
`...`	for extra arguments

Details

The function `gamlssNP()` is a modification of the R functions `alldist()` and `allvc` created by Jochen Einbeck and John Hinde. Both functions were originally created by Ross Darnell (2002). Here the two functions are merged to one `gamlssNP` and allows finite mixture from gamlss family of distributions.

The following are comments from the original Einbeck and Hinde documentation.

"The nonparametric maximum likelihood (NPML) approach was introduced in Aitkin (1996) as a tool to fit overdispersed generalized linear models. Aitkin (1999) extended this method to generalized linear models with shared random effects arising through variance component or repeated measures structure. Applications are two-stage sample designs, when firstly the primary sampling units (the upper-level units, e.g. classes) and then the secondary sampling units (lower-level units, e.g. students) are selected, or longitudinal data. Models of this type have also been referred to as multi-level models (Goldstein, 2003). This R function is restricted to 2-level models. The idea of NPML is to approximate the unknown and unspecified distribution of the random effect by a discrete mixture of k exponential family densities, leading to a simple expression of the marginal likelihood, which can then be maximized using a standard EM algorithm. When option 'gq' is set, then Gauss-Hermite masses and mass points are used and considered as fixed, otherwise they serve as starting points for the EM algorithm. The position of the starting points can be concentrated or extended by setting tol smaller or larger than one, respectively. Variance component models with random coefficients (Aitkin, Hinde & Francis, 2005, p. 491) are also possible, in this case the option random.distribution is restricted to the setting 'np' . The weights have to be understood as frequency weights, i.e. setting all weights equal to 2 will duplicate each data point and hence double the disparity and deviance. Warning: There might be some options and circumstances which had not been tested and where the weights do not work." Note that in keeping with the gamlss notation disparity is called global deviance.

Value

The function `gamlssNP` produces an object of class "gamlssNP". This object contain several components.

`family`	the name of the gamlss family
`type`	the type of distribution which in this case is "Mixture"
`parameters`	the parameters for the kernel gamlss family distribution
`call`	the call of the gamlssNP function
`y`	the response variable
`bd`	the binomial demominator, only for BI and BB models
`control`	the NP.control settings
`weights`	the vector of weights of te expanded fit
`G.deviance`	the global deviance
`N`	the number of observations in the fit
`rqres`	a function to calculate the normalized (randomized) quantile residuals of the object (here is the gamlss object rather than gamlssNP and it should change??)
`iter`	the number of external iterations in the last gamlss fitting (?? do we need this?)

- `type` — the type of the distribution or the response variable here set to "Mixture"
- `method` — which algorithm is used for the gamlss fit, RS(), CG() or mixed()
- `contrasts` — the type of contrasts use in the fit
- `converged` — whether the gamlss fit has converged
- `residuals` — the normalized (randomized) quantile residuals of the model
- `mu.fv` — the fitted values of the extended mu model, also sigma.fv, nu.fv, tau.fv for the other parameters if present
- `mu.lp` — the linear predictor of the extended mu model, also sigma.lp, nu.lp, tau.lp for the other parameters if present
- `mu.wv` — the working variable of the extended mu model, also sigma.wv, nu.wv, tau.wv for the other parameters if present
- `mu.wt` — the working weights of the mu model, also sigma.wt, nu.wt, tau.wt for the other parameters if present
- `mu.link` — the link function for the mu model, also sigma.link, nu.link, tau.link for the other parameters if present
- `mu.terms` — the terms for the mu model, also sigma.terms, nu.terms, tau.terms for the other parameters if present
- `mu.x` — the design matrix for the mu, also sigma.x, nu.x, tau.x for the other parameters if present
- `mu.qr` — the QR decomposition of the mu model, also sigma.qr, nu.qr, tau.qr for the other parameters if present
- `mu.coefficients` — the linear coefficients of the mu model, also sigma.coefficients, nu.coefficients, tau.coefficients for the other parameters if present
- `mu.formula` — the formula for the mu model, also sigma.formula, nu.formula, tau.formula for the other parameters if present
- `mu.df` — the mu degrees of freedom also sigma.df, nu.df, tau.df for the other parameters if present
- `mu.nl.df` — the non linear degrees of freedom, also sigma.nl.df, nu.nl.df, tau.nl.df for the other parameters if present
- `df.fit` — the total degrees of freedom use by the model
- `df.residual` — the residual degrees of freedom left after the model is fitted
- `data` — the original data set
- `EMiter` — the number of EM iterations
- `EMconverged` — whether the EM has converged
- `allresiduals` — the residuas for the long fit
- `mass.points` — the estimates mass point (if "np" mixture is used)
- `K` — the number of mass points used
- `post.prob` — contains a matrix of posteriori probabilities,
- `prob` — the estimated mixture probalilities

aic	the Akaike information criterion
sbc	the Bayesian information criterion
formula	the formula used in the expanded fit
random	the random effect formula
pweights	prior weights
ebp	the Empirical Bayes Predictions (Aitkin, 1996b) on the scale of the linear predictor

Note that in case of Gaussian quadrature, the coefficient given at 'z' in coefficients corresponds to the standard deviation of the mixing distribution.

As a by-product, gamlssNP produces a plot showing the global deviance against the iteration number. Further, a plot with the EM trajectories is given. The x-axis corresponds to the iteration number, and the y-axis to the value of the mass points at a particular iteration. This plot is not produced when mixture is set to "gq"

Author(s)

Mikis Stasinopoulos based on function created by Jochen Einbeck John Hinde and Ross Darnell

References

Aitkin, M. and Francis, B. (1995). Fitting overdispersed generalized linear models by nonparametric maximum likelihood. GLIM Newsletter 25 , 37-45.

Aitkin, M. (1996a). A general maximum likelihood analysis of overdispersion in generalized linear models. Statistics and Computing 6 , 251-262.

Aitkin, M. (1996b). Empirical Bayes shrinkage using posterior random effect means from nonparametric maximum likelihood estimation in general random effect models. Statistical Modelling: Proceedings of the 11th IWSM 1996 , 87-94.

Aitkin, M., Francis, B. and Hinde, J. (2005) Statistical Modelling in GLIM 4. Second Edition, Oxford Statistical Science Series, Oxford, UK.

Einbeck, J. & Hinde, J. (2005). A note on NPML estimation for exponential family regression models with unspecified dispersion parameter. Technical Report IRL-GLWY-2005-04, National University of Ireland, Galway.

Einbeck, J. Darnell R. and Hinde J. (2006) npmlreg: Nonparametric maximum likelihood estimation for random effect models, R package version 0.34

Hinde, J. (1982). Compound Poisson regression models. Lecture Notes in Statistics 14 ,109-121.

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.

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

See Also

gamlss, gamlss.family

Examples

```
data(enzyme)
# equivalent model using gamlssNP
mmNP1 <- gamlssNP(act~1, data=enzyme, random=~1,family=NO, K=2)
mmNP2 <- gamlssNP(act~1, data=enzyme, random=~1, sigma.fo=~MASS, family=NO, K=2)
AIC(mmNP1, mmNP2)
```

MX.control *The control function for gamlssMX*

Description

The function sets controls for the gamlssMX function.

Usage

```
MX.control(cc = 1e-04, n.cyc = 200, trace = FALSE,
        seed = NULL, plot = TRUE, sample = NULL, ...)
```

Arguments

cc	convergent criterion for the EM
n.cyc	number of cycles for EM
trace	whether to print the EM iterations
seed	a number for setting the seeds for starting values
plot	whether to plot the sequence of global deviance up to convergence
sample	how large the sample to be in the starting values
...	for extra arguments

Value

Returns a list

Author(s)

Mikis Stasinopoulos and Bob Rigby

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

See Also

`gamlss`, `gamlssMX`, `gamlssMXfits`

`NP.control` *Control function for gamlssNP*

Description

This is a control function for `gamlssNP` function.

Usage

```
NP.control(EMcc = 0.001, EMn.cyc = 200, damp = TRUE,
           trace = TRUE, plot.opt = 3, ...)
```

Arguments

`EMcc`	convergence criterion for the EM
`EMn.cyc`	number of cycles for the EM
`damp`	Not in used
`trace`	whether to print the EM iterations
`plot.opt`	plotting the
`...`	for extra arguments

Value

Returns a list.

Author(s)

Mikis Stasinopoulos

References

Einbeck, J. Darnell R. and Hinde J. (2006) npmlreg: Nonparametric maximum likelihood estimation for random effect models, R package version 0.34

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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

See Also

gamlss, gamlssNP

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plotMP *plotting mass points*

Description

A utility function for plotting two dimension non-parametric distribution. The function uses the `persp()` function.

Usage

```
plotMP(x, y, prob, theta = 20, phi = 20, expand = 0.5, col = "lightblue",
      xlab = "intercept", ylab = "slope", ...)
```

Arguments

`x`	a vector containg points in the x axis
`y`	a vector containg points in the y axis
`prob`	vector containing probabilities which should add up to one
`theta, phi, expand, col`	arguments to pass to the `persp()` function
`xlab`	the x label
`ylab`	the y label
`...`	additinal argument to be passed to `persp()`

Details

The function call

Value

A graph is produced.

Author(s)

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References

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

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Stasinopoulos D. M. Rigby R.A. (2007) Generalized additive models for location scale and shape (GAMLSS) in R. *Journal of Statistical Software*, Vol. **23**, Issue 7, Dec 2007, 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, Heller GZ. (2024) Generalized Additive Models for Location, Scale and Shape: A Distributional Regression Approach, with Applications. Cambridge University Press.

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

See Also

`gamlssNP`, `persp`

Examples

```
gamma_0 <- c( -4.4, -3,-2.2, -.5, 0.1, 1, 1.5, 2.2,  3.5, 4.1 )
gamma_1 <- c( 2.2, 1.2, 0.1, -1, -2.3, -4.6 , 5.1, -3.2, 0.1, -1.2)
   prob <- c(0.1, .05, .12, 0.25, 0.08, 0.12, 0.10, 0.05, 0.10, 0.03 )
plotMP(gamma_0, gamma_1,prob)
```

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