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npmlreg-package

Description

Nonparametric maximum likelihood estimation or Gaussian quadrature for overdispersed generalized linear models and variance component models. The main functions are `alldist` and `allvc`.

Details

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Author(s)

Jochen Einbeck, Ross Darnell and John Hinde.

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References


See Also

glm

Description

Fits a random effect model using Gaussian quadrature (Hinde, 1982) or nonparametric maximum likelihood estimation (Aitkin, 1996a). The function alldist is designed to account for overdispersion, while allvc fits variance component models.

Usage

alldist(formula,
random = ~1,
family = gaussian(),
data,
k = 4,
random.distribution = "np",
tol = 0.5,
offset,
weights,
pluginz,
na.action,
EMmaxit = 500,
EMdev.change = 0.001,
lambda = 0,
damp = TRUE,
damp.power = 1,
spike.protect = 0,
sdev,
shape,
plot.opt = 3,
verbose = TRUE,
...)

allvc(formula,
random = ~1,
family = gaussian(),
data,
k = 4,
random.distribution = "np",
tol = 0.5,
offset,
weights,
pluginz,
na.action,
EMmaxit = 500,
EMdev.change = 0.001,
lambda=0,
damp = TRUE,
damp.power = 1,
spike.protect=0,
sdev,
shape,
plot.opt = 3,
verbose = TRUE,
...)

Arguments

- **formula** a formula defining the response and the fixed effects (e.g. \( y \sim x \)).
- **random** a formula defining the random model. In the case of `alldist`, set `random = ~1` to model overdispersion, and for instance `random = ~x` to introduce a random coefficient \( x \). In the case of `allvc`, set `random=~1|PSU` to model overdispersion on the upper level, where PSU is a factor for the primary sampling units, e.g. groups, clusters, classes, or individuals in longitudinal data, and define random coefficients accordingly.
- **family** conditional distribution of responses: "gaussian", "poisson", "binomial", "Gamma", or "inverse.gaussian" can be set. If "gaussian", "Gamma", or "inverse.gaussian", then equal component dispersion parameters are assumed, except if the optional parameter `lambda` is modified. The same link functions as for function `glm` are supported.
- **data** the data frame (mandatory, even if it is attached to the workspace!).
- **k** the number of mass points/integration points (supported are up to 600 mass points).
- **random.distribution** the mixing distribution, Gaussian Quadrature (gq) or NPML (np) can be set.
- **tol** the tol scalar (usually, \( 0 < \text{tol} \leq 1 \))
- **offset** an optional offset to be included in the model.
- **weights** optional prior weights for the data.
- **pluginz** optional numerical vector of length \( k \) specifying the starting mass points of the EM algorithm.
**Details**

The nonparametric maximum likelihood (NPML) approach was introduced in Aitkin (1996) as a tool to fit overdispersed generalized linear models. The idea is to approximate the unknown and unspecified distribution of the random effect by a discrete mixture of exponential family densities, leading to a simple expression of the marginal likelihood which can then be maximized using a standard EM algorithm.

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
The number of components \( k \) of the finite mixture has to be specified beforehand. When option 'gq' is set, then Gauss-Hermite masses and mass points are used, assuming implicitly a normally distributed random effect. When option 'np' is chosen, the EM algorithm uses the Gauss-Hermite masses and mass points as starting points. The position of the starting points can be concentrated or extended by setting \( \text{tol} \) smaller or larger than one, respectively.

Fitting random coefficient models (Aitkin, Francis & Hinde, 2009, pp. 496, p. 514) is possible by specifying the random term explicitly. Note that the setting \( \text{random} \sim x \) gives a model with a random slope and a random intercept, and that only one random coefficient can be specified. The option \( \text{random.distribution} \) is restricted to np in this case, i.e. Gaussian Quadrature is not supported for random coefficient models (see also Aitkin, Francis & Hinde (2005), page 475 bottom).

As for \( \text{glm} \), there are three different ways of specifying a binomial model, namely through

- a two-column matrix before the ‘\( \sim \)’ symbol, specifying the counts of successes and non-successes.
- a vector of proportions of successes before the ‘\( \sim \)’ symbol, and the associated number of trials provided in the \( \text{weights} \) argument.
- a two-level factor before the ‘\( \sim \)’ symbol (only for Bernoulli-response).

The weights have to be understood as frequency weights, i.e. setting all weights in \text{alldist} equal to 2 will duplicate each data point and hence double the disparity and deviance.

The Inverse Gaussian (IG) response distribution is parametrized as usual through the mean and a scaling parameter. We refer to the latter, which is the inverse of the dispersion parameter in exponential family formulation, as shape. The canonical \( 1/\mu^2 \) link is supported, but it is quite tenuous since the linear predictor is likely to become negative after adding the random effect. The \( \log \) link behaves more reliably for this distribution.

For \( k \geq 54 \), mass points with negligible mass (i.e. < 1e-50) are omitted. The maximum number of 'effective' mass points is then 198.

**Value**

The function \text{alldist} produces an object of class \text{glmNPML} (if \text{random.distribution} is set to 'np') or \text{glmGQ} ('gq'). Both objects contain the following 29 components:

- **coefficients**: a named vector of coefficients (including the mass points). In case of Gaussian quadrature, the coefficient given at \( z \) corresponds to the standard deviation of the mixing distribution.
- **residuals**: the difference between the true response and the empirical Bayes predictions.
- **fitted.values**: the empirical Bayes predictions (Aitkin, 1996b) on the scale of the responses.
- **family**: the ‘family’ object used.
- **linear.predictors**: the extended linear predictors \( \hat{\eta}_{jk} \).
disparity the disparity (-2logL) of the fitted mixture regression model.
deviance the deviance of the fitted mixture regression model.
null.deviance the deviance for the null model (just containing an intercept), comparable with deviance.
df.residual the residual degrees of freedom of the fitted model (including the random part).
df.null the residual degrees of freedom for the null model.
y the (extended) response vector.
call the matched call.
formula the formula supplied.
random the random term of the model formula.
data the data argument.
model the (extended) design matrix.
weights the case weights initially supplied.
offset the offset initially supplied.
mass.points the fitted mass points.
masses the mixture probabilities corresponding to the mass points.
sdev a list of the two elements sdev$sdev and sdev$sdevk. The former is the estimated standard deviation of the Gaussian mixture components (estimated over all mixture components), and the latter gives the unequal or smooth component-specific standard deviations. All values are equal if \( \lambda = 0 \).
shape a list of the two elements shape$shape and shape$shapek, to be interpreted in analogy to sdev.
rsdev estimated random effect standard deviation.
post.prob a matrix of posteriori probabilities.
post.int a vector of 'posteriori intercepts' (as in Sofroniou et al. (2006)).
ebp the empirical Bayes Predictions on the scale of the linear predictor. For compatibility with older versions.
EMiter gives the number of iterations of the EM algorithm.
EMconverged logical value indicating if the EM algorithm converged.
lastglm the fitted glm object from the last EM iteration.
Misc contains additional information relevant for the summary and plot functions, in particular the disparity trend and the EM trajectories.

If a binomial model is specified by giving a two-column response, the weights returned by weights are the total numbers of cases (factored by the supplied case weights) and the component y of the result is the proportion of successes.

As a by-product, alldist produces a plot showing the disparity in dependence of 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 for GQ.
Note

In contrast to the GLIM 4 version, this R implementation uses for Gaussian (as well Gamma and IG) mixtures by default a damping procedure in the first cycles of the EM algorithm (Einbeck & Hinde, 2006), which stabilizes the algorithm and makes it less sensitive to the optimal choice of tol. If tol is very small (i.e. less than 0.1), it can be useful to set damp.power to values larger than 1 in order to accelerate convergence. Do not use damp.power=0, as this would mean permanent damping during EM. Using the option pluginz, one can to some extent circumvent the necessity to specify tol by giving the starting points explicitly. However, when using pluginz for normal, Gamma- or IG- distributed response, damping will be strictly necessary to ensure that the imposed starting points don’t get blurred immediately due to initial fluctuations, implying that tol still plays a role in this case.

Author(s)


References


See Also

 glm, summary.glmmNPML, predict.glmmNPML family.glmmNPML, plot.glmmNPML.

Examples

# The first three examples (galaxy data, toxoplasmosis data, fabric faults)
# are based on GLIM examples in Aitkin et al. (2005), and the forth example using
# the Hospital-Stay-Data (Rosner, 2000) is taken from Einbeck & Hinde (2006).
# The fifth data example using the Oxford boys is again inspired by Aitkin et al. (2005).
# The sixth example on Irish suicide rates is taken from Sofroniou et al. (2006).

# The galaxy data
data(galaxies, package="MASS")
gal <- as.data.frame(galaxies)
galaxy.np6 <- alldist(galaxies/1000~1, random=~1, random.distribution="np",
data=gal, k=6)
galaxy.np8u <- alldist(galaxies/1000~1, random=~1, random.distribution="np",
data=gal, k=8, lambda=0.99)
round(galaxy.np8u$dev$devk, digits=3)
# [1] 0.912 0.435 0.220 0.675 1.214 0.264 0.413 0.297

# The toxoplasmosis data
data(rainfall, package="forward")
fall$<-= rainfall$Rain/1000
fall$x2<-= rainfall$x^2; rainfall$x3<-= rainfall$x^3
toxo.np3<-= alldist(cbind(Cases, Total-Cases) ~ x+x2+x3, random=~1,
random.distribution="np", family=binomial(link=logit), data=rainfall, k=3)
toxo.np3<-= alldist(cbind(Cases, Total-Cases) ~ x, random=~x,
random.distribution="np", family=binomial(link=logit), data=rainfall, k=3)
# is the same as
toxo.np3<-= alldist(Cases/Total ~ x, random =~x, weights=Total,
family=binomial(link=logit), data=rainfall, k=3)
# or
toxo.np3<-=update(toxo.np3, .~.x2-x3, random = ~x)

# The fabric faults data
data(fabric)
coefficients(alldist(y ~ x, random=~1, family=poisson(link=log),
random.distribution="gq", data= fabric, k=3, verbose=FALSE))
# (Intercept) x z
# -3.3088663 0.8488060 0.3574909

# The Pennsylvanian hospital stay data
data(hosp)
fitnp3<-= alldist(duration~age+temp1, data=hosp, k=3, family=Gamma(link=log),
tol=0.5)
fitnp3$shape$shape
# [1] 50.76636
fitnp3<-= alldist(duration~age+temp1, data=hosp, k=3, family=Gamma(link=log),
tol=0.5, lambda=0.9)
fitnp3$shape$shape
# [1] 49.03101 42.79522 126.64077

# The Oxford boys data
data(Oxboys, package="nlme")
Oxboys$boy <- gl(26,9)
allvc(height~age, random=~1|boy, data=Oxboys, random.distribution="gq", k=20)
alvc(height~age, random=~1|boy, data=Oxboys,random.distribution="np",k=8)
# with random coefficients:
allvc(height~age,random=~age|boy, data=0xboys, random.distribution='np', k=8)

# Irish suicide data
data(irlsuicide)
# Crude rate model:
crude<- allvc(death~sex* age, random=~1|ID, offset=log(pop),
    k=3, data=irlsuicide, family=poisson)
crude$disparity
# [1] 654.021
# Relative risk model:
relrisk<- allvc(death~1, random=~1|ID, offset=log(expected),
    k=3, data=irlsuicide, family=poisson)
relrisk$disparity
# [1] 656.4955

dkern  

Aitchison-Aitken kernel

Description

Discrete kernel for categorical data with \( k \) unordered categories.

Usage

dkern(x, y, k, lambda)

Arguments

- \( x \) : categorical data vector
- \( y \) : positive integer defining a fixed category
- \( k \) : positive integer giving the number of categories
- \( \lambda \) : smoothing parameter

Details

This kernel was introduced in Aitchison & Aitken (1976); see also Titterington (1980).

The setting \( \lambda = 1/k \) corresponds to the extreme case ‘maximal smoothing’, while \( \lambda = 1 \) means ‘no smoothing’. Statistically sensible settings are only \( 1/k \leq \lambda \leq 1 \).

Author(s)

Jochen Einbeck (2006)
**References**


**Examples**

```r
k<-6;
dkern(1:k,4,k,0.99)
# Kernel centered at the 4th component with a very small amount of smoothing.

## The function is currently defined as
function(x,y,k,lambda){
  ifelse(y==x, lambda, (1-lambda)/(k-1))
}
```

**fabric**  
*The Fabric Data*

**Description**

The data are 32 observations on faults in rolls of fabric.

**Usage**

```r
data(fabric)
```

**Format**

A data frame with 32 observations on the following 3 variables.

- `leng` the length of the roll : a numeric vector
- `y` the number of faults in the roll of fabric : a discrete vector
- `x` the log of the length of the roll : a numeric vector

**Details**

The data are 32 observations on faults in rolls of fabric taken from Hinde (1982) who used the EM algorithm to fit a Poisson-normal model. The response variable is the number of faults in the roll of fabric and the explanatory variable is the log of the length of the roll.

**Note**

This data set and help file is an identical copy of the `fabric` data in package `gamlss.data`. 
family.glmmNPML

Source

John Hinde.

References


Examples

data(fabric)
attach(fabric)
plot(x,y)
detach(fabric)

Methods for objects of class glmmNPML or glmmGQ

Description

Methods for the generic family and model.matrix functions

Usage

## S3 method for class 'glmmNPML'
family(object, ...)
## S3 method for class 'glmmGQ'
family(object, ...)
## S3 method for class 'glmmNPML'
model.matrix(object, ...)
## S3 method for class 'glmmGQ'
model.matrix(object, ...)

Arguments

object object of class glmmNPML or glmmGQ.

... further arguments, ensuring compatibility with generic functions.

Note

The generic R functions update(), coefficients(), coef(), fitted(), fitted.values(), and df.residual() can also be applied straightforwardly on all objects of class glmmNPML or glmmGQ. They are not listed above as they use the generic default functions and are not separately implemented.

Explicit implementations exist for predict, summary, print, and plot, and these functions are explained in the corresponding help files.
**gqz**

**Author(s)**

Jochen Einbeck and John Hinde (2007)

**See Also**

`summary.glmmNPML`, `predict.glmmNPML`, `family`, `model.matrix`, `update`, `coefficients`, `alldist`.

---

### gqz

**Gauss-Hermite integration points**

**Description**

Calculate Gaussian Quadrature points for the Normal distribution using the abscissas and weights for Hermite integration.

**Usage**

```r
gqz(numnodes=20, minweight=0.000001)
```

**Arguments**

- `numnodes` theoretical number of quadrature points.
- `minweight` locations with weights that are less than this value will be omitted.

**Details**

The conversion of the locations and weights is given in Lindsey (1992, page 169:3) and Skrondal & Rabe-Hesketh (2004, page 165:1). The argument `numnodes` is the theoretical number of quadrature points, locations with weights that are less than the argument `minweight` will be omitted. The default value of `minweight`=0.000001 returns 14 masspoints for the default `numnodes`=20 as in Aitkin, Francis & Hinde (2005).

**Value**

A list with two vectors:

- `location` locations of mass points
- `weight` masses

**Author(s)**

Nick Sofroniou (2005)
References


See Also

alldist, allvc

Examples

gqz(20, minweight=1e-14)
   # gives k=20 GH integration points. These are used in alldist
   # and allvc as fixed mass point locations when working with
   # option random.distribution='gq', and serve as EM starting points
   # otherwise.

hosp

The Pennsylvanian Hospital Stay Data

Description

The data, 25 observations, are a subset from a larger data set collected on persons discharged from a selected Pennsylvania hospital as part of a retrospective chart review of antibiotic use in hospitals (Towensend et al., 1979, Rosner, 2000).

Usage

data(hosp)

Format

A data frame with 25 observations on the following 9 variables. All variables are given as numerical vectors.

id  patient ID.
duration the total number of days patients spent in hospital.
age  age of patient in whole years.
sex  gender: 1=M, 2=F.
temp1  first temperature following admission.
wbc1  first WBC count \((\times 10^3)\) following admission. [WBC= white blood cells].
antib  received antibiotic: 1=yes, 2=no.
bact  received bacterial culture: 1=yes, 2=no.
serv  service: 1=med., 2=surg.
**Warnings**

Don’t confuse with the Barcelona ‘Hospital stay data’ aep in package `gamlss`.

**Source**

B. Rosner, Harvard University.

**References**


**Examples**

```r
data(hosp)
glm1 <- glm(dur~age+temp+wbc1, data=hosp, family=Gamma(link=log))
```

---

**irlsuicide**  
*Irish Suicide Data*

**Description**


**Usage**

```r
data(irlsuicide)
```

**Format**

A data frame with 104 observations on the following 8 variables.

- **id**: a factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 corresponding to Regions.
- **pop**: a numeric vector giving the population sizes (estimated for 1994).
- **death**: a numeric vector giving the total number of deaths.
- **sex**: a factor for gender with levels 0 (female) and 1 (male).
- **age**: a factor for age with levels 1 (0-29), 2 (30-39), 3 (40-59), 4 (60+ years).
- **smr**: a numeric vector with standardized mortality ratios (SMRs)
- **expected**: a numeric vector with ‘expected’ number of cases obtained from a reference population (Ahlbom, 1993).
Details

The data set is examined in Sofroniou et al. (2006), using a variance component model with regions as upper level.

Source


References


Examples

data(irlsuicide)
library(lattice)
trellis.device(color=FALSE)
plot2age<-rep(gl(4,2),13)
xyplot(irlsuicide$death/irlsuicide$pop~plot2age|irlsuicide$Region,
pch=(1+(irlsuicide$sex==1)),xlab="age",ylab="Crude rates")

missouri

Missouri lung cancer data

Description


Usage

data(missouri)

Format

A data frame with 84 observations on the following 2 variables.

Size  population of the city.
Deaths  number of lung cancer deaths.
The data set was analyzed using a Poisson model with normal random effect in Tsutakawa (1985), and using a binomial logit model with unspecified random effect distribution in Aitkin (1996b). Aitkin fitted this model with GLIM4.

Source


References


Examples

data(missouri)
alldist(Deaths=1, offset=log(Size), random=~1, k=2,
family=poisson(link='log'), data=missouri)

---

plot.glmmNPML

Plot Diagnostics for objects of class glmmNPML or glmmGQ

Description

The functions alldist and allvc produce objects of type glmmGQ, if Gaussian quadrature (Hinde, 1982, random.distribution="gq") was applied for computation, and objects of class glmmNPML, if parameter estimation was carried out by nonparametric maximum likelihood (Aitkin, 1996a, random.distribution="np"). The functions presented here give some useful diagnostic plotting functionalities to analyze these objects.

Usage

## S3 method for class 'glmmNPML'
plot(x, plot.opt = 15, noformat=FALSE, ...)

## S3 method for class 'glmmGQ'
plot(x, plot.opt = 3, noformat=FALSE, ...)

Arguments

x a fitted object of class glmmNPML or glmmGQ.
plot.opt an integer with values $0 \leq \text{plot.opt} \leq 15$. 
**noformat** if TRUE, then any formatting of the plots is omitted (useful if the user wants to include the plots into a panel of several other plots, possibly generated by other functions).

... further arguments which will mostly not have any effect (and are included only to ensure compatibility with the generic `plot()`-function.)

**Details**

See the help pages to `alldist` and the vignette (Einbeck & Hinde, 2007). It is sufficient to write `plot` instead of `plot.glmmNPML` or `plot.glmmGQ`, since the generic `plot` function provided in R automatically selects the right model class.

**Value**

For class `glmmNPML`: Depending on the choice of `plot.opt`, a subset of the following four plots:

1. Disparity trend.
2. EM Trajectories.
3. Empirical Bayes Predictions against observed response.
4. Individual posterior probabilities.

The number given in `plot.opt` is transformed into a binary number indicating which plots are to be selected. The first digit (from the right!) refers to plot 1, the second one to plot 2, and so on. For example, `plot.opt=4` gives the binary number 0100 and hence selects just plot 3.

For class `glmmGQ`: Depending on the choice of `plot.opt`, a subset of plots 1 and 3. Again, the number is transformed into binary coding, yielding only the disparity trend for `plot.opt=1`, only the EBP’s for `plot.opt=2`, and both plots for `plot.opt=3`.

**Author(s)**

Jochen Einbeck and John Hinde (2007)

**References**


**See Also**

`alldist`, `allvc`
Examples

data(galaxies, package="MASS")
gal<-as.data.frame(galaxies)
galaxy.np4u <- alldist(galaxies/1000-1,random=-1,k=4,tol=0.5,data=gal,lambda=1)
predict(galaxy.np4u, type="response") # EBP on scale of responses

plot(galaxy.np4u, plot.opt=4) # plots only EBP vs. response
plot(galaxy.np4u, plot.opt=3) # gives same output as given by default when executing alldist
plot(galaxy.np4u) # gives all four plots.

post

Posterior probabilities/intercepts, and mass point classifications

Description

Takes an object of class glmmNPML or glmmGQ and displays the posterior probabilities \( w_{ik} \) as well as the posterior intercepts (Sofroniou et. al, 2006). Further it classifies the observations to mass points according to their posterior probability. The level on which the information in all three cases is displayed can be chosen by the user via the level argument ("upper" or "lower"). The actual information in both cases is identical, the latter is just an expanded version of the former. In case of simple overdispersion models, the level argument is not relevant.

Usage

post(object, level="upper")

Arguments

object an object of class glmmNPML or glmmGQ.
level "upper" or "lower".

Value

A list of the following four items:

\texttt{prob} posterior probabilities (identical to \texttt{object$post.prob} in case of "lower" and for one-level models).
\texttt{int} posterior intercepts (identical to \texttt{object$post.int} in case of "lower" and for one-level models).
\texttt{classif} a numerical vector containing the class numbers (the order of the classes corresponds to the order of the mass points given in the output of alldist or allvc).
\texttt{level} either "lower", "upper", or "none" (for one-level models).

Author(s)

References


See Also

alldist, allvc

Examples

data(galaxies, package="MASS")
gal <- as.data.frame(galaxies)
post(alldist(galaxies/1000~1, random=-1, data=gal, k=5))$classif
  # classifies the 82 galaxies to one of the five mass points

predict.glmmNPML       Prediction from objects of class glmmNPML or glmmGQ

Description

The functions alldist and allvc produce objects of type glmmGQ, if Gaussian quadrature (Hinde, 1982, random.distribution="gq") was applied for computation, and objects of class glmmNPML, if parameter estimation was carried out by nonparametric maximum likelihood (Aitkin, 1996a, random.distribution="np"). The functions presented here give predictions from those objects.

Usage

## S3 method for class 'glmmNPML'
predict(object, newdata, type = "link", ...)
## S3 method for class 'glmmGQ'
predict(object, newdata, type = "link", ...)

Arguments

object  a fitted object of class glmmNPML or glmmGQ.
newdata a data frame with covariates from which prediction is desired. If omitted, empirical Bayes predictions for the original data will be given.
type    if set to link, the prediction is given on the linear predictor scale. If set to response, prediction is given on the scale of the responses.
...     further arguments which will mostly not have any effect (and are included only to ensure compatibility with the generic predict()- function.)
The predicted values are obtained by

- Empirical Bayes (Aitkin, 1996b), if newdata has not been specified. That is, the prediction on
  the linear predictor scale is given by $\sum \eta_{ik} w_{ik}$, whereby $\eta_{ik}$ are the fitted linear predictors,
  $w_{ik}$ are the weights in the final iteration of the EM algorithm (corresponding to the posterior
  probability for observation $i$ to come from component $k$), and the sum is taken over the
  number of components $k$ for fixed $i$.

- the marginal model, if object is of class glmmNPML and newdata has been specified. That is,
  computation is identical as above, but with $w_{ik}$ replaced by the masses $\pi_k$ of the fitted model.

- the analytical expression for the marginal mean of the responses, if object is of class glmmGQ
  and newdata has been specified. See Aitkin et al. (2009), p. 481, for the formula. This method
  is only supported for the logarithmic link function, as otherwise no analytical expression for
  the marginal mean of the responses exists.

It is sufficient to call predict instead of predict.glmmNPML or predict.glmmGQ, since the generic
predict function provided in R automatically selects the right model class.

Value

A vector of predicted values.

Note

The results of the generic fitted() method correspond to predict(object, type="response").
Note that, as we are working with random effects, fitted values are never really ‘fitted’ but rather
‘predicted’.

Author(s)


References


Aitkin, M. (1996b). Empirical Bayes shrinkage using posterior random effect means from non-
parametric maximum likelihood estimation in general random effect models. Statistical Modelling:

Series, Oxford, UK.


See Also

alldist, allvc, predict
Examples

# Toxoplasmosis data:

data(rainfall, package="forward")
rainfall$x <- rainfall$Rain/1000
toxo.0.3x <- alldist(cbind(Cases, Total-Cases)-1, random=-x,
data=rainfall, k=3, family=binomial(link=logit))
toxo.1.3x <- alldist(cbind(Cases, Total-Cases)-x, random=-x,
data=rainfall, k=3, family=binomial(link=logit))
predict(toxo.0.3x, type="response", newdata=data.frame(x=2))
# [1] 0.4608
predict(toxo.1.3x, type="response", newdata=data.frame(x=2))
# [1] 0.4608
# gives the same result, as both models are equivalent and only differ
# by a parameter transformation.

# Fabric faults data:

data(fabric)
names(fabric)
# [1] "leng" "y" "x"
faults.g2 <- alldist(y - x, family=poisson(link=log), random=-1,
data= fabric, k=2, random.distribution="gq")
predict(faults.g2, type="response", newdata=fabric[1:6,])
# is not the same as
predict(faults.g2, type="response"[1:6]
# since in the first case prediction is done using the analytical
# mean of the marginal distribution, and in the second case using the
# individual posterior probabilities in an empirical Bayes approach.

summary.glmmNPML

Summarizing finite mixture regression fits

Description

These functions are the summary and print methods for objects of type glmmNPML and glmmGQ.

Usage

## S3 method for class 'glmmNPML'
summary(object, digits = max(3, getOption("digits") - 3), ...)

## S3 method for class 'glmmGQ'
summary(object, digits = max(3, getOption("digits") - 3), ...)

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

## S3 method for class 'glmmGQ'
print(x, digits=max(3,getOption('digits')-3), ...)
Arguments

- **object**: a fitted object of class `glmmNPML` or `glmmGQ`.
- **x**: a fitted object of class `glmmNPML` or `glmmGQ`.
- **digits**: number of digits; applied on various displayed quantities.
- **...**: further arguments, which will mostly be ignored.

Details

The `summary(...)` and `print(...)` -functions invoke the generic `useMethod(...)` function and detect the right model class automatically. In other words, it is enough to write `summary(...)` or `print(...)`.

Value

Prints regression output or summary on screen.

Objects returned by `summary.glmmNPML` or `summary.glmmGQ` are essentially identical to objects of class `glmmNPML` or `glmmGQ`. However, their `$coef` component contains the parameter standard errors and t values (taken from the GLM fitted in the last EM iteration), and they have two additional components `$dispersion` and `$lastglmsum` providing the estimated dispersion parameter and a summary of the glm fitted in the last EM iteration.

Note

Please note that the provided parameter standard errors tend to be underestimated as the uncertainty due to the EM algorithm is not incorporated into them. According to Aitkin et al (2009), Section 7.5, page 440, more accurate standard errors can be obtained by dividing the (absolute value of the) parameter estimate through the square root of the change in disparity when omitting/not omitting the variable from the model.

Author(s)


References


See Also

`alldist, allvc, summary, print, family.glmmNPML`
tolfind  

**Grid search over tol for NPML estimation of (generalized) random effect models**

**Description**

Performs a grid search to select the parameter `tol`, which is a tuning parameter for starting point selection of the EM algorithm for NPML estimation (see e.g. Aitkin, Hinde & Francis, 2009, p. 437)

**Usage**

```r
tolfind(formula, random = ~1, family = gaussian(), data, k = 4, random.distribution="np", offset, weights, na.action, EMmaxit = 500, EMdev.change = 0.001, lambda = 0, damp = TRUE, damp.power = 1, spike.protect = 1, sdev, shape, plot.opt = 1, steps = 15, find.in.range = c(0.05, 0.8), verbose = FALSE, noformat = FALSE, ...)
```

**Arguments**

- `formula`: a formula defining the response and the fixed effects (e.g. `y ~ x`).
- `random`: a formula defining the random model. Set `random=~1` to model overdispersion.
- `family`: conditional distribution of responses: "gaussian", "poisson", "binomial", "Gamma", or "inverse.gaussian" can be set.
- `data`: the data frame (mandatory, even if it is attached to the workspace!).
- `k`: the number of mass points/integration points (supported are up to 600 mass points).
tolfind

random.distribution
the mixing distribution, Gaussian Quadrature (gq) or NPML (np) can be set.

offset
an optional offset to be included in the model.

weights(optional prior weights for the data.

na.action
a function indicating what should happen when NA’s occur, with possible arguments na.omit and na.fail. The default is set by the na.action setting in options().

EMmaxit
maximum number of EM iterations.

EMdev.change
stops EM algorithm when deviance change falls below this value.

lambda
see the help file for alldist.

damp
switches EM damping on or off.

damp.power
steers degree of damping.

spike.protect
see the help file for alldist. For unequal or smooth component dispersion parameters, the setting spike.protect=1 is strongly recommended.

sdev
optional fixed standard deviation for normal mixture.

shape
optional fixed shape parameter for Gamma and IG mixtures.

plot.opt
For plot.opt=1 the EM trajectories are plotted, for plot.opt=2 the development of the disparity $-2 \log L$ over iteration number is plotted, for plot.opt=3 both plots are shown, and for plot.opt=0 none of them.

steps
number of grid points for the search of tol.

find.in.range
range for the search of tol.

verbose
If set to FALSE, no printed output is given during execution of alldist or allvc.

noformat
If TRUE, then any formatting of the plots is omitted.

... further arguments which will be ignored.

Details

The EM algorithm for NPML estimation (Aitkin, 1996) uses the Gauss-Hermite masses and mass points as starting points. The position of the starting points can be concentrated or extended by setting tol smaller or larger than 1, respectively. The tuning parameter tol is, as in GLIM4, responsible for this scaling. A careful selection of tol may be necessary for some data sets. The reason is that NPML has a tendency to get stuck in local maxima, as the log-likelihood function is not concave for fixed k (Boehning, 1999).

For Gaussian, Gamma, and IG mixtures this R implementation uses by default a damping procedure in the first cycles of the EM algorithm (Einbeck & Hinde, 2006), which stabilizes the algorithm and makes it less sensitive to the optimal choice of tol. Application of tolfind to check that the optimal solution has not been overlooked may nevertheless be advisable.

tolfind works for alldist and allvc. The tolfind function is mainly designed for NPML (random.distribution="np"). It can also be applied to Gaussian Quadrature (random.distribution="gq"), though tol is of little importance for this and primarily influences the speed of convergence.
Value

A list of 5 items:

- **MinDisparity**: the minimal disparity achieved (for which EM converged).
- **Mintol**: the tol value at which this disparity is achieved.
- **AllDisparities**: a vector containing all disparities calculated on the grid.
- **Alltol**: all corresponding tol values making up the grid.
- **AllEMconverged**: a vector of Booleans indicating if EM converged for the particular tol values.

Author(s)


References


See Also

- `alldist`, `allvc`

Examples

data(galaxies, package="MASS")
gal<-as.data.frame(galaxies)
tolfind(galaxies/1000~1, random=-1, k=5, data=gal, lambda=1, damp=TRUE,
        find.in.range=c(0,1), steps=10)
# Minimal Disparity: 380.1444 at tol= 0.5
Usage

weightslog1.calc.w(p, fjk, weights)
expand(x, k)
expand.vc(x, ni)
binomial.expand(Y, k, w)

Arguments

p ................
fjk ..............
weights ..........
x ................
k ..............
ni ..............
Y .............
w .............

Author(s)

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