Package 'gnm'

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Title Generalized Nonlinear Models

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Description Functions to specify and fit generalized nonlinear models,including models with multiplicative interaction terms such as
the UNIDIFF model from sociology and the AMMI model from crop
science, and many others. Over-parameterized representations
of models are used throughout; functions are provided for
inference on estimable parameter combinations, as well as standard methods for diagnostics etc.

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URL http://go.warwick.ac.uk/gnm

License GPL (>= 2)

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gnm-package *Generalized Nonlinear Models*

Description

Functions to specify, fit and evaluate generalized nonlinear models.

Details

gnm provides functions to fit generalized nonlinear models by maximum likelihood. Such models extend the class of generalized linear models by allowing nonlinear terms in the predictor.

Some special cases are models with multiplicative interaction terms, such as the UNIDIFF and row-column association models from sociology and the AMMI and GAMMI models from crop science; stereotype models for ordered categorical response, and diagonal reference models for dependence on a square two-way classification.

gnm is a major re-working of an earlier Xlisp-Stat package, "Llama". Over-parameterized representations of models are used throughout; functions are provided for inference on estimable parameter combinations, as well as standard methods for diagnostics etc.

The following documentation provides further information on the gnm package:

gnmOverview `vignette("gnmOverview", package = "gnm")`

NEWS `file.show(system.file("NEWS", package = "gnm"))`

Author(s)

Heather Turner and David Firth

Maintainer: Heather Turner <ht@heatherturner.net>

References

http://www.warwick.ac.uk/go/gnm

See Also

gnm for the model fitting function, with links to associated functions.

Examples

```
demo(gnm)
```

anova.gnm *Analysis of Deviance for Generalized Nonlinear Models*

Description

Compute an analysis of deviance table for one or more generalized nonlinear models

Usage

```
## S3 method for class 'gnm'
anova(object, ..., dispersion = NULL, test = NULL)
```

Arguments

object	an object of class gnm
...	additional objects of class gnm or glm
dispersion	the dispersion parameter for the fitting family. By default it is derived from object
test	(optional) a character string, (partially) matching one of "Chisq", "F", or "Cp". See stat.anova.

Details

Specifying a single object gives a sequential analysis of deviance table for that fit. The rows of the table show the reduction in the residual deviance and the current residual deviance as each term in the formula is added in turn.

If more than one object is specified, the rows of the table show the residual deviance of the current model and the change in the residual deviance from the previous model. (This only makes statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

If test is specified, the table will include test statistics and/or p values for the reduction in deviance. For models with known dispersion (e.g., binomial and Poisson fits) the chi-squared test is most appropriate, and for those with dispersion estimated by moments (e.g., 'gaussian', 'quasibinomial' and 'quasipoisson' fits) the F test is most appropriate. Mallows' Cp statistic is the residual deviance plus twice the estimate of σ^2 times the residual degrees of freedom, which is closely related to AIC (and a multiple of it if the dispersion is known).

Value

An object of class "anova" inheriting from class "data.frame".

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of na.action = na.omit is used; an error will be given in this case.

Author(s)

Heather Turner

See Also

gnm, anova

Examples

```
set.seed(1)
data(occupationalStatus)

##  Fit a uniform association model separating diagonal effects
Rscore <- scale(as.numeric(row(occupationalStatus)), scale = FALSE)
Cscore <- scale(as.numeric(col(occupationalStatus)), scale = FALSE)
Uniform <- glm(Freq ~ origin + destination + Diag(origin, destination) +
               Rscore:Cscore, family = poisson, data = occupationalStatus)

##  Fit an association model with homogeneous row-column effects
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination), family = poisson,
               data = occupationalStatus)

##  Fit an association model with separate row and column effects
RC <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
          Mult(origin, destination), family = poisson,
          data = occupationalStatus)

anova(RC, test = "Chisq")

anova(Uniform, RChomog, RC, test = "Chisq")
```

---

asGnm *Coerce Linear Model to gnm Object*

Description

asGnm is a generic function which coerces objects of class "glm" or "lm" to an object of class "gnm".

Usage

```
asGnm(object, ...)
```

Arguments

object	an object of class "glm" or "lm".
...	additional arguments for method functions.

Details

Components are added to or removed from `object` to produce an object of class "gnm". This can be useful in model building, see examples.

Value

An object of class "gnm" - see `gnm` for full description.

Author(s)

Heather Turner

References

Vargas, M, Crossa, J, van Eeuwijk, F, Sayre, K D and Reynolds, M P (2001). Interpreting treatment by environment interaction in agronomy trials. *Agronomy Journal* **93**, 949–960.

See Also

`gnm`, `glm`, `lm`

Examples

```
set.seed(1)
data(wheat)

##  Scale yields to reproduce analyses reported in Vargas et al (2001)
yield.scaled <- wheat$yield * sqrt(3/1000)
treatment <- interaction(wheat$tillage, wheat$summerCrop, wheat$manure,
                         wheat$N, sep = "")
##  Fit linear model
mainEffects <- lm(yield.scaled ~ year + treatment, data = wheat)

##  Convert to gnm object to allow addition of Mult() term
svdStart <- residSVD(mainEffects, year, treatment, 3)
bilinear1 <- update(asGnm(mainEffects), . ~ . +
                    Mult(year, treatment),
                    start = c(coef(mainEffects), svdStart[,1]))
```

---

backPain *Data on Back Pain Prognosis, from Anderson (1984)*

Description

Data from a study of patients suffering from back pain. Prognostic variables were recorded at presentation and progress was categorised three weeks after treatment.

Usage

```
data(backPain)
```

Format

A data frame with 101 observations on the following 4 variables.

x1 length of previous attack.

x2 pain change.

x3 lordosis.

pain an ordered factor describing the progress of each patient with levels `worse` < `same` < `slight.improvement` < `moderate.improvement` < `marked.improvement` < `complete.relief`.

Source

http://ideas.repec.org/c/boc/bocode/s419001.html

References

Anderson, J. A. (1984) Regression and Ordered Categorical Variables. *J. R. Statist. Soc. B*, **46(1)**, 1-30.

Examples

```
set.seed(1)
data(backPain)
summary(backPain)

### Re-express as count data
backPainLong <- expandCategorical(backPain, "pain")

### Fit models described in Table 5 of Anderson (1984)

### Logistic family models
noRelationship <- gnm(count ~ pain, eliminate = id,
                      family = "poisson", data = backPainLong)

## stereotype model
oneDimensional <- update(noRelationship,
                         ~ . + Mult(pain, x1 + x2 + x3))

## multinomial logistic
threeDimensional <- update(noRelationship, ~ . + pain:(x1 + x2 + x3))

### Models to determine distinguishability in stereotype model
## constrain scale of category-specific multipliers
oneDimensional <- update(noRelationship,
                         ~ . + Mult(pain, offset(x1) + x2 + x3))
## obtain identifiable contrasts & id possibly indistinguishable slopes
getContrasts(oneDimensional, pickCoef(oneDimensional, "[.]pain"))
```

```
## Not run:
## (this part not needed for package testing)
## fit simpler models and compare
.pain <- backPainLong$pain

levels(.pain)[2:3] <- paste(levels(.pain)[2:3], collapse = " | ")
fiveGroups <- update(noRelationship,
                     ~ . + Mult(.pain, x1 + x2 + x3))

levels(.pain)[4:5] <- paste(levels(.pain)[4:5], collapse = " | ")
fourGroups <- update(fiveGroups)

levels(.pain)[2:3] <- paste(levels(.pain)[2:3], collapse = " | ")
threeGroups <- update(fourGroups)

### Grouped continuous model, aka proportional odds model
library(MASS)
sixCategories <- polr(pain ~ x1 + x2 + x3, data = backPain)

### Obtain number of parameters and log-likelihoods for equivalent
### multinomial models as presented in Anderson (1984)
logLikMultinom <- function(model, size){
    object <- get(model)
    if (inherits(object, "gnm")) {
        l <- sum(object$y * log(object$fitted/size))
        c(nParameters = object$rank - nlevels(object$eliminate),
          logLikelihood = l)
    }
    else
        c(nParameters = object$edf, logLikelihood = -deviance(object)/2)
}
size <- tapply(backPainLong$count, backPainLong$id, sum)[backPainLong$id]
models <- c("threeDimensional", "oneDimensional", "noRelationship",
            "fiveGroups", "fourGroups", "threeGroups", "sixCategories")
t(sapply(models, logLikMultinom, size))

## End(Not run)
```

---

barley *Jenkyn's Data on Leaf-blotch on Barley*

Description

Incidence of *R. secalis* on the leaves of ten varieties of barley grown at nine sites.

Usage

```
data(barley)
```

Format

A data frame with 90 observations on the following 3 variables.

y the proportion of leaf affected (values in [0,1])

site a factor with 9 levels `A` to `I`

variety a factor with 10 levels `c(1:9, "X")`

Note

This dataset was used in Wedderburn's original paper (1974) on quasi-likelihood.

Source

Originally in an unpublished Aberystwyth PhD thesis by J F Jenkyn.

References

Gabriel, K R (1998). Generalised bilinear regression. *Biometrika* **85**, 689–700.

McCullagh, P and Nelder, J A (1989) *Generalized Linear Models* (2nd ed). Chapman and Hall.

Wedderburn, R W M (1974). Quasilikelihood functions, generalized linear models and the Gauss-Newton method. *Biometrika* **61**, 439–47.

Examples

```
data(barley)
set.seed(1)

###  Fit Wedderburn's logit model with variance proportional to [mu(1-mu)]^2
logitModel <- glm(y ~ site + variety, family = wedderburn, data = barley)
fit <- fitted(logitModel)
print(sum((barley$y - fit)^2 / (fit * (1-fit))^2))
##  Agrees with the chi-squared value reported in McCullagh and Nelder
##  (1989, p331), which differs slightly from Wedderburn's reported value.

###  Fit the biplot model as in Gabriel (1998, p694)
biplotModel <- gnm(y ~ -1 + instances(Mult(site, variety), 2),
                   family = wedderburn, data = barley)
barleySVD <- svd(matrix(biplotModel$predictors, 10, 9))
A <- sweep(barleySVD$v, 2, sqrt(barleySVD$d), "*")[, 1:2]
B <- sweep(barleySVD$u, 2, sqrt(barleySVD$d), "*")[, 1:2]
##  These are essentially A and B as in Gabriel (1998, p694), from which
##  the biplot is made by
plot(rbind(A, B), pch = c(levels(barley$site), levels(barley$variety)))

##  Fit the double-additive model as in Gabriel (1998, p697)
variety.binary <- factor(match(barley$variety, c(2,3,6), nomatch = 0) > 0,
                         labels = c("rest", "2,3,6"))
doubleAdditive <- gnm(y ~ variety + Mult(site, variety.binary),
                      family = wedderburn, data = barley)
##  It is unclear why Gabriel's chi-squared statistics differ slightly
```

```
##  from the ones produced in these fits.  Possibly Gabriel adjusted the
##  data somehow prior to fitting?
```

---

barleyHeights *Heights of Barley Plants*

Description

Average heights for 15 genotypes of barley recorded over 9 years.

Usage

```
data(barleyHeights)
```

Format

A data frame with 135 observations on the following 3 variables.

`height` average height over 4 replicates (cm)

`year` a factor with 9 levels `1974` to `1982`

`genotype` a factor with 15 levels `1:15`

Source

Aastveit, A. H. \& Martens, H. (1986). ANOVA interactions interpreted by partial least squares regression. *Biometrics*, **42**, 829–844.

References

Chadoeuf, J \& Denis, J B (1991). Asymptotic variances for the multiplicative interaction model. *J. App. Stat.* **18(3)**, 331–353.

Examples

```
data(barleyHeights)
set.seed(1)
## Fit AMMI-1 model
barleyModel <- gnm(height ~ year + genotype + Mult(year, genotype),
                   data = barleyHeights)

## Get row and column scores with se's
gamma <- getContrasts(barleyModel, pickCoef(barleyModel, "[.]y"),
                      ref = "mean", scaleWeights = "unit")
delta <- getContrasts(barleyModel, pickCoef(barleyModel, "[.]g"),
                      ref = "mean", scaleWeights = "unit")

## Corresponding CI's similar to Chadoeuf & Denis (1991) Table 8
## (allowing for change in sign)
gamma[[2]][,1] + (gamma[[2]][,2]) %o% c(-1.96, 1.96)
```

```
delta[[2]][,1] + (delta[[2]][,2]) %o% c(-1.96, 1.96)

## Multiplier of row and column scores
height <- matrix(scale(barleyHeights$height, scale = FALSE), 15, 9)
R <- height - outer(rowMeans(height), colMeans(height), "+")
svd(R)$d[1]
```

`cautres` *Data on Class, Religion and Vote in France*

Description

A 4-way contingency table of vote by class by religion in four French elections

Usage

```
data(cautres)
```

Format

A table of counts, with classifying factors `vote` (levels `1:2`), `class` (levels `1:6`) and `religion` (levels `1:4`) and `election` (levels `1:4`).

Source

Bruno Cautres

References

Cautres, B, Heath, A F and Firth, D (1998). Class, religion and vote in Britain and France. *La Lettre de la Maison Francaise* **8**.

Examples

```
set.seed(1)
data(cautres)

##  Fit a "double UNIDIFF" model with the religion-vote and class-vote
##  interactions both modulated by nonnegative election-specific multipliers
doubleUnidiff <- gnm(Freq ~ election*vote + election*class*religion +
                     Mult(Exp(election), religion:vote) +
                     Mult(Exp(election), class:vote),
                     family = poisson, data = cautres)
##  Deviance should be 133.04

##  Examine the multipliers of the class-vote log odds ratios
ofInterest(doubleUnidiff) <- pickCoef(doubleUnidiff, "class:vote[).]")
coef(doubleUnidiff)
## Coefficients of interest:
## Mult(Exp(.), class:vote).election1
```

```
##                         -0.38357138
## Mult(Exp(.), class:vote).election2
##                          0.29816599
## Mult(Exp(.), class:vote).election3
##                          0.06580307
## Mult(Exp(.), class:vote).election4
##                         -0.02174104
##  Re-parameterize by setting Mult2.Factor1.election1 to zero
getContrasts(doubleUnidiff, ofInterest(doubleUnidiff))
##                                     estimate        SE
## Mult(Exp(.), class:vote).election1 0.0000000 0.0000000
## Mult(Exp(.), class:vote).election2 0.6817374 0.2401644
## Mult(Exp(.), class:vote).election3 0.4493745 0.2473521
## Mult(Exp(.), class:vote).election4 0.3618301 0.2534754
##                                       quasiSE    quasiVar
## Mult(Exp(.), class:vote).election1 0.22854401 0.052232363
## Mult(Exp(.), class:vote).election2 0.07395886 0.005469913
## Mult(Exp(.), class:vote).election3 0.09475938 0.008979340
## Mult(Exp(.), class:vote).election4 0.10934798 0.011956981

##  Same thing but with election 4 as reference category:
getContrasts(doubleUnidiff, rev(ofInterest(doubleUnidiff)))
##                                       estimate        SE
## Mult(Exp(.), class:vote).election4  0.00000000 0.0000000
## Mult(Exp(.), class:vote).election3  0.08754436 0.1446833
## Mult(Exp(.), class:vote).election2  0.31990727 0.1320022
## Mult(Exp(.), class:vote).election1 -0.36183013 0.2534754
##                                       quasiSE    quasiVar
## Mult(Exp(.), class:vote).election4 0.10934798 0.011956981
## Mult(Exp(.), class:vote).election3 0.09475938 0.008979340
## Mult(Exp(.), class:vote).election2 0.07395886 0.005469913
## Mult(Exp(.), class:vote).election1 0.22854401 0.052232363
```

---

checkEstimable *Check Whether One or More Parameter Combinations in a gnm Model are Identified*

Description

For each of a specified set of linear combinations of parameters from a gnm model, checks numerically whether the combination's estimate is invariant to re-parameterization of the model.

Usage

```
checkEstimable(model, combMatrix = diag(length(coef(model))),
               tolerance = NULL)
```

Arguments

model	a model object of class "gnm"
combMatrix	numeric: either a vector of length the same as length(coef(model)), or a matrix with that number of rows. Coefficients of one or more linear combinations of the model's parameters.
tolerance	numeric: a threshold value for detection of non-estimability. If NULL, the default value of the tol argument to rankMatrix is used.

Value

A logical vector of length equal to the number of parameter combinations tested; NA where a parameter combination is identically zero.

Author(s)

David Firth

References

Catchpole, E.A. and Morgan, B.J.T. (1997). Detecting parameter redundancy. *Biometrika*, **84**, 187–196.

See Also

gnm, se, getContrasts

Examples

```
data(yaish)
set.seed(1)

## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest), family = poisson,
               data = yaish, subset = (dest != 7))

## Check whether multiplier contrast educ4 - educ5 is estimable
ofInterest(unidiff) <- pickCoef(unidiff, "[.]educ")
mycontrast <- numeric(length(coef(unidiff)))
mycontrast[ofInterest(unidiff)[4:5]] <- c(1, -1)
checkEstimable(unidiff, mycontrast)
## should be TRUE

## Check whether multiplier educ4 itself is estimable
mycontrast[ofInterest(unidiff)[5]] <- 0
checkEstimable(unidiff, mycontrast)
## should be FALSE -- only *differences* are identified here
```

confint.gnm *Compute Confidence Intervals of Parameters in a Generalized Nonlinear Model*

Description

Computes confidence intervals for one or more parameters in a generalized nonlinear model, based on the profiled deviance.

Usage

```
## S3 method for class 'gnm'
confint(object, parm = ofInterest(object), level = 0.95,
    trace = FALSE, ...)

## S3 method for class 'profile.gnm'
confint(object, parm = names(object), level = 0.95, ...)
```

Arguments

object	an object of class "gnm" or "profile.gnm"
parm	(optional) either a numeric vector of indices or a character vector of names, specifying the parameters for which confidence intervals are to be estimated. If parm is missing, confidence intervals are found for all parameters.
level	the confidence level required.
trace	a logical value indicating whether profiling should be traced.
...	arguments passed to or from other methods

Details

These are methods for the generic function confint in the base package.

For "gnm" objects, profile.gnm is first called to profile the deviance over each parameter specified by parm, or over all parameters in the model if parm is missing.

The method for "profile.gnm" objects is then called, which interpolates the deviance profiles to estimate the limits of the confidence interval for each parameter, see profile.gnm for more details.

If a "profile.gnm" object is passed directly to confint, parametrs specified by parm must be a subset of the profiled parameters.

For unidentified parameters a confidence interval cannot be calculated and the limits will be returned as NA. If the deviance curve has an asymptote and a limit of the confidence interval cannot be reached, the limit will be returned as -Inf or Inf appropriately. If the range of the profile does not extend far enough to estimate a limit of the confidence interval, the limit will be returned as NA. In such cases, it may be desirable create a profile object directly, see profile.gnm for more details.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%).

Author(s)

Heather Turner

See Also

profile.gnm, gnm, profile.glm

Examples

```
### Example in which profiling doesn't take too long
data(voting)
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     constrain = "delta1", family = binomial,
                     data = voting)
## profile diagonal effects
confint(classMobility, parm = 3:7, trace = TRUE)

## Not run:
### Profiling takes much longer here, but example more interesting!
data(yaish)
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               ofInterest = "[.]educ", constrain = "[.]educ1",
               family = poisson, data = yaish, subset = (dest != 7))

## Letting 'confint' compute profile
confint(unidiff, trace = TRUE)
##                                                    2.5 %     97.5 %
## Mult(Exp(.), orig:dest).educ1         NA         NA
## Mult(Exp(.), orig:dest).educ2 -0.5978901  0.1022447
## Mult(Exp(.), orig:dest).educ3 -1.4836854 -0.2362378
## Mult(Exp(.), orig:dest).educ4 -2.5792398 -0.2953420
## Mult(Exp(.), orig:dest).educ5       -Inf -0.7007616

## Creating profile object first with user-specified stepsize
prof <- profile(unidiff, trace = TRUE, stepsize = 0.1)
confint(prof, ofInterest(unidiff)[2:5])
##                                      2.5 %     97.5 %
## Mult(Exp(.), orig:dest).educ2 -0.5978324  0.1022441
## Mult(Exp(.), orig:dest).educ3 -1.4834753 -0.2362138
## Mult(Exp(.), orig:dest).educ4         NA -0.2950790
## Mult(Exp(.), orig:dest).educ5         NA         NA

## For 95% confidence interval, need to estimate parameters for which
## z = +/- 1.96. Profile has not gone far enough for last two parameters
```

```
range(prof[[4]]$z)
## -1.566601  2.408650
range(prof[[5]]$z)
## -0.5751376  1.1989487

## End(Not run)
```

Const *Specify a Constant in a "nonlin" Function Predictor*

Description

A symbolic wrapper to specify a constant in the predictor of a "nonlin" function.

Usage

```
Const(const)
```

Arguments

const	a numeric value.

Value

A call to rep used to create a variable representing the constant in the model frame.

Note

Const may only be used in the predictor of a "nonlin" function. Use offset to specify a constant in the model formula.

Author(s)

Heather Turner

See Also

gnm, formula, offset

Examples

```
## One way to fit the logistic function without conditional
## linearity as in ?nls
library(gnm)
set.seed(1)
DNase1 <- subset(DNase, Run == 1)

test <- gnm(density ~ -1 +
            Mult(1, Inv(Const(1) + Exp(Mult(1 + offset(-log(conc)),
```

```
                                                  Inv(1))))),
            start = c(NA, 0, 1), data = DNase1, trace = TRUE)
coef(test)
```

`Diag` *Equality of Two or More Factors*

Description

Converts two or more factors into a new factor whose value is 0 where the original factors are not all equal, and nonzero otherwise.

Usage

```
Diag(..., binary = FALSE)
```

Arguments

`...`	One or more factors
`binary`	Logical

Details

Used mainly in regression models for data classified by two or more factors with the same levels. By default, operates on k-level factors to produce a new factor having k+1 levels; if `binary = TRUE` is specified, the result is a coarser binary variable equal to 1 where all of the input factors are equal and 0 otherwise.

Value

Either a factor (if `binary = FALSE`) or a 0-1 numeric vector (if `binary = TRUE`).

Author(s)

David Firth

See Also

`Symm`

Examples

```
row <- gl(4, 4, 16)
col <- gl(4, 1, 16)
diag4by4 <- Diag(row, col)
matrix(Diag(row, col, binary = TRUE), 4, 4)
```

Dref *Specify a Diagonal Reference Term in a gnm Model Formula*

Description

Dref is a function of class "nonlin" to specify a diagonal reference term in the formula argument to gnm.

Usage

```
Dref(..., delta = ~ 1)
```

Arguments

...	a comma-separated list of two or more factors.
delta	a formula with no left-hand-side specifying the model for each factor weight.

Details

Dref specifies diagonal reference terms as introduced by Sobel (1981, 1985). Such terms comprise an additive component for each factor of the form

$$w_f \gamma_l$$

where w_f is the weight for factor f, γ_l is the diagonal effect for level l and l is the level of factor f for the given data point.

The weights are constrained to be nonnegative and to sum to one as follows

$$w_f = \frac{e^{\delta_f}}{\sum_i e^{\delta_i}}$$

and the δ_f are modelled as specified by the delta argument (constant weights by default). The returned parameters are those in the model for δ_f, rather than the implied weights w_f. The DrefWeights function will take a fitted gnm model and return the weights w_f, along with their standard errors.

If the factors passed to Dref do not have exactly the same levels, the set of levels in the diagonal reference term is taken to be the union of the factor levels, sorted into increasing order.

Value

A list with the anticipated components of a "nonlin" function:

predictors	the factors passed to Dref and the formulae for the weights.
common	an index to specify that common effects are to be estimated across the factors.
term	a function to create a deparsed mathematical expression of the term, given labels for the predictors.
start	a function to generate starting values for the parameters.
call	the call to use as a prefix for parameter labels.

Author(s)

Heather Turner

References

Sobel, M. E. (1981), Diagonal mobility models: A substantively motivated class of designs for the analysis of mobility effects. *American Sociological Review* **46**, 893–906.

Sobel, M. E. (1985), Social mobility and fertility revisited: Some new models for the analysis of the mobility effects hypothesis. *American Sociological Review* **50**, 699–712.

Clifford, P. and Heath, A. F. (1993) The Political Consequences of Social Mobility. *J. Roy. Stat. Soc. A*, **156(1)**, 51-61.

Van der Slik, F. W. P., De Graaf, N. D and Gerris, J. R. M. (2002) Conformity to Parental Rules: Asymmetric Influences of Father's and Mother's Levels of Education. *European Sociological Review* **18(4)**, 489 – 502.

See Also

gnm, formula, nonlin.function

Examples

```
### Examples from Clifford and Heath paper
### (Results differ slightly - possible transcription error in
### published data?)
set.seed(1)
data(voting)
## reconstruct counts voting Labour/non-Labour
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)

## fit diagonal reference model with constant weights
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting)
DrefWeights(classMobility)

## create factors indicating movement in and out of salariat (class 1)
upward <- with(voting, origin != 1 & destination == 1)
downward <- with(voting, origin == 1 & destination != 1)

## fit separate weights for the "socially mobile" groups
socialMobility <- gnm(yvar ~ -1 + Dref(origin, destination,
                                       delta = ~ 1 + downward + upward),
                      family = binomial, data = voting)
DrefWeights(socialMobility)

## fit separate weights for downwardly mobile groups only
downwardMobility <- gnm(yvar ~ -1 + Dref(origin, destination,
                                         delta = ~ 1 + downward),
                        family = binomial, data = voting)
DrefWeights(downwardMobility)
```

```
## Not run:
### Examples from Van der Slik paper
### For illustration only - data not publically available
### Using data in data.frame named 'conformity', with variables
### MCFM - mother's conformity score
### FCFF - father's conformity score
### MOPLM - a factor describing the mother's education with 7 levels
### FOPLF - a factor describing the father's education with 7 levels
### AGEM - mother's birth cohort
### MRMM - mother's traditional role model
### FRMF - father's traditional role model
### MWORK - mother's employment
### MFCM - mother's family conflict score
### FFCF - father's family conflict score

set.seed(1)

## Models for mothers' conformity score as specified in Figure 1
A <- gnm(MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
         Dref(MOPLM, FOPLF), family = gaussian, data = conformity,
         verbose = FALSE)
A
## Call:
## gnm(formula = MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
##     Dref(MOPLM, FOPLF), family = gaussian, data = conformity,
##     verbose = FALSE)
##
## Coefficients:
##                     AGEM                      MRMM
##                  0.06363                  -0.32425
##                     FRMF                     MWORK
##                 -0.25324                  -0.06430
##                     MFCM  Dref(MOPLM, FOPLF)delta1
##                 -0.06043                  -0.33731
## Dref(MOPLM, FOPLF)delta2   Dref(., .).MOPLM|FOPLF1
##                 -0.02505                   4.95121
##  Dref(., .).MOPLM|FOPLF2   Dref(., .).MOPLM|FOPLF3
##                  4.86329                   4.86458
##  Dref(., .).MOPLM|FOPLF4   Dref(., .).MOPLM|FOPLF5
##                  4.72343                   4.43516
##  Dref(., .).MOPLM|FOPLF6   Dref(., .).MOPLM|FOPLF7
##                  4.18873                   4.43378
##
## Deviance:            425.3389
## Pearson chi-squared: 425.3389
## Residual df:         576

## Weights as in Table 4
DrefWeights(A)
## Refitting with parameters of first Dref weight constrained to zero
## $MOPLM
##    weight        se
```

```
## 0.4225636 0.1439829
##
## $FOPLF
##    weight        se
## 0.5774364 0.1439829

F <- gnm(MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
         Dref(MOPLM, FOPLF, delta = ~1 + MFCM), family = gaussian,
         data = conformity, verbose = FALSE)
F
## Call:
## gnm(formula = MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
##     Dref(MOPLM, FOPLF, delta = ~1 + MFCM), family = gaussian,
##     data = conformity, verbose = FALSE)
##
##
## Coefficients:
##                                                      AGEM
##                                                   0.05818
##                                                      MRMM
##                                                  -0.32701
##                                                      FRMF
##                                                  -0.25772
##                                                     MWORK
##                                                  -0.07847
##                                                      MFCM
##                                                  -0.01694
## Dref(MOPLM, FOPLF, delta = ~ . + MFCM).delta1(Intercept)
##                                                   1.03515
##           Dref(MOPLM, FOPLF, delta = ~ 1 + .).delta1MFCM
##                                                  -1.77756
## Dref(MOPLM, FOPLF, delta = ~ . + MFCM).delta2(Intercept)
##                                                  -0.03515
##           Dref(MOPLM, FOPLF, delta = ~ 1 + .).delta2MFCM
##                                                   2.77756
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF1
##                                                   4.82476
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF2
##                                                   4.88066
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF3
##                                                   4.83969
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF4
##                                                   4.74850
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF5
##                                                   4.42020
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF6
##                                                   4.17957
##              Dref(., ., delta = ~ 1 + MFCM).MOPLM|FOPLF7
##                                                   4.40819
##
## Deviance:            420.9022
## Pearson chi-squared: 420.9022
## Residual df:         575
```

```
##
##

## Standard error for MFCM == 1 lower than reported by Van der Slik et al
DrefWeights(F)
## Refitting with parameters of first Dref weight constrained to zero
## $MOPLM
##   MFCM     weight        se
## 1    1 0.02974675 0.2277711
## 2    0 0.74465224 0.2006916
##
## $FOPLF
##   MFCM    weight        se
## 1    1 0.9702532 0.2277711
## 2    0 0.2553478 0.2006916

## End(Not run)
```

`erikson` *Intergenerational Class Mobility in England/Wales, France and Sweden*

Description

Intergenerational class mobility among the male populations of England and Wales; France, and Sweden.

Usage

```
data(erikson)
```

Format

A table of counts, with classifying factors `origin` (father's class; levels `I`, `II`, `III`, `IVa`, `IVb`, `IVc`, `V/VI`, `VIIa`, `VIIb`) `destination` (son's class; levels as before), and `country` (son's country of residence; levels `EW`, `F`, `S`).

Source

Hauser, R. M. (1984) Vertical Class Mobility in England, France and Sweden. *Acta Sociol.*, **27(2)**, 87-110.

References

Erikson, R., GoldThorpe, J. H. and Portocarero, L. (1982) Social Fluidity in Industrial Nations: England, France and Sweden. *Brit. J. Sociol.* **33(1)**, 1-34.

Xie, Y. (1992) The Log-multiplicative Layer Effect Model for Comparing Mobility Tables. *Am. Sociol. Rev.* **57(3)**, 380-395.

Examples

```
set.seed(1)
data(erikson)

### Collapse to 7 by 7 table as in Erikson (1982)

erikson <- as.data.frame(erikson)
lvl <- levels(erikson$origin)
levels(erikson$origin) <- levels(erikson$destination) <-
    c(rep(paste(lvl[1:2], collapse = " + "), 2), lvl[3],
      rep(paste(lvl[4:5], collapse = " + "), 2), lvl[6:9])
erikson <- xtabs(Freq ~ origin + destination + country, data = erikson)

### Fit the models given in first half of Table 3 of Xie (1992)

## Null association between origin and destination
nullModel <- gnm(Freq ~ country*origin + country*destination,
                 family = poisson, data = erikson)

## Full interaction, common to all countries
commonInteraction <- update(nullModel, ~ . + origin:destination)

## Full Interaction, different multiplier for each country
multInteraction <- update(nullModel,
                          ~ . + Mult(Exp(country), origin:destination))

### Create array of interaction levels as in Table 2 of Xie (1992)

levelMatrix <- matrix(c(2, 3, 4, 6, 5, 6, 6,
                        3, 3, 4, 6, 4, 5, 6,
                        4, 4, 2, 5, 5, 5, 5,
                        6, 6, 5, 1, 6, 5, 2,
                        4, 4, 5, 6, 3, 4, 5,
                        5, 4, 5, 5, 3, 3, 5,
                        6, 6, 5, 3, 5, 4, 1), 7, 7, byrow = TRUE)

### Fit models in second half of Table 3 in Xie (1992)

## Interaction specified by levelMatrix, common to all countries
commonTopo <- update(nullModel, ~ . +
                     Topo(origin, destination, spec = levelMatrix))

## Interaction specified by levelMatrix, different multiplier for
## each country
multTopo <- update(nullModel, ~ . +
                   Mult(Exp(country),
                        Topo(origin, destination, spec = levelMatrix)))

## Interaction specified by levelMatrix, different effects for
## each country
separateTopo <- update(nullModel, ~ . +
                       country:Topo(origin, destination,
```

```
                                    spec = levelMatrix))
```

`exitInfo` *Print Exit Information for gnm Fit*

Description

A utility function to print information on final iteration in `gnm` fit, intended for use when `gnm` has not converged.

Usage

```
exitInfo(object)
```

Arguments

`object`	a `gnm` object.

Details

If `gnm` has not converged within the pre-specified maximum number of iterations, it may be because the algorithm has converged to a non-solution of the likelihood equations. In order to determine appropriate action, it is necessary to differentiate this case from one of near-convergence to the solution.

`exitInfo` prints the absolute score and the corresponding convergence criterion for all parameters which failed to meet the convergence criterion at the last iteration. Clearly a small number of parameters with scores close to the criterion suggests near-convergence.

Author(s)

Heather Turner

References

Vargas, M, Crossa, J, van Eeuwijk, F, Sayre, K D and Reynolds, M P (2001). Interpreting treatment by environment interaction in agronomy trials. *Agronomy Journal* **93**, 949–960.

See Also

`gnm`

Examples

```
data(cautres)

##  Fit a "double UNIDIFF" model with low iterMax for illustration!
set.seed(1)
doubleUnidiff <- gnm(Freq ~ election*vote + election*class*religion +
                     Mult(Exp(election), religion:vote) +
                     Mult(Exp(election), class:vote),
                     family = poisson, data = cautres, iterMax = 10)
exitInfo(doubleUnidiff)
```

Exp *Specify the Exponential of a Predictor in a gnm Model Formula*

Description

A function of class "nonlin" to specify the exponential of a predictor in the formula argument to gnm.

Usage

```
Exp(expression, inst = NULL)
```

Arguments

expression	a symbolic expression representing the (possibly nonlinear) predictor.
inst	(optional) an integer specifying the instance number of the term.

Details

The expression argument is interpreted as the right hand side of a formula in an object of class "formula", except that an intercept term is not added by default. Any function of class "nonlin" may be used in addition to the usual operators and functions.

Value

A list with the components required of a "nonlin" function:

predictors	the expression argument passed to Exp
term	a function to create a deparsed mathematical expression of the term, given a label for the predictor.
call	the call to use as a prefix for parameter labels.

Author(s)

Heather Turner

See Also

gnm, formula, nonlin.function

Examples

```
set.seed(1)

## Using 'Mult' with 'Exp' to constrain the first constituent multiplier
##  to be non-negative
data(yaish)
## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               family = poisson, data = yaish, subset = (dest != 7))
```

---

expandCategorical *Expand Data Frame by Re-expressing Categorical Data as Counts*

Description

Expands the rows of a data frame by re-expressing observations of a categorical variable specified by catvar, such that the column(s) corresponding to catvar are replaced by a factor specifying the possible categories for each observation and a vector of 0/1 counts over these categories.

Usage

```
expandCategorical(data, catvar, sep = ".", countvar = "count",
                  idvar = "id", as.ordered = FALSE, group = TRUE)
```

Arguments

data	a data frame.
catvar	a character vector specifying factors in data whose interaction will form the basis of the expansion.
sep	a character string used to separate the concatenated values of catvar in the name of the new interaction factor.
countvar	(optional) a character string to be used for the name of the new count variable.
idvar	(optional) a character string to be used for the name of the new factor identifying the original rows (cases).
as.ordered	logical - whether the new interaction factor should be of class "ordered".
group	logical: whether or not to group individuals with common values over all covariates.

Details

Each row of the data frame is replicated c times, where c is the number of levels of the interaction of the factors specified by `catvar`. In the expanded data frame, the columns specified by `catvar` are replaced by a factor specifying the r possible categories for each case, named by the concatenated values of `catvar` separated by `sep`. The ordering of factor levels will be preserved in the creation of the new factor, but this factor will not be of class `"ordered"` unless the argument `as.ordered = TRUE`. A variable with name `countvar` is added to the data frame which is equal to 1 for the observed category in each case and 0 elsewhere. Finally a factor with name `idvar` is added to index the cases.

Value

The expanded data frame as described in Details.

Note

Re-expressing categorical data in this way allows a multinomial response to be modelled as a poisson response, see examples.

Author(s)

Heather Turner

References

Anderson, J. A. (1984) Regression and Ordered Categorical Variables. *J. R. Statist. Soc. B*, **46(1)**, 1-30.

See Also

`gnm`, `multinom`, `reshape`, `mclgen`

Examples

```
### Example from help(multinom, package = "nnet")
library(MASS)
data(birthwt)
example(birthwt)
library(nnet)
bwt.mu <- multinom(low ~ ., data = bwt)

## Equivalent using gnm - include unestimable main effects in model so
## that interactions with low0 automatically set to zero, else could use
## 'constrain' argument.
bwtLong <- expandCategorical(bwt, "low", group = FALSE)
bwt.po <- gnm(count ~  low*(. - id), eliminate = id, data = bwtLong, family =
              "poisson")
summary(bwt.po) # same deviance; df reflect extra id parameters

### Example from ?backPain
set.seed(1)
```

```
data(backPain)
summary(backPain)
backPainLong <- expandCategorical(backPain, "pain")

## Fit models described in Table 5 of Anderson (1984)

noRelationship <- gnm(count ~ pain, eliminate = id,
                      family = "poisson", data = backPainLong)

oneDimensional <- update(noRelationship,
                         ~ . + Mult(pain, x1 + x2 + x3))
```

`friend` *Occupation of Respondents and Their Closest Friend*

Description

Cross-classification of the occupation of respondent and that of their closest friend. Data taken from wave 10 (year 2000) of the British Household Panel Survey.

Usage

```
data(friend)
```

Format

A table of counts, with classifying factors `r` (respondent's occupational category; levels `1:31`) and `c` (friend's occupational category; levels `1:31`).

Source

Chan, T.W. and Goldthorpe, J.H. (2004) Is there a status order in contemporary British society: Evidence from the occupational structure of friendship, *European Sociological Review*, **20**, 383–401.

Examples

```
set.seed(1)
data(friend)

###  Fit an association model with homogeneous row-column effects
rc1 <- gnm(Freq ~ r + c + Diag(r,c) + MultHomog(r, c),
           family = poisson, data = friend)
rc1

## Not run:
###  Extend to two-component interaction
rc2 <- update(rc1, . ~ . + MultHomog(r, c, inst = 2),
              etastart = rc1$predictors)
```

```
rc2

## End(Not run)
```

`getContrasts` *Estimated Contrasts and Standard Errors for Parameters in a gnm Model*

Description

Computes contrasts or scaled contrasts for a set of (non-eliminated) parameters from a `gnm` model, and computes standard errors for the estimated contrasts. Where possible, quasi standard errors are also computed.

Usage

```
getContrasts(model, set = NULL,  ref = "first", scaleRef = "mean",
  scaleWeights = NULL, dispersion = NULL, check = TRUE, ...)
```

Arguments

`model`	a model object of class `"gnm"`.
`set`	a vector of indices (numeric) or coefficient names (character). If `NULL`, a dialog will open for parameter selection.
`ref`	either a single numeric index, or a vector of real numbers which sum to 1, or one of the character strings `"first"`, `"last"` or `"mean"`.
`scaleRef`	as for `ref`
`scaleWeights`	either `NULL`, a vector of real numbers, `"unit"` or `"setLength"`.
`dispersion`	either `NULL`, or a positive number by which the model's variance-covariance matrix should be scaled.
`check`	`TRUE` or `FALSE` or a numeric vector – for which of the specified parameter combinations should estimability be checked? If `TRUE`, all are checked; if `FALSE`, none is checked.
`...`	arguments to pass to other functions.

Details

The indices in `set` must all be in `1:length(coef(object))`. If `set = NULL`, a dialog is presented for the selection of indices (model coefficients).

For the set of coefficients selected, contrasts and their standard errors are computed. A check is performed first on the estimability of all such contrasts (if `check = TRUE`) or on a specified subset (if `check` is a numeric index vector). The specific contrasts to be computed are controlled by the choice of `ref`: this may be `"first"` (the default), for contrasts with the first of the selected coefficients, or `"last"` for contrasts with the last, or `"mean"` for contrasts with the arithmetic mean

of the coefficients in the selected set; or it may be an arbitrary vector of weights (summing to 1, not necessarily all non-negative) which specify a weighted mean against which contrasts are taken; or it may be a single index specifying one of the coefficients with which all contrasts should be taken. Thus, for example, `ref = 1` is equivalent to `ref = "first"`, and `ref = c(1/3, 1/3, 1/3)` is equivalent to `ref = "mean"` when there are three coefficients in the selected `set`.

The contrasts may be scaled by

$$\frac{1}{\sqrt{\sum_r v_r * d_r^2}}$$

where d_r is a contrast of the r'th coefficient in `set` with the reference level specified by `scaleRef` and v is a vector of weights (of the same length as `set`) specified by `scaleWeights`. If `scaleWeights` is `NULL` (the default), `scaleRef` is ignored and no scaling is performed. Other options for `scaleWeights` are `"unit"` for weights equal to one and `"setLength"` for weights equal to the reciprocal of `length(set)`. If `scaleRef` is the same as `ref`, these options constrain the sum of squared contrasts to 1 and `length(set)` respectively.

Quasi-variances (and corresponding quasi standard errors) are reported for **unscaled** contrasts where possible. These statistics are invariant to the choice of `ref`, see Firth (2003) or Firth and Menezes (2004) for more details.

Value

An object of class `qv` — see `qvcalc`.

Author(s)

David Firth

References

Firth, D (2003). Overcoming the reference category problem in the presentation of statistical models. *Sociological Methodology* **33**, 1–18.

Firth, D and Menezes, R X de (2004). Quasi-variances. *Biometrika* **91**, 65–80.

See Also

`gnm`, `se`, `checkEstimable`, `qvcalc`, `ofInterest`

Examples

```
### Unscaled contrasts ###
set.seed(1)
data(yaish)

## Fit the "UNIDIFF" mobility model across education levels -- see ?yaish
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               ofInterest = "[.]educ", family = poisson,
               data = yaish,  subset = (dest != 7))
## Examine the education multipliers (differences on the log scale):
unidiffContrasts <- getContrasts(unidiff, ofInterest(unidiff))
```

```
plot(unidiffContrasts,
  main = "Unidiff multipliers (log scale): intervals based on
           quasi standard errors",
  xlab = "Education level", levelNames = 1:5)


### Scaled contrasts (elliptical contrasts) ###
set.seed(1)
data(mentalHealth)

##  Goodman Row-Column association model fits well (deviance 3.57, df 8)
mentalHealth$MHS <- C(mentalHealth$MHS, treatment)
mentalHealth$SES <- C(mentalHealth$SES, treatment)
RC1model <- gnm(count ~ SES + MHS + Mult(SES, MHS),
                family = poisson, data = mentalHealth)
## Row scores and column scores are both unnormalized in this
## parameterization of the model

## The scores can be normalized as in Agresti's eqn (9.15):
rowProbs <- with(mentalHealth, tapply(count, SES, sum) / sum(count))
colProbs <- with(mentalHealth, tapply(count, MHS, sum) / sum(count))
mu <- getContrasts(RC1model, pickCoef(RC1model, "[.]SES"),
                   ref = rowProbs, scaleRef = rowProbs,
                   scaleWeights = rowProbs)
nu <- getContrasts(RC1model, pickCoef(RC1model, "[.]MHS"),
                   ref = colProbs, scaleRef = colProbs,
                   scaleWeights = colProbs)
all.equal(sum(mu$qv[,1] * rowProbs), 0)
all.equal(sum(nu$qv[,1] * colProbs), 0)
all.equal(sum(mu$qv[,1]^2 * rowProbs), 1)
all.equal(sum(nu$qv[,1]^2 * colProbs), 1)
```

---

gnm *Fitting Generalized Nonlinear Models*

Description

gnm fits generalised nonlinear models using an over-parameterised representation. Nonlinear terms are specified by calls to functions of class "nonlin".

Usage

```
gnm(formula, eliminate = NULL, ofInterest = NULL, constrain = numeric(0),
    constrainTo = numeric(length(constrain)), family = gaussian,
    data = NULL, subset, weights, na.action,  method = "gnmFit",
    checkLinear = TRUE, offset, start = NULL, etastart = NULL,
    mustart = NULL, tolerance = 1e-06, iterStart = 2, iterMax = 500,
    trace = FALSE, verbose = TRUE, model = TRUE, x = TRUE,
    termPredictors = FALSE, ridge = 1e-08, ...)
```

Arguments

formula	a symbolic description of the nonlinear predictor.
eliminate	a factor to be included as the first term in the model. gnm will exploit the structure of this factor to improve computational efficiency. See details.
ofInterest	optional coefficients of interest, specified by a regular expression, a numeric vector of indices, a character vector of names, or "[?]" to select from a Tk dialog. If missing, it is assumed that all non-eliminated coefficients are of interest.
constrain	(non-eliminated) coefficients to constrain, specified by a regular expression, a numeric vector of indices, a logical vector, a character vector of names, or "[?]" to select from a Tk dialog.
constrainTo	a numeric vector of the same length as constrain specifying the values to constrain to. By default constrained parameters will be set to zero.
family	a specification of the error distribution and link function to be used in the model. This can be a character string naming a family function; a family function, or the result of a call to a family function. See family and wedderburn for possibilities.
data	an optional data frame containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which gnm is called.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional vector of weights to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. If data is a contingency table, the default is "exclude". Otherwise the default is first, any na.action attribute of data; second, any na.action setting of options, and third, na.fail.
method	the method to be used: either "gnmFit" to fit the model using the default maximum likelihood algorithm, "coefNames" to return a character vector of names for the coefficients in the model, "model.matrix" to return the model matrix, "model.frame" to return the model frame, or the name of a function providing an alternative fitting algorithm.
checkLinear	logical: if TRUE glm.fit is used when the predictor is found to be linear
offset	this can be used to specify an a priori known component to be added to the predictor during fitting. offset terms can be included in the formula instead or as well, and if both are specified their sum is used.
start	a vector of starting values for the parameters in the model; if a starting value is NA, the default starting value will be used. Starting values need not be specified for eliminated parameters.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
tolerance	a positive numeric value specifying the tolerance level for convergence.
iterStart	a positive integer specifying the number of start-up iterations to perform.
iterMax	a positive integer specifying the maximum number of main iterations to perform.

trace	a logical value indicating whether the deviance should be printed after each iteration.
verbose	logical: if TRUE and model includes nonlinear terms, progress indicators are printed as the model is fitted, including a diagnostic error message if the algorithm fails.
model	logical: if TRUE the model frame is returned.
x	logical: if TRUE the local design matrix from the last iteration is included as a component of returned model object.
termPredictors	logical: if TRUE, a matrix is returned with a column for each term in the model, containing the additive contribution of that term to the predictor.
ridge	numeric, a positive value for the ridge constant to be used in the fitting algorithm
...	further arguments passed to fitting function.

Details

Models for gnm are specified by giving a symbolic description of the nonlinear predictor, of the form response ~ terms. The response is typically a numeric vector, see later in this section for alternatives. The usual symbolic language may be used to specify any linear terms, see formula for details.

Nonlinear terms may be specified by calls to functions of class "nonlin". There are several "nonlin" functions in the gnm package. Some of these specify simple mathematical functions of predictors: Exp, Mult, and Inv. Others specify more specialised nonlinear terms, in particular MultHomog specifies homogeneous multiplicative interactions and Dref specifies diagonal reference terms. Users may also define their own "nonlin" functions, see nonlin.function for details.

The eliminate argument may be used to specify a factor that is to be included as the first term in the model (since an intercept is then redundant, none is fitted). The structure of the factor is exploited to improve computational efficiency — substantially so if the eliminated factor has a large number of levels. Use of eliminate is designed for factors that are required in the model but are not of direct interest (e.g., terms needed to fit multinomial-response models as conditional Poisson models). See backPain for an example.

The ofInterest argument may be used to specify coefficients of interest, the indices of which are returned in the ofInterest component of the model object. print() displays of the model object or its components obtained using accessor functions such as coef() etc, will only show these coefficients. In addition methods for "gnm" objects which may be applied to a subset of the parameters are by default applied to the coefficients of interest. See ofInterest for accessor and replacement functions.

For contingency tables, the data may be provided as an object of class "table" from which the frequencies will be extracted to use as the response. In this case, the response should be specified as Freq in the model formula. The "predictors", "fitted.values", "residuals", "prior.weights", "weights", "y" and "offset" components of the returned gnm fit will be tables with the same format as the data, completed with NAs where necessary.

For binomial models, the response may be specified as a factor in which the first level denotes failure and all other levels denote success, as a two-column matrix with the columns giving the numbers of successes and failures, or as a vector of the proportions of successes.

The gnm fitting algorithm consists of two stages. In the start-up iterations, any nonlinear parameters that are not specified by either the start argument of gnm or a plug-in function are updated one parameter at a time, then the linear parameters are jointly updated before the next iteration. In the main iterations, all the parameters are jointly updated, until convergence is reached or the number or iterations reaches iterMax. To solve the (typically rank-deficient) least squares problem at the heart of the gnm fitting algorithm, the design matrix is standardized and regularized (in the Levenberg-Marquardt sense) prior to solving; the ridge argument provides a degree of control over the regularization performed (smaller values may sometimes give faster convergence but can lead to numerical instability).

Convergence is judged by comparing the squared components of the score vector with corresponding elements of the diagonal of the Fisher information matrix. If, for all components of the score vector, the ratio is less than tolerance^2, or the corresponding diagonal element of the Fisher information matrix is less than 1e-20, iterations cease. If the algorithm has not converged by iterMax iterations, exitInfo can be used to print information on the parameters which failed the convergence criteria at the last iteration.

By default, gnm uses an over-parameterized representation of the model that is being fitted. Only minimal identifiability constraints are imposed, so that in general a random parameterization is obtained. The parameter estimates are ordered so that those for any linear terms appear first.

getContrasts may be used to obtain estimates of specified scaled contrasts, if these contrasts are identifiable. For example, getContrasts may be used to estimate the contrasts between the first level of a factor and the rest, and obtain standard errors.

If appropriate constraints are known in advance, or have been determined from a gnm fit, the model may be (re-)fitted using the constrain argument to specify coefficients which should be set to values specified by constrainTo. Constraints should only be specified for non-eliminated parameters. update provides a convenient way of re-fitting a gnm model with new constraints.

Value

If method = "gnmFit", gnm returns NULL if the algorithm has failed and an object of class "gnm" otherwise. A "gnm" object inherits first from "glm" then "lm" and is a list containing the following components:

call	the matched call.
formula	the formula supplied.
constrain	a numeric vector specifying any coefficients that were constrained in the fitting process.
constrainTo	a numeric vector of the same length as constrain specifying the values which constrained parameters were set to.
family	the family object used.
prior.weights	the case weights initially supplied.
terms	the terms object used.
data	the data argument.
na.action	the na.action attribute of the model frame
xlevels	a record of the levels of the factors used in fitting.

y	the response used.
offset	the offset vector used.
coefficients	a named vector of non-eliminated coefficients, with an attribute "eliminated" specifying the eliminated coefficients if eliminate is non-NULL.
eliminate	the eliminate argument.
ofInterest	a named numeric vector of indices corresponding to non-eliminated coefficients, or NULL.
predictors	the fitted values on the link scale.
fitted.values	the fitted mean values, obtained by transforming the predictors by the inverse of the link function.
deviance	up to a constant, minus twice the maximised log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.
aic	Akaike's *An Information Criterion*, minus twice the maximized log-likelihood plus twice the number of parameters (so assuming that the dispersion is known).
iter	the number of main iterations.
conv	logical indicating whether the main iterations converged, with an attribute for use by exitInfo if FALSE.
weights	the *working* weights, that is, the weights used in the last iteration.
residuals	the *working* residuals, that is, the residuals from the last iteration.
df.residual	the residual degrees of freedom.
rank	the numeric rank of the fitted model.

The list may also contain the components model, x, or termPredictors if requested in the arguments to gnm.

If a table was passed to data and the default for na.action was not overridden, the list will also contain a table.attr component, for use by the extractor functions.

If a binomial gnm model is specified by giving a two-column response, the weights returned by prior.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.

The function summary.gnm may be used to obtain and print a summary of the results, whilst plot.gnm may be used for model diagnostics.

The generic functions formula, family, terms, coefficients, fitted.values, deviance, extractAIC, weights, residuals, df.residual, model.frame, model.matrix, vcov and termPredictors maybe used to extract components from the object returned by gnm or to construct the relevant objects where necessary.

Note that the generic functions weights and residuals do not act as straight-forward accessor functions for gnm objects, but return the prior weights and deviance residuals respectively, as for glm objects.

Note

Regular expression matching is performed using grep with default settings.

Author(s)

Heather Turner, David Firth

References

Cautres, B, Heath, A F and Firth, D (1998). Class, religion and vote in Britain and France. *La Lettre de la Maison Francaise* **8**.

See Also

`formula` for the symbolic language used to specify formulae.

`Diag` and `Symm` for specifying special types of interaction.

`Exp`, `Mult`, `Inv`, `MultHomog`, `Dref` and `nonlin.function` for incorporating nonlinear terms in the `formula` argument to `gnm`.

`residuals.glm` and the generic functions `coef`, `fitted`, etc. for extracting components from `gnm` objects.

`exitInfo` to print more information on last iteration when `gnm` has not converged.

`getContrasts` to estimate (identifiable) scaled contrasts from a `gnm` model.

Examples

```
###  Analysis of a 4-way contingency table
set.seed(1)
data(cautres)
print(cautres)

##  Fit a "double UNIDIFF" model with the religion-vote and class-vote
##  interactions both modulated by nonnegative election-specific
##  multipliers.
doubleUnidiff <- gnm(Freq ~ election:vote + election:class:religion
                     + Mult(Exp(election), religion:vote) +
                     Mult(Exp(election), class:vote), family = poisson,
                     data = cautres)

##  Examine the multipliers of the class-vote log odds ratios
ofInterest(doubleUnidiff) <- pickCoef(doubleUnidiff, "class:vote[).]")
coef(doubleUnidiff)
## Coefficients of interest:
## Mult(Exp(.), class:vote).election1
##                        -0.38357138
## Mult(Exp(.), class:vote).election2
##                         0.29816599
## Mult(Exp(.), class:vote).election3
##                         0.06580307
## Mult(Exp(.), class:vote).election4
##                        -0.02174104

##  Re-parameterize by setting first multiplier to zero
getContrasts(doubleUnidiff, ofInterest(doubleUnidiff))
```

```
##                                      estimate        SE
## Mult(Exp(.), class:vote).election1 0.0000000 0.0000000
## Mult(Exp(.), class:vote).election2 0.6817374 0.2401644
## Mult(Exp(.), class:vote).election3 0.4493745 0.2473521
## Mult(Exp(.), class:vote).election4 0.3618301 0.2534754
##                                        quasiSE    quasiVar
## Mult(Exp(.), class:vote).election1 0.22854401 0.052232363
## Mult(Exp(.), class:vote).election2 0.07395886 0.005469913
## Mult(Exp(.), class:vote).election3 0.09475938 0.008979340
## Mult(Exp(.), class:vote).election4 0.10934798 0.011956981

##  Same thing but with last multiplier as reference category:
getContrasts(doubleUnidiff, rev(ofInterest(doubleUnidiff)))
##                                        estimate        SE
## Mult(Exp(.), class:vote).election4  0.00000000 0.0000000
## Mult(Exp(.), class:vote).election3  0.08754436 0.1446833
## Mult(Exp(.), class:vote).election2  0.31990727 0.1320022
## Mult(Exp(.), class:vote).election1 -0.36183013 0.2534754
##                                        quasiSE    quasiVar
## Mult(Exp(.), class:vote).election4 0.10934798 0.011956981
## Mult(Exp(.), class:vote).election3 0.09475938 0.008979340
## Mult(Exp(.), class:vote).election2 0.07395886 0.005469913
## Mult(Exp(.), class:vote).election1 0.22854401 0.052232363

##  Re-fit model with first multiplier set to zero
doubleUnidiffConstrained <-
    update(doubleUnidiff, constrain = ofInterest(doubleUnidiff)[1])

##  Examine the multipliers of the class-vote log odds ratios
coef(doubleUnidiffConstrained)[ofInterest(doubleUnidiff)]
##  ...as using 'getContrasts' (to 4 d.p.).
```

`House2001` *Data on twenty roll calls in the US House of Representatives, 2001*

Description

The voting record of every representative in the 2001 House, on 20 roll calls selected by *Americans for Democratic Action*. Each row is the record of one representative; the first column records the representative's registered party allegiance.

Usage

```
data(House2001)
```

Format

A data frame with 439 observations on the following 21 variables.

`party` a factor with levels `D` `I` `N` `R`

`HR333.BankruptcyOverhaul.Yes` a numeric vector

`SJRes6.ErgonomicsRuleDisapproval.No` a numeric vector

`HR3.IncomeTaxReduction.No` a numeric vector

`HR6.MarriageTaxReduction.Yes` a numeric vector

`HR8.EstateTaxRelief.Yes` a numeric vector

`HR503.FetalProtection.No` a numeric vector

`HR1.SchoolVouchers.No` a numeric vector

`HR1836.TaxCutReconciliationBill.No` a numeric vector

`HR2356.CampaignFinanceReform.No` a numeric vector

`HJRes36.FlagDesecration.No` a numeric vector

`HR7.FaithBasedInitiative.Yes` a numeric vector

`HJRes50.ChinaNormalizedTradeRelations.Yes` a numeric vector

`HR4.ANWRDrillingBan.Yes` a numeric vector

`HR2563.PatientsRightsHMOLiability.No` a numeric vector

`HR2563.PatientsBillOfRights.No` a numeric vector

`HR2944.DomesticPartnerBenefits.No` a numeric vector

`HR2586.USMilitaryPersonnelOverseasAbortions.Yes` a numeric vector

`HR2975.AntiTerrorismAuthority.No` a numeric vector

`HR3090.EconomicStimulus.No` a numeric vector

`HR3000.TradePromotionAuthorityFastTrack.No` a numeric vector

Details

Coding of the votes is as described in ADA (2002).

Source

Originally printed in ADA (2002). Kindly supplied in electronic format by Jan deLeeuw, who used the data to illustrate methods developed in deLeeuw (2006).

References

Americans for Democratic Action, ADA (2002). 2001 voting record: Shattered promise of liberal progress. *ADA Today* **57**(1), 1–17.

deLeeuw, J (2006). Principal component analysis of binary data by iterated singular value decomposition. *Computational Statistics and Data Analysis* **50**, 21–39.

Examples

```
## Not run:
## This example takes some time to run!
data(House2001)
summary(House2001)
## Put the votes in a matrix, and discard members with too many NAs etc:
House2001m <- as.matrix(House2001[-1])
informative <- apply(House2001m, 1, function(row){
    valid <- !is.na(row)
    validSum <- if (any(valid)) sum(row[valid]) else 0
    nValid <- sum(valid)
    uninformative <- (validSum == nValid) || (validSum == 0) || (nValid < 10)
    !uninformative})
House2001m <- House2001m[informative, ]
## Make a vector of colours, blue for Republican and red for Democrat:
parties <- House2001$party[informative]
partyColors <- rep("black", length(parties))
partyColors <- ifelse(parties == "D", "red", partyColors)
partyColors <- ifelse(parties == "R", "blue", partyColors)
## Expand the data for statistical modelling:
House2001v <- as.vector(House2001m)
House2001f <- data.frame(member = rownames(House2001m),
                         party = parties,
                         rollCall = factor(rep((1:20),
                                         rep(nrow(House2001m), 20))),
                         vote = House2001v)
## Now fit an "empty" model, in which all members vote identically:
baseModel <- glm(vote ~ -1 + rollCall, family = binomial, data = House2001f)
## From this, get starting values for a one-dimensional multiplicative term:
Start <- residSVD(baseModel, rollCall, member)
##
## Now fit the logistic model with one multiplicative term.
## For the response variable, instead of vote=0,1 we use 0.03 and 0.97,
## corresponding approximately to a bias-reducing adjustment of p/(2n),
## where p is the number of parameters and n the number of observations.
##
voteAdj <- 0.5 + 0.94*(House2001f$vote - 0.5)
House2001model1 <- gnm(voteAdj ~ Mult(rollCall, member),
              eliminate = rollCall,
              family = binomial, data = House2001f,
              na.action = na.exclude, trace = TRUE, tolerance = 1e-03,
              start = -Start)
## Deviance is 2234.847, df = 5574
##
## Plot the members' positions as estimated in the model:
##
memberParameters <- pickCoef(House2001model1, "member")
plot(coef(House2001model1)[memberParameters], col = partyColors,
     xlab = "Alphabetical index (Abercrombie 1 to Young 301)",
     ylab = "Member's relative position, one-dimensional model")
## Can do the same thing with two dimensions, but gnm takes around 40
## slow iterations to converge (there are more than 600 parameters):
```

```
Start2 <- residSVD(baseModel, rollCall, member, d = 2)
House2001model2 <- gnm(
              voteAdj ~ instances(Mult(rollCall - 1, member - 1), 2),
              eliminate = rollCall,
              family = binomial, data = House2001f,
              na.action = na.exclude, trace = TRUE, tolerance = 1e-03,
              start = Start2, lsMethod = "qr")
## Deviance is 1545.166, df = 5257
##
memberParameters1 <- pickCoef(House2001model2, "1).member")
memberParameters2 <- pickCoef(House2001model2, "2).member")
plot(coef(House2001model2)[memberParameters1],
     coef(House2001model2)[memberParameters2],
     col = partyColors,
     xlab = "Dimension 1",
     ylab = "Dimension 2",
     main = "House2001 data: Member positions, 2-dimensional model")
##
## The second dimension is mainly due to rollCall 12, which does not
## correlate well with the rest -- look at the coefficients of
## House2001model1, or at the 12th row of
cormat <- cor(na.omit(House2001m))

## End(Not run)
```

`instances` *Specify Multiple Instances of a Nonlinear Term in a gnm Model Formula*

Description

A symbolic wrapper, for use in the formula argument to `gnm`, to specify multiple instances of a term specified by a function with an `inst` argument.

Usage

```
instances(term, instances = 1)
```

Arguments

`term`	a call to a function with an inst argument, which specifies some term.
`instances`	the desired number of instances of the term.

Value

A deparsed expression representing the summation of `term` specified with `inst = 1`, `inst = 2`, ..., `inst = instances`, which is used to create an expanded formula.

Author(s)

Heather Turner

See Also

gnm, formula, nonlin.function, Mult, MultHomog

Examples

```
## Not run:
## (this example can take quite a while to run)
##
## Fitting two instances of a multiplicative interaction (i.e. a
## two-component interaction)
data(wheat)
yield.scaled <- wheat$yield * sqrt(3/1000)
treatment <- factor(paste(wheat$tillage, wheat$summerCrop, wheat$manure,
                          wheat$N, sep = ""))
bilinear2 <- gnm(yield.scaled ~ year + treatment +
                 instances(Mult(year, treatment), 2),
                 family = gaussian, data = wheat)

## End(Not run)
```

Inv *Specify the Reciprocal of a Predictor in a gnm Model Formula*

Description

A function of class "nonlin" to specify the reciprocal of a predictor in the formula argument to gnm.

Usage

```
Inv(expression, inst = NULL)
```

Arguments

expression	a symbolic expression representing the (possibly nonlinear) predictor.
inst	(optional) an integer specifying the instance number of the term.

Details

The expression argument is interpreted as the right hand side of a formula in an object of class "formula", except that an intercept term is not added by default. Any function of class "nonlin" may be used in addition to the usual operators and functions.

Value

A list with the components required of a "nonlin" function:

predictors	the expression argument passed to Inv
term	a function to create a deparsed mathematical expression of the term, given a label for the predictor.
call	the call to use as a prefix for parameter labels.

Author(s)

Heather Turner

See Also

gnm, formula, nonlin.function

Examples

```
## One way to fit the logistic function without conditional
## linearity as in ?nls
library(gnm)
set.seed(1)
DNase1 <- subset(DNase, Run == 1)

test <- gnm(density ~ -1 +
            Mult(1, Inv(Const(1) + Exp(Mult(1 + offset(-log(conc)),
                                            Inv(1))))),
            start = c(NA, 0, 1), data = DNase1, trace = TRUE)
coef(test)
```

---

meanResiduals *Average Residuals within Factor Levels*

Description

Computes the mean working residuals from a model fitted using Iterative Weighted Least Squares for each level of a factor or interaction of factors.

Usage

```
meanResiduals(object, by, standardized=TRUE, as.table=TRUE, ...)
```

Arguments

object	model object for which object$residuals gives the working residuals and object$weights gives the working weights.
by	either a formula specifying a factor or interaction of factors (recommended), or a list of factors (the elements of which must correspond exactly to observations in the model frame). When a list of factors is specified, their interaction is used to specify the grouping factor.
standardized	logical: if TRUE, the mean residuals are standardized to be approximately standard normal.
as.table	logical: logical: if TRUE and by specifies an interaction of factors, the result is returned as a table cross-classified by these factors.
...	currently ignored

Details

For level i of the grouping factor A the mean working residual is defined as

$$\frac{r_{ij} * w_{ij}}{\sum_{j=1}^{n_i} w_{ij}}$$

where r_{ij} is the j'th residual for level i, w_{ij} is the corresponding working weight and n_i is the number of observations for level i. The denominator gives the weight corresponding to mean residual.

For non-aggregated residuals, i.e. when the factor has one level per observation, the residuals are the same as Pearson residuals.

Value

An object of class "meanResiduals", for which print and summary methods are provided. A "meanResiduals" object is a list containing the following elements:

call	the call used to create the model object from which the mean residuals are derived.
by	a label for the grouping factor.
residuals	the mean residuals.
df	the degrees of freedom associated with the mean residuals.
standardized	the standardized argument.
weights	the weights corresponding to the mean residuals.

Author(s)

Heather Turner

Examples

```
data(yaish)
## Fit a conditional independence model, leaving out
## the uninformative subtable for dest == 7:
CImodel <- gnm(Freq ~ educ*orig + educ*dest, family = poisson,
               data = yaish, subset = (dest != 7))

## compute mean residuals over origin and destination
meanRes <- meanResiduals(CImodel, ~ orig:dest)
meanRes
summary(meanRes)

## Not run:
## requires vcdExtra package
## display mean residuals for origin and destination
library(vcdExtra)
mosaic(CImodel, ~orig+dest)

## End(Not run)

## non-aggregated residuals
res1 <- meanResiduals(CImodel, ~ educ:orig:dest)
res2 <- residuals(CImodel, type = "pearson")
all.equal(as.numeric(res1), as.numeric(res2))
```

---

mentalHealth *Data on Mental Health and Socioeconomic Status*

Description

A 2-way contingency table from a sample of residents of Manhattan. Classifying variables are child's mental impairment (MHS) and parents' socioeconomic status (SES).

Usage

```
data(mentalHealth)
```

Format

A data frame with 24 observations on the following 3 variables.

`count` a numeric vector

`SES` an ordered factor with levels A < B < C < D < E < F

`MHS` an ordered factor with levels well < mild < moderate < impaired

Source

From Agresti (2002, p381); originally in Srole et al. (1978, p289).

References

Agresti, A. (2002). *Categorical Data Analysis* (2nd edn). New York: Wiley.

Srole, L, Langner, T. S., Michael, S. T., Opler, M. K. and Rennie, T. A. C. (1978), *Mental Health in the Metropolis: The Midtown Manhattan Study*. New York: NYU Press.

Examples

```
set.seed(1)
data(mentalHealth)

##  Goodman Row-Column association model fits well (deviance 3.57, df 8)
mentalHealth$MHS <- C(mentalHealth$MHS, treatment)
mentalHealth$SES <- C(mentalHealth$SES, treatment)
RC1model <- gnm(count ~ SES + MHS + Mult(SES, MHS),
                family = poisson, data = mentalHealth)
## Row scores and column scores are both unnormalized in this
## parameterization of the model

## The scores can be normalized as in Agresti's eqn (9.15):
rowProbs <- with(mentalHealth, tapply(count, SES, sum) / sum(count))
colProbs <- with(mentalHealth, tapply(count, MHS, sum) / sum(count))
mu <- getContrasts(RC1model, pickCoef(RC1model, "[.]SES"),
                   ref = rowProbs, scaleRef = rowProbs,
                   scaleWeights = rowProbs)
nu <- getContrasts(RC1model, pickCoef(RC1model, "[.]MHS"),
                   ref = colProbs, scaleRef = colProbs,
                   scaleWeights = colProbs)
all.equal(sum(mu$qv[,1] * rowProbs), 0)
all.equal(sum(nu$qv[,1] * colProbs), 0)
all.equal(sum(mu$qv[,1]^2 * rowProbs), 1)
all.equal(sum(nu$qv[,1]^2 * colProbs), 1)
```

---

model.matrix.gnm *Local Design Matrix for a Generalized Nonlinear Model*

Description

This method extracts or evaluates a local design matrix for a generalized nonlinear model

Usage

```
## S3 method for class 'gnm'
model.matrix(object, coef = NULL, ...)
```

Arguments

object	an object of class gnm.
coef	if specified, the vector of (non-eliminated) coefficients at which the local design matrix is evaluated.
...	further arguments.

Value

If coef = NULL, the local design matrix with columns corresponding to the non-eliminated parameters evaluated at coef(object) (extracted from object if possible).

Otherwise, the local design matrix evaluated at coef.

Author(s)

Heather Turner

See Also

gnm, model.matrix

Examples

```
example(mentalHealth)
model.matrix(RC1model)
model.matrix(RC1model, coef = seq(coef(RC1model)))
```

MPinv *Moore-Penrose Pseudoinverse of a Real-valued Matrix*

Description

Computes the Moore-Penrose generalized inverse.

Usage

```
MPinv(mat, tolerance = 100*.Machine$double.eps,
      rank = NULL, method = "svd")
```

Arguments

mat	a real matrix.
tolerance	A positive scalar which determines the tolerance for detecting zeroes among the singular values.
rank	Either NULL, in which case the rank of mat is determined numerically; or an integer specifying the rank of mat if it is known. No check is made on the validity of any non-NULL value.
method	Character, one of "svd", "chol". The specification method = "chol" is valid only for symmetric matrices.

Details

Real-valuedness is not checked, neither is symmetry when `method = "chol"`.

Value

A matrix, with an additional attribute named `"rank"` containing the numerically determined rank of the matrix.

Author(s)

David Firth

References

Harville, D. A. (1997). *Matrix Algebra from a Statistician's Perspective*. New York: Springer.

Courrieu, P. (2005). Fast computation of Moore-Penrose inverse matrices. *Neural Information Processing* **8**, 25–29

See Also

`ginv`

Examples

```
A <- matrix(c(1, 1, 0,
              1, 1, 0,
              2, 3, 4), 3, 3)
B <- MPinv(A)
A %*% B %*% A - A  # essentially zero
B %*% A %*% B - B  # essentially zero
attr(B, "rank")    # here 2

## demonstration that "svd" and "chol" deliver essentially the same
## results for symmetric matrices:
A <- crossprod(A)
MPinv(A) - MPinv(A, method = "chol") ##  (essentially zero)
```

`MultHomog` *Specify a Multiplicative Interaction with Homogeneous Effects in a gnm Model Formula*

Description

A function of class `"nonlin"` to specify a multiplicative interaction with homogeneous effects in the formula argument to `gnm`.

Usage

```
MultHomog(..., inst = NULL)
```

Arguments

`...`	a comma-separated list of two or more factors.
`inst`	(optional) an integer specifying the instance number of the term.

Details

`MultHomog` specifies instances of a multiplicative interaction in which the constituent multipliers are the effects of two or more factors and the effects of these factors are constrained to be equal when the factor levels are equal. Thus the interaction effect would be

$$\gamma_i \gamma_j \cdots$$

for an observation with level i of the first factor, level j of the second factor and so on, where γ_l is the effect for level l of the homogeneous multiplicative factor.

If the factors passed to `MultHomog` do not have exactly the same levels, the set of levels is taken to be the union of the factor levels, sorted into increasing order.

Value

A list with the anticipated components of a `"nonlin"` function:

`predictors`	the factors passed to `MultHomog`
`common`	an index to specify that common effects are to be estimated across the factors
`term`	a function to create a deparsed mathematical expression of the term, given labels for the predictors.
`call`	the call to use as a prefix for parameter labels.

Note

Currently, `MultHomog` can only be used to specify a one-dimensional interaction. See examples for a workaround to specify interactions with more than one dimension.

Author(s)

Heather Turner

References

Goodman, L. A. (1979) Simple Models for the Analysis of Association in Cross-Classifications having Ordered Categories. *J. Am. Stat. Assoc.*, **74(367)**, 537-552.

See Also

`gnm`, `formula`, `instances`, `nonlin.function`, `Mult`

Examples

```
set.seed(1)
data(friend)

###  Fit an association model with homogeneous row-column effects
rc1 <- gnm(Freq ~ r + c + Diag(r,c) + MultHomog(r, c),
           family = poisson, data = friend)
rc1

## Not run:
###  Extend to two-component interaction
rc2 <- update(rc1, . ~ . + MultHomog(r, c, inst = 2),
              etastart = rc1$predictors)
rc2

## End(Not run)

### For factors with a large number of levels, save time by
### setting diagonal elements to NA rather than fitting exactly;
### skipping start-up iterations may also save time
dat <- as.data.frame(friend)
id <- with(dat, r == c)
dat[id,] <- NA
rc2 <- gnm(Freq ~ r + c + instances(MultHomog(r, c), 2),
           family = poisson, data = dat, iterStart = 0)
```

Multiplicative interaction

Specify a Product of Predictors in a gnm Model Formula

Description

A function of class "nonlin" to specify a multiplicative interaction in the formula argument to gnm.

Usage

```
Mult(..., inst = NULL)
```

Arguments

...	a comma-separated list of two or more symbolic expressions representing the constituent multipliers in the interaction.
inst	a positive integer specifying the instance number of the term.

Details

`Mult` specifies instances of a multiplicative interaction, i.e. a product of the form

$$m_1 m_2 ... m_n,$$

where the constituent multipliers $m_1, m_2, ..., m_n$ are linear or nonlinear predictors.

Models for the constituent multipliers are specified symbolically as unspecified arguments to `Mult`. These symbolic expressions are interpreted in the same way as the right hand side of a formula in an object of class `"formula"`, except that an intercept term is not added by default. Offsets can be added to constituent multipliers, using `offset`.

The family of multiplicative interaction models include row-column association models for contingency tables (e.g., Agresti, 2002, Sec 9.6), log-multiplicative or UNIDIFF models (Erikson and Goldthorpe, 1992; Xie, 1992), and GAMMI models (van Eeuwijk, 1995).

Value

A list with the required components of a `"nonlin"` function:

`predictors`	the expressions passed to `Mult`
`term`	a function to create a deparsed mathematical expression of the term, given labels for the predictors.
`call`	the call to use as a prefix for parameter labels.

Author(s)

Heather Turner

References

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van Eeuwijk, F A (1995). Multiplicative interaction in generalized linear models. *Biometrics* **51**, 1017-1032.

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Xie, Y (1992). The log-multiplicative layer effect model for comparing mobility tables. *American Sociological Review* **57**, 380-395.

See Also

`gnm`, `formula`, `instances`, `nonlin.function`, `MultHomog`

Examples

```
set.seed(1)

## Using 'Mult' with 'Exp' to constrain the first constituent multiplier
##  to be non-negative
data(yaish)
## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               family = poisson, data = yaish, subset = (dest != 7))

## Not run:
## (this example can take quite a while to run)
##
## Fitting two instances of a multiplicative interaction (i.e. a
## two-component interaction)
data(wheat)
yield.scaled <- wheat$yield * sqrt(3/1000)
treatment <- factor(paste(wheat$tillage, wheat$summerCrop, wheat$manure,
                          wheat$N, sep = ""))
bilinear2 <- gnm(yield.scaled ~ year + treatment +
                 instances(Mult(year, treatment), 2),
                 family = gaussian, data = wheat)
formula(bilinear2)
## yield.scaled ~ year + treatment + Mult(year, treatment, inst = 1) +
##     Mult(year, treatment, inst = 2)

## End(Not run)
```

`nonlin.function` *Functions to Specify Nonlinear Terms in gnm Models*

Description

Nonlinear terms maybe be specified in the formula argument to gnm by a call to a function of class `"nonlin"`. A `"nonlin"` function takes a list of arguments and returns a list of arguments for the internal `nonlinTerms` function.

Arguments

`...`	arguments required to define the term, e.g. symbolic representations of predictors in the term.
`inst`	(optional) an integer specifying the instance number of the term - for compatibility with `instances`.

Value

The function should return a list with the following components:

predictors	a list of symbolic expressions or formulae with no left hand side which represent (possibly nonlinear) predictors that form part of the term. Intercepts will be added by default to predictors specified by formulae. If predictors are named, these names will be used as a prefix for parameter labels or the parameter label itself in the single parameter case (in either case, prefixed by the call if supplied.) Predictors that may include an intercept should always be named or matched to a call.
variables	an optional list of expressions representing variables in the term.
term	a function which takes the arguments predLabels and varLabels, which are vectors of labels defined by gnm that correspond to the specified predictors and variables, and returns a deparsed mathematical expression of the full term. Only functions recognised by deriv should be used in the expression, e.g. + rather than sum.
common	an optional numeric index of predictors with duplicated indices identifying single factor predictors for which homologous effects are to be estimated.
call	an optional call to be used as a prefix for parameter labels, specified as an R expression.
match	(if call is non-NULL) a numeric index of predictors specifying which arguments of call the predictors match to - zero indicating no match. If NULL, predictors will not be matched. It is recommended that matches are specified wherever possible, to ensure parameter labels are well-defined. Parameters in matched predictors are labelled using "dot-style" labelling, see examples.
start	an optional function which takes a named vector of parameters corresponding to the predictors and returns a vector of starting values for those parameters. This function is ignored if the term is nested within another nonlinear term.

Author(s)

Heather Turner

See Also

Const to specify a constant, Dref to specify a diagonal reference term, Exp to specify the exponential of a predictor, Inv to specify the reciprocal of a predictor,

Mult to specify a multiplicative interaction, MultHomog to specify a homogeneous multiplicative interaction,

Examples

```
### Equivalent of weighted.MM function in ?nls
weighted.MM <- function(resp, conc){
    list(predictors = list(Vm = substitute(conc), K = 1),
         variables = list(substitute(resp), substitute(conc)),
         term = function(predictors, variables) {
```

```
            pred <- paste("(", predictors[1], "/(", predictors[2],
                          " + ", variables[2], "))", sep = "")
            pred <- paste("(", variables[1], " - ", pred, ")/sqrt(",
                          pred, ")", sep = "")
        })
}
class(weighted.MM) <- "nonlin"

## use to fitted weighted Michaelis-Menten model
Treated <- Puromycin[Puromycin$state == "treated", ]
Pur.wt.2 <- gnm( ~ -1 + weighted.MM(rate, conc), data = Treated,
               start = c(Vm = 200, K = 0.1), verbose = FALSE)
Pur.wt.2
##
## Call:
## gnm(formula = ~-1 + weighted.MM(rate, conc), data = Treated,
##     start = c(Vm = 200, K = 0.1), verbose = FALSE)
##
## Coefficients:
##        Vm          K
## 206.83477    0.05461
##
## Deviance:            14.59690
## Pearson chi-squared: 14.59690
## Residual df:         10

### The definition of MultHomog
data(occupationalStatus)
MultHomog <- function(..., inst = NULL){
    dots <- match.call(expand.dots = FALSE)[["..."]]
    list(predictors = dots,
         common = rep(1, length(dots)),
         term = function(predictors, ...) {
             paste("(", paste(predictors, collapse = ")*("), ")", sep = "")
         },
         call = as.expression(match.call()))
}
class(MultHomog) <- "nonlin"
## use to fit homogeneous multiplicative interaction
set.seed(1)
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination), ofInterest = "MultHomog",
               family = poisson, data = occupationalStatus,
               verbose = FALSE)
RChomog
##
## Call:
##
## gnm(formula = Freq ~ origin + destination + Diag(origin, destination) +
##     MultHomog(origin, destination), ofInterest = "MultHomog", family = poisson,
##     data = occupationalStatus, verbose = FALSE)
##
## Coefficients of interest:
```

```
## MultHomog(origin, destination)1
##                               -1.50089
## MultHomog(origin, destination)2
##                               -1.28260
## MultHomog(origin, destination)3
##                               -0.68443
## MultHomog(origin, destination)4
##                               -0.10055
## MultHomog(origin, destination)5
##                               -0.08338
## MultHomog(origin, destination)6
##                                0.42838
## MultHomog(origin, destination)7
##                                0.84452
## MultHomog(., .).`origin|destination`8
##                                1.08809
##
## Deviance:            32.56098
## Pearson chi-squared: 31.20716
## Residual df:         34
##

## the definition of Exp
Exp <- function(expression, inst = NULL){
    list(predictors = list(substitute(expression)),
         term = function(predictors, ...) {
             paste("exp(", predictors, ")", sep = "")
         },
         call = as.expression(match.call()),
         match = 1)
}
class(Exp) <- "nonlin"


## use to fit exponentional model
x <- 1:100
y <- exp(- x / 10)
set.seed(4)
exp1 <- gnm(y ~ Exp(1 + x), verbose = FALSE)
exp1
##
## Call:
## gnm(formula = y ~ Exp(1 + x), verbose = FALSE)
##
## Coefficients:
##            (Intercept)  Exp(. + x).(Intercept)
##              1.549e-11               -7.934e-11
##           Exp(1 + .).x
##             -1.000e-01
##
## Deviance:            9.342418e-20
## Pearson chi-squared: 9.342418e-20
## Residual df:         97
```

`ofInterest` *Coefficents of Interest in a Generalized Nonlinear Model*

Description

Retrieve or set the `"ofInterest"` component of a `"gnm"` (generalized nonlinear model) object.

Usage

```
ofInterest(object)
ofInterest(object) <- value
```

Arguments

`object`	an object of class `"gnm"`.
`value`	a numeric vector of indices specifying the subset of (non-eliminated) coefficients of interest, or `NULL` to specify that all non-eliminated coefficients are of interest.

Details

The `"ofInterest"` component of a `"gnm"` object is a named numeric vector of indices specifying a subset of the non-eliminated coefficients which are of specific interest.

If the `"ofInterest"` component is non-NULL, printed summaries of the model only show the coefficients of interest. In addition methods for `"gnm"` objects which may be applied to a subset of the parameters are by default applied to the coefficients of interest.

These functions provide a way of extracting and replacing the `"ofInterest"` component. The replacement function prints the replacement value to show which parameters have been specified by `value`.

Value

A named vector of indices, or `NULL`.

Note

Regular expression matching is performed using `grep` with default settings.

Author(s)

Heather Turner

See Also

`grep`, `gnm`, `se`, `getContrasts`,`profile.gnm`, `confint.gnm`

Examples

```
data(yaish)
set.seed(1)

## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               ofInterest = "[.]educ", family = poisson,
               data = yaish,  subset = (dest != 7))
ofInterest(unidiff)

## Get all of the contrasts with educ1 in the UNIDIFF multipliers
getContrasts(unidiff, ofInterest(unidiff))

## Get estimate and se for the contrast between educ4 and educ5 in the
## UNIDIFF multiplier
mycontrast <- numeric(length(coef(unidiff)))
mycontrast[ofInterest(unidiff)[4:5]] <- c(1, -1)
se(unidiff, mycontrast)
```

---

parameters *Extract Constrained and Estimated Parameters from a gnm Object*

Description

A function to extract non-eliminated parameters from a "gnm" object, including parameters that were constrained.

Usage

```
parameters(object)
```

Arguments

object	an object of class "gnm".

Details

parameters acts like coefficients except that for constrained parameters, the value at which the parameter was constrained is returned instead of NA.

Value

A vector of parameters.

Author(s)

Heather Turner

See Also

coefficients, gnm

Examples

```
data(occupationalStatus)
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination), family = poisson,
               data = occupationalStatus, ofInterest = "MultHomog",
               constrain = "MultHomog.*1")
coefficients(RChomog)
parameters(RChomog)
```

---

pickCoef *Get Indices or Values of Selected Model Coefficients*

Description

Get the indices or values of a subset of non-eliminated coefficients selected via a Tk dialog or by pattern matching.

Usage

```
pickCoef(object, pattern = NULL, value = FALSE, ...)
```

Arguments

object	a model object.
pattern	character string containing a regular expression or (with fixed = TRUE) a pattern to be matched exactly. If missing, a Tk dialog will open for coefficient selection.
value	if FALSE, a named vector of indices, otherwise the value of the selected coefficients.
...	arguments to pass on to pickFrom if pattern is missing, otherwise grep. In particular, fixed = TRUE specifies that pattern is a string to be matched as is.

Value

If value = FALSE (the default), a named vector of indices, otherwise the values of the selected coefficients. If no coefficients are selected the returned value will be NULL.

Author(s)

Heather Turner

See Also

regexp, grep, pickFrom, ofInterest

Examples

```
set.seed(1)

### Extract indices for use with ofInterest

data(yaish)
## fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               family = poisson, data = yaish, subset = (dest != 7))

## set coefficients in first constituent multiplier as 'ofInterest'
## using regular expression
ofInterest(unidiff) <- pickCoef(unidiff, "[.]educ")

## summarise model, only showing coefficients of interest
summary(unidiff)

## get contrasts of these coefficients
getContrasts(unidiff, ofInterest(unidiff))

### Extract coefficients to use as starting values

## fit diagonal reference model with constant weights
set.seed(1)
data(voting)
## reconstruct counts voting Labour/non-Labour
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)

classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting)

## create factors indicating movement in and out of salariat (class 1)
upward <- with(voting, origin != 1 & destination == 1)
downward <- with(voting, origin == 1 & destination != 1)

## extract diagonal effects from first model to use as starting values
diagCoef <- pickCoef(classMobility, "Dref(., .)", fixed = TRUE,
                     value = TRUE)

## fit separate weights for the "socially mobile" groups
## -- there are now 3 parameters for each weight
socialMobility <- gnm(yvar ~ -1 + Dref(origin, destination,
                                       delta = ~ 1 + downward + upward),
                      family = binomial, data = voting,
                      start = c(rep(NA, 6), diagCoef))
```

plot.gnm *Plot Diagnostics for a gnm Object*

Description

Five plots are available: a plot of residuals against fitted values, a Scale-Location plot of $\sqrt{|residuals|}$ against fitted values, a Normal Q-Q plot, a plot of Cook's distances versus row labels, and a plot of residuals against leverages. By default, all except the fourth are produced.

Usage

```
## S3 method for class 'gnm'
plot(x, which = c(1:3, 5), caption = c("Residuals vs Fitted",
         "Normal Q-Q", "Scale-Location", "Cook's distance",
         "Residuals vs Leverage"),
         panel = if (add.smooth) panel.smooth else points,
         sub.caption = NULL, main = "",
         ask = prod(par("mfcol")) < length(which) && dev.interactive(),
         ..., id.n = 3, labels.id = names(residuals(x)), cex.id = 0.75,
         qqline = TRUE, cook.levels = c(0.5, 1),
         add.smooth = getOption("add.smooth"), label.pos = c(4, 2),
         cex.caption = 1)
```

Arguments

x	a "gnm" object.
which	a subset of the numbers 1:5 specifying which plots to produce (out of those listed in Description section).
caption	captions to appear above the plots.
panel	panel function. The useful alternative to points, panel.smooth can be chosen by add.smooth = TRUE.
sub.caption	common title - above figures if there are multiple; used as sub (s.title) otherwise. If NULL, as by default, a possible shortened version of deparse(x$call) is used.
main	title to each plot - in addition to the above caption.
ask	logical; if TRUE, the user is asked before each plot, see par(ask = .).
...	other parameters to be passed through to plotting functions.
id.n	number of points to be labelled in each plot starting with the most extreme.
labels.id	vector of labels, from which the labels for extreme points will be chosen. NULL uses observation numbers.
cex.id	magnification of point labels.
qqline	logical indicating if a qqline() should be added to the normal Q-Q plot.
cook.levels	levels of Cook's distance at which to draw contours.

add.smooth	logical indicating if a smoother should be added to most plots; see also panel above.
label.pos	positioning of labels, for the left half and right half of the graph respectively, for plots 1-3.
cex.caption	controls the size of 'caption'.

Details

sub.caption - by default the function call - is shown as a subtitle (under the x-axis title) on each plot when plots are on separate pages, or as a subtitle in the outer margin (if any) when there are multiple plots per page.

The "Scale-Location" plot, also called "Spread-Location" or "S-L" plot, takes the square root of the absolute residuals in order to diminish skewness ($\sqrt{|E|}$ is much less skewed than $|E|$ for Gaussian zero-mean E).

The S-L, the Q-Q, and the Residual-Leverage plot, use *standardized* residuals which have identical variance (under the hypothesis). They are given as $R[i]/(s * \sqrt{(1 - h_{ii})})$ where h_{ii} are the diagonal entries of the hat matrix, influence()$hat, see also hat.

The Residual-Leverage plot shows contours of equal Cook's distance, for values of cook.levels (by default 0.5 and 1) and omits cases with leverage one. If the leverages are constant, as typically in a balanced aov situation, the plot uses factor level combinations instead of the leverages for the x-axis.

Author(s)

Heather Turner (adaptation of plot.lm, as of R 2.2.1)

See Also

gnm, plot.lm

Examples

```
set.seed(1)
data(occupationalStatus)

##  Fit an association model with homogeneous row-column effects
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination), family = poisson,
               data = occupationalStatus)

## Plot model diagnostics
plot(RChomog)

## Put 4 plots on 1 page; allow room for printing model formula in outer margin:
par(mfrow = c(2, 2), oma = c(0, 0, 3, 0))
title <- paste(deparse(RChomog$formula, width.cutoff = 50), collapse = "\n")
plot(RChomog, sub.caption = title)

## Fit smoother curves
```

```
plot(RChomog, sub.caption = title, panel = panel.smooth)
plot(RChomog, sub.caption = title, panel = function(x,y) panel.smooth(x, y, span = 1))
```

---

predict.gnm *Predict Method for Generalized Nonlinear Models*

Description

Obtains predictions and optionally estimates standard errors of those predictions from a fitted generalized nonlinear model object.

Usage

```
## S3 method for class 'gnm'
predict(object, newdata = NULL,
type = c("link", "response", "terms"), se.fit = FALSE, dispersion =
NULL, terms = NULL, na.action = na.exclude, ...)
```

Arguments

object	a fitted object of class inheriting from "gnm".
newdata	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted predictors are used.
type	the type of prediction required. The default is on the scale of the predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities. The "terms" option returns a matrix giving the fitted values of each term in the model formula on the predictor scale. The value of this argument can be abbreviated.
se.fit	logical switch indicating if standard errors are required.
dispersion	the dispersion of the fit to be assumed in computing the standard errors. If omitted, that returned by summary applied to the object is used.
terms	with type="terms" by default all terms are returned. A character vector specifies which terms are to be returned
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
...	further arguments passed to or from other methods.

Details

If newdata is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the na.action argument of that fit. If na.action = na.omit omitted cases will not appear in the residuals, whereas if na.action = na.exclude they will appear (in predictions and standard errors), with residual value NA. See also napredict.

Value

If `se = FALSE`, a vector or matrix of predictions. If `se = TRUE`, a list with components

`fit`	predictions.
`se.fit`	estimated standard errors.
`residual.scale`	a scalar giving the square root of the dispersion used in computing the standard errors.

Note

Variables are first looked for in 'newdata' and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in 'newdata' if it was supplied.

Author(s)

Heather Turner

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*

See Also

`gnm`

Examples

```
set.seed(1)
data(occupationalStatus)

##  Fit an association model with homogeneous row-column effects
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination), family = poisson,
               data = occupationalStatus)

## Fitted values (expected counts)
predict(RChomog, type = "response", se.fit = TRUE)

## Fitted values on log scale
predict(RChomog, type = "link", se.fit = TRUE)
```

profile.gnm *Profile Deviance for Parameters in a Generalized Nonlinear Model*

Description

For one or more parameters in a generalized nonlinear model, profile the deviance over a range of values about the fitted estimate.

Usage

```
## S3 method for class 'gnm'
profile(fitted, which = ofInterest(fitted), alpha = 0.05, maxsteps = 10,
            stepsize = NULL, trace = FALSE, ...)
```

Arguments

fitted	an object of class "gnm".
which	(optional) either a numeric vector of indices or a character vector of names, specifying the parameters over which the deviance is to be profiled. If missing, the deviance is profiled over all parameters.
alpha	the significance level of the z statistic, indicating the range that the profile must cover (see details).
maxsteps	the maximum number of steps to take either side of the fitted parameter.
stepsize	(optional) a numeric vector of length two, specifying the size of steps to take when profiling down and up respectively, or a single number specifying the step size in both directions. If missing, the step sizes will be determined automatically.
trace	logical, indicating whether profiling should be traced.
...	further arguments.

Details

This is a method for the generic function profile in the base package.

For a given parameter, the deviance is profiled by constraining that parameter to certain values either side of its estimate in the fitted model and refitting the model.

For each updated model, the following "z statistic" is computed

$$z(\theta) = (\theta - \hat{\theta}) * \sqrt{\frac{D_{theta} - D_{\hat{theta}}}{\delta}}$$

where θ is the constrained value of the parameter; $\hat{\theta}$ is the original fitted value; D_θ is the deviance when the parameter is equal to θ, and δ is the dispersion parameter.

When the deviance is quadratic in θ, z will be linear in θ. Therefore departures from quadratic behaviour can easily be identified by plotting z against θ using plot.profile.gnm.

confint.profile.gnm estimates confidence intervals for the parameters by interpolating the deviance profiles and identifying the parameter values at which z is equal to the relevant percentage points of the normal distribution. The alpha argument to profile.gnm specifies the significance level of z which must be covered by the profile. In particular, the profiling in a given direction will stop when maxsteps is reached or two steps have been taken in which

$$z(\theta) > (\theta - \hat{\theta}) * z_{(1-\alpha)/2}$$

By default, the stepsize is

$$z_{(1-\alpha)/2} * s_{\hat{\theta}}$$

where $s_{\hat{\theta}}$ is the standard error of $\hat{\theta}$. Strong assymetry is detected and the stepsize is adjusted accordingly, to try to ensure that the range determined by alpha is adequately covered. profile.gnm will also attempt to detect if the deviance is asymptotic such that the desired significance level cannot be reached. Each profile has an attribute "asymptote", a two-length logical vector specifying whether an asymptote has been detected in either direction.

For unidentified parameters the profile will be NA, as such parameters cannot be profiled.

Value

A list of profiles, with one named component for each parameter profiled. Each profile is a data.frame: the first column, "z", contains the z statistics and the second column "par.vals" contains a matrix of parameter values, with one column for each parameter in the model.

The list has two attributes: "original.fit" containing fitted and "summary" containing summary(fitted).

Author(s)

Heather Turner

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*

See Also

confint.gnm, gnm, profile.glm, ofInterest

Examples

```
set.seed(1)

### Example in which deviance is near quadratic
data(voting)
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     constrain = "delta1", family = binomial,
                     data = voting)
prof <- profile(classMobility, trace = TRUE)
plot(prof)
```

```
## confint similar to MLE +/- 1.96*s.e.
confint(prof, trace = TRUE)
coefData <- se(classMobility)
cbind(coefData[1] - 1.96 * coefData[2], coefData[1] + 1.96 * coefData[2])

## Not run:
### These examples take longer to run
### Another near quadratic example
data(occupationalStatus)
RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
               MultHomog(origin, destination),
               ofInterest = "MultHomog", constrain = "MultHomog.*1",
               family = poisson, data = occupationalStatus)
prof <- profile(RChomog, trace = TRUE)
plot(prof)
## confint similar to MLE +/- 1.96*s.e.
confint(prof)
coefData <- se(RChomog)
cbind(coefData[1] - 1.96 * coefData[2], coefData[1] + 1.96 * coefData[2])

## Another near quadratic example, with more complex constraints
data(voting)
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting)
wts <- prop.table(exp(coef(classMobility))[1:2])
classMobility <- update(classMobility, constrain = "delta1",
                        constrainTo = log(wts[1]))
sum(exp(parameters(classMobility))[1:2]) #=1
prof <- profile(classMobility, trace = TRUE)
plot(prof)
## confint similar to MLE +/- 1.96*s.e.
confint(prof, trace = TRUE)
coefData <- se(classMobility)
cbind(coefData[1] - 1.96 * coefData[2], coefData[1] + 1.96 * coefData[2])

### An example showing asymptotic deviance
data(yaish)
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               ofInterest = "[.]educ", constrain = "[.]educ1",
               family = poisson, data = yaish, subset = (dest != 7))
prof <- profile(unidiff, trace = TRUE)
plot(prof)
## clearly not quadratic for Mult1.Factor1.educ4 or Mult1.Factor1.educ5!
confint(prof)
##                            2.5 %     97.5 %
## Mult(Exp(.), orig:dest).educ1         NA         NA
## Mult(Exp(.), orig:dest).educ2 -0.5978901  0.1022447
## Mult(Exp(.), orig:dest).educ3 -1.4836854 -0.2362378
## Mult(Exp(.), orig:dest).educ4 -2.5792398 -0.2953420
## Mult(Exp(.), orig:dest).educ5       -Inf -0.7006889
```

```
coefData <- se(unidiff)
cbind(coefData[1] - 1.96 * coefData[2], coefData[1] + 1.96 * coefData[2])

### A far from quadratic example, also with eliminated parameters
data(backPain)
backPainLong <- expandCategorical(backPain, "pain")

oneDimensional <- gnm(count ~ pain + Mult(pain, x1 + x2 + x3),
                      eliminate = id,  family = "poisson",
                      constrain = "[.](painworse|x1)", constrainTo = c(0, 1),
                      data = backPainLong)
prof <- profile(oneDimensional, trace = TRUE)
plot(prof)
## not quadratic for any non-eliminated parameter
confint(prof)
coefData <- se(oneDimensional)
cbind(coefData[1] - 1.96 * coefData[2], coefData[1] + 1.96 * coefData[2])

## End(Not run)
```

`residSVD` *Multiplicative Approximation of Model Residuals*

Description

This function uses the first `d` components of the singular value decomposition in order to approximate a vector of model residuals by a sum of `d` multiplicative terms, with the multiplicative structure determined by two specified factors. It applies to models of class `lm`, `glm` or `gnm`.

Usage

```
residSVD(model, fac1, fac2, d = 1)
```

Arguments

`model`	an object of class `gnm`, `glm` or `lm`
`fac1`	a factor
`fac2`	a factor
`d`	integer, the number of multiplicative terms to use in the approximation

Details

This function operates on the matrix of mean residuals, with rows indexed by `fac1` and columns indexed by `fac2`. For `glm` and `glm` models, the matrix entries are weighted working residuals. The primary use of `residSVD` is to generate good starting values for the parameters in `Mult` terms in models to be fitted using `gnm`.

Value

If `d = 1`, a numeric vector; otherwise a numeric matrix with `d` columns.

Author(s)

David Firth and Heather Turner

See Also

`gnm`, `Mult`

Examples

```
set.seed(1)
data(mentalHealth)
##  Goodman RC1  association model fits well (deviance 3.57, df 8)
mentalHealth$MHS <- C(mentalHealth$MHS, treatment)
mentalHealth$SES <- C(mentalHealth$SES, treatment)
## independence model
indep <- gnm(count ~ SES + MHS, family = poisson, data = mentalHealth)
mult1 <- residSVD(indep, SES, MHS)
## Now use mult1 as starting values for the RC1 association parameters
RC1model <- update(indep, . ~ . + Mult(SES, MHS),
                   start = c(coef(indep), mult1), trace = TRUE)
##  Similarly for the RC2 model:
mult2 <- residSVD(indep, SES, MHS, d = 2)
RC2model <- update(indep, . ~ . + instances(Mult(SES, MHS), 2),
                   start = c(coef(indep), mult2), trace = TRUE)
##
## See also example(House2001), where good starting values matter much more!
##
```

---

se *Standard Errors of Linear Parameter Combinations in gnm Models*

Description

Computes approximate standard errors for (a selection of) individual parameters or one or more linear combinations of the parameters in a `gnm` (generalized nonlinear model) object. By default, a check is made first on the estimability of each specified combination.

Usage

```
se(model, estimate = NULL, checkEstimability = TRUE, Vcov =
NULL, dispersion = NULL, ...)
```

Arguments

model	a model object of class "gnm".
estimate	(optional) specifies parameters or linear combinations of parameters for which to find standard errors. In the first case either a character vector of names, a numeric vector of indices or "[?]" to select from a Tk dialog. In the second case coefficients given as a vector or the rows of a matrix, such that NROW(estimate) is equal to length(coef(model)). If missing, standard errors are returned for all (non-eliminated) parameters in the model.
checkEstimability	logical: should the estimability of all specified combinations be checked?
Vcov	either NULL, or a matrix
dispersion	either NULL, or a positive number
...	possible further arguments for checkEstimable.

Value

A data frame with two columns:

Estimate	The estimated parameter combinations
Std. Error	Their estimated standard errors

If available, the column names of coefMatrix will be used to name the rows.

Note

In the case where estimate is a numeric vector, se will assume that indices have been specified if all the values of estimate are in seq(length(coef(model))).

Where both Vcov and dispersion are supplied, the variance-covariance matrix of estimated model coefficients is taken to be Vcov * dispersion.

Author(s)

David Firth

See Also

gnm, getContrasts, checkEstimable, ofInterest

Examples

```
data(yaish)
set.seed(1)

## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest),
               ofInterest = "[.]educ", family = poisson,
               data = yaish,  subset = (dest != 7))
```

```
## Deviance is 200.3

## Get estimate and se for the contrast between educ4 and educ5 in the
## UNIDIFF multiplier
mycontrast <- numeric(length(coef(unidiff)))
mycontrast[ofInterest(unidiff)[4:5]] <- c(1, -1)
se(unidiff, mycontrast)

## Get all of the contrasts with educ5 in the UNIDIFF multipliers
getContrasts(unidiff, rev(ofInterest(unidiff)))
```

---

summary.gnm *Summarize Generalized Nonlinear Model Fits*

Description

summary method for objects of class "gnm"

Usage

```
## S3 method for class 'gnm'
summary(object, dispersion = NULL, correlation = FALSE,
                      symbolic.cor = FALSE, with.eliminate = FALSE, ...)

## S3 method for class 'summary.gnm'
print(x, digits = max(3, getOption("digits") - 3),
                            signif.stars = getOption("show.signif.stars"),
                            symbolic.cor = x$symbolic.cor, ...)
```

Arguments

object	an object of class "gnm".
x	an object of class "summary.gnm".
dispersion	the dispersion parameter for the fitting family. By default it is obtained from object.
correlation	logical: if TRUE, the correlation matrix of the estimated parameters is returned.
digits	the number of siginificant digits to use when printing.
symbolic.cor	logical: if TRUE, the correlations are printed in a symbolic form rather than numbers (see symnum).
signif.stars	logical. If TRUE, "significance stars" are printed for each coefficient.
with.eliminate	Logical. If TRUE, any eliminated coefficients are included in the summary.
...	further arguments passed to or from other methods.

Details

print.summary.gnm prints the original call to gnm; a summary of the deviance residuals from the model fit; the coefficients of the model; the residual deviance; the Akaike's Information Criterion value, and the number of main iterations performed.

Standard errors, z-values and p-values are printed alongside the coefficients, with "significance stars" if signif.stars is TRUE.

When the "summary.gnm" object has a "correlation" component, the lower triangle of this matrix is also printed, to two decimal places (or symbolically); to see the full matrix of correlations print summary(object, correlation = TRUE)$correlation directly.

The standard errors returned by summary.gnm are scaled by sqrt(dispersion). If the dispersion is not specified, it is taken as 1 for the binomial and Poisson families, and otherwise estimated by the residual Chi-squared statistic divided by the residual degrees of freedom. For coefficients that have been constrained or are not estimable, the standard error is returned as NA.

Value

summary.gnm returns an object of class "summary.gnm", which is a list with components

call	the "call" component from object.
ofInterest	the "ofInterest" component from object.
family	the "family" component from object.
deviance	the "deviance" component from object.
aic	the "aic" component from object.
df.residual	the "df.residual" component from object.
iter	the "iter" component from object.
deviance.resid	the deviance residuals, see residuals.glm.
coefficients	the matrix of coefficients, standard errors, z-values and p-values.
elim.coefs	if with.eliminate = TRUE a matrix of eliminated coefficients, standard errors, z-values and p-values.
dispersion	either the supplied argument or the estimated dispersion if the latter is NULL.
df	a 3-vector of the rank of the model; the number of residual degrees of freedom, and number of unconstrained coefficients.
cov.scaled	the estimated covariance matrix scaled by dispersion (see vcov.gnm for more details).
correlation	(only if correlation is TRUE) the estimated correlations of the estimated coefficients.
symbolic.cor	(only if correlation is TRUE) the value of the argument symbolic.cor.

Note

The gnm class includes generalized linear models, and it should be noted that summary.gnm differs from summary.glm in that it does not omit coefficients which are NA from the objects it returns. (Such coefficients are NA since they have been fixed at 0 either by use of the constrain argument to gnm or by a convention to handle linear aliasing).

Author(s)

Heather Turner

See Also

gnm, summary

Examples

```
### First example from ?Dref
set.seed(1)
data(voting)

## reconstruct counts voting Labour/non-Labour
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)

## fit diagonal reference model with constant weights
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting)

## summarize results - note diagonal weights are over-parameterised
summary(classMobility)

## refit setting first weight to zero (as DrefWeights() does)
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting,
                     constrain = "delta1")
summary(classMobility)
```

Symm *Symmetric Interaction of Factors*

Description

Symm codes the symmetric interaction of factors having the same set of levels, for use in regression models of symmetry or quasi-symmetry.

Usage

```
Symm(...)
```

Arguments

...	one or more factors.

Value

A factor whose levels index the symmetric interaction of all factors supplied as input.

Note

Symm relies on the gtools package from CRAN

Author(s)

David Firth

See Also

Diag

Examples

```
row <- gl(4, 4, 16)
col <- gl(4, 1, 16)
symm4by4 <- Symm(row, col)
matrix(symm4by4, 4, 4)
```

---

termPredictors *Extract Term Contributions to Predictor*

Description

termPredictors is a generic function which extracts the contribution of each term to the predictor from a fitted model object.

Usage

```
termPredictors(object, ...)
```

Arguments

object	a fitted model object.
...	additional arguments for method functions.

Details

The default method assumes that the predictor is linear and calculates the contribution of each term from the model matrix and fitted coefficients. A method is also available for gnm objects.

Value

A matrix with the additive components of the predictor in labelled columns.

Author(s)

Heather Turner

See Also

gnm

Examples

```
## Linear model
G <- gl(4, 6)
x <- 1:24
y <- rnorm(24, 0, 1)
lmGx <- lm(y ~ G + x)
contrib <- termPredictors(lmGx)
contrib
all.equal(as.numeric(rowSums(contrib)), as.numeric(lmGx$fitted)) #TRUE

## Generalized linear model
y <- cbind(rbinom(24, 10, 0.5), rep(10, 24))
glmGx <- glm(y ~ G + x, family = binomial)
contrib <- termPredictors(glmGx)
contrib
all.equal(as.numeric(rowSums(contrib)),
          as.numeric(glmGx$linear.predictors)) #TRUE

## Generalized nonlinear model
A <- gl(4, 6)
B <- gl(6, 1, 24)
y <- cbind(rbinom(24, 10, 0.5), rep(10, 24))
set.seed(1)
gnmAB <- gnm(y ~ A + B + Mult(A, B), family = binomial)
contrib <- termPredictors(gnmAB)
contrib
all.equal(as.numeric(rowSums(contrib)),
          as.numeric(gnmAB$predictors)) #TRUE
```

Topo *Topological Interaction of Factors*

Description

Given two or more factors Topo creates an interaction factor as specified by an array of levels, which may be arbitrarily structured.

Usage

```
Topo(..., spec = NULL)
```

Arguments

...	two or more factors
spec	an array of levels, with dimensions corresponding to the number of levels of each factor in the interaction

Value

A factor of levels extracted from the levels array given in spec, using the given factors as index variables.

Author(s)

David Firth

References

Erikson, R., GoldThorpe, J. H. and Portocarero, L. (1982) Social Fluidity in Industrial Nations: England, France and Sweden. *Brit. J. Sociol.* **33(1)**, 1-34.

Xie, Y. (1992) The Log-multiplicative Layer Effect Model for Comparing Mobility Tables. *Am. Sociol. Rev.* **57(3)**, 380-395.

See Also

Symm and Diag for special cases

Examples

```
set.seed(1)
data(erikson)

### Collapse to 7 by 7 table as in Erikson (1982)

erikson <- as.data.frame(erikson)
lvl <- levels(erikson$origin)
levels(erikson$origin) <- levels(erikson$destination) <-
    c(rep(paste(lvl[1:2], collapse = " + "), 2), lvl[3],
      rep(paste(lvl[4:5], collapse = " + "), 2), lvl[6:9])
erikson <- xtabs(Freq ~ origin + destination + country, data = erikson)

### Create array of interaction levels as in Table 2 of Xie (1992)

levelMatrix <- matrix(c(2, 3, 4, 6, 5, 6, 6,
                        3, 3, 4, 6, 4, 5, 6,
                        4, 4, 2, 5, 5, 5, 5,
                        6, 6, 5, 1, 6, 5, 2,
                        4, 4, 5, 6, 3, 4, 5,
                        5, 4, 5, 5, 3, 3, 5,
                        6, 6, 5, 3, 5, 4, 1), 7, 7, byrow = TRUE)

### Fit the levels models given in Table 3 of Xie (1992)

## Null association between origin and destination
nullModel <- gnm(Freq ~ country:origin + country:destination,
                 family = poisson, data = erikson)

## Interaction specified by levelMatrix, common to all countries
commonTopo <- update(nullModel, ~ . +
```

```
                    Topo(origin, destination, spec = levelMatrix))

## Interaction specified by levelMatrix, different multiplier for
## each country
multTopo <- update(nullModel, ~ . +
                   Mult(Exp(country),
                        Topo(origin, destination, spec = levelMatrix)))

## Interaction specified by levelMatrix, different effects for
## each country
separateTopo <- update(nullModel, ~ . +
                       country:Topo(origin, destination,
                                    spec = levelMatrix))
```

---

vcov.gnm *Variance-covariance Matrix for Parameters in a Generalized Nonlinear Model*

Description

This method extracts or computes a variance-covariance matrix for use in approximate inference on estimable parameter combinations in a generalized nonlinear model.

Usage

```
## S3 method for class 'gnm'
vcov(object, dispersion = NULL, with.eliminate = FALSE, ...)
```

Arguments

object	a model object of class gnm.
dispersion	the dispersion parameter for the fitting family. By default it is obtained from object.
with.eliminate	logical; should parts of the variance-covariance matrix corresponding to eliminated coefficients be computed?
...	as for vcov.

Details

The resultant matrix does not itself necessarily contain variances and covariances, since gnm typically works with over-parameterized model representations in which parameters are not all identified. Rather, the resultant matrix is to be used as the kernel of quadratic forms which are the variances or covariances for estimable parameter combinations.

The matrix values are scaled by dispersion. If the dispersion is not specified, it is taken as 1 for the binomial and Poisson families, and otherwise estimated by the residual Chi-squared statistic divided by the residual degrees of freedom. The dispersion used is returned as an attribute of the matrix.

The dimensions of the matrix correspond to the non-eliminated coefficients of the "gnm" object. If use.eliminate = TRUE then setting can sometimes give appreciable speed gains; see gnm for details of the eliminate mechanism. The use.eliminate argument is currently ignored if the model has full rank.

Value

A matrix with number of rows/columns equal to length(coef(object)). If there are eliminated coefficients and use.eliminate = TRUE, the matrix will have the following attributes:

covElim	a matrix of covariances between the eliminated and non-eliminated parameters.
varElim	a vector of variances corresponding to the eliminated parameters.

Note

The gnm class includes generalized linear models, and it should be noted that the behaviour of vcov.gnm differs from that of vcov.glm whenever any(is.na(coef(object))) is TRUE. Whereas vcov.glm drops all rows and columns which correspond to NA values in coef(object), vcov.gnm keeps those columns (which are full of zeros, since the NA represents a parameter which is fixed either by use of the constrain argument to gnm or by a convention to handle linear aliasing).

Author(s)

David Firth

References

Turner, H and Firth, D (2005). Generalized nonlinear models in R: An overview of the gnm package. At http://cran.r-project.org

See Also

getContrasts, se

Examples

```
set.seed(1)
data(yaish)
## Fit the "UNIDIFF" mobility model across education levels
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
               Mult(Exp(educ), orig:dest), family = poisson,
               data = yaish, subset = (dest != 7))
## Examine the education multipliers (differences on the log scale):
ind <- pickCoef(unidiff, "[.]educ")
educMultipliers <- getContrasts(unidiff, rev(ind))
## Now get the same standard errors using a suitable set of
## quadratic forms, by calling vcov() directly:
cmat <- contr.sum(ind)
sterrs <- sqrt(diag(t(cmat)
                    %*% vcov(unidiff)[ind, ind]
                    %*% cmat))
all(sterrs == (educMultipliers$SE)[-1]) ## TRUE
```

voting *Data on Social Mobility and the Labour Vote*

Description

Voting data from the 1987 British general election, cross-classified by the class of the head of household and the class of their father.

Usage

```
data(voting)
```

Format

A data frame with 25 observations on the following 4 variables.

`percentage` the percentage of the cell voting Labour.

`total` the cell count.

`origin` a factor describing the father's class with levels `1:5`.

`destination` a factor describing the head of household's class with levels `1:5`.

Source

Clifford, P. and Heath, A. F. (1993) The Political Consequences of Social Mobility. *J. Roy. Stat. Soc. A*, **156(1)**, 51-61.

Examples

```
### Examples from Clifford and Heath paper
### (Results differ slightly - possible transcription error in
### published data?)
set.seed(1)
data(voting)
## reconstruct counts voting Labour/non-Labour
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)

## fit diagonal reference model with constant weights
classMobility <- gnm(yvar ~ -1 + Dref(origin, destination),
                     family = binomial, data = voting)
DrefWeights(classMobility)

## create factors indicating movement in and out of salariat (class 1)
upward <- with(voting, origin != 1 & destination == 1)
downward <- with(voting, origin == 1 & destination != 1)

## fit separate weights for the "socially mobile" groups
socialMobility <- gnm(yvar ~ -1 + Dref(origin, destination,
```

```
                                        delta = ~ 1 + downward + upward),
                      family = binomial, data = voting)
DrefWeights(socialMobility)

## fit separate weights for downwardly mobile groups only
downwardMobility <- gnm(yvar ~ -1 + Dref(origin, destination,
                                         delta = ~ 1 + downward),
                        family = binomial, data = voting)
DrefWeights(downwardMobility)
```

---

wedderburn *Wedderburn Quasi-likelihood Family*

Description

Creates a family object for use with glm, gnm, etc., for the variance function $[\mu(1-\mu)]^2$ introduced by Wedderburn (1974) for response values in [0,1].

Usage

```
wedderburn(link = "logit")
```

Arguments

link	The name of a link function. Allowed are "logit", "probit" and "cloglog".

Value

An object of class family.

Note

The reported deviance involves an arbitrary constant (see McCullagh and Nelder, 1989, p330); for estimating dispersion, use the Pearson chi-squared statistic instead.

Author(s)

David Firth

References

Gabriel, K R (1998). Generalised bilinear regression. *Biometrika* **85**, 689–700.

McCullagh, P and Nelder, J A (1989). *Generalized Linear Models* (2nd ed). Chapman and Hall.

Wedderburn, R W M (1974). Quasilikelihood functions, generalized linear models and the Gauss-Newton method. *Biometrika* **61**, 439–47.

See Also

glm, gnm, family

Examples

```
set.seed(1)
data(barley)  ##  data from Wedderburn (1974), see ?barley

###  Fit Wedderburn's logit model with variance proportional to the
###  square of mu(1-mu)
logitModel <- glm(y ~ site + variety, family = wedderburn, data = barley)
fit <- fitted(logitModel)
print(sum((barley$y - fit)^2 / (fit * (1-fit))^2))
##  Agrees with the chi-squared value reported in McCullagh and Nelder
##  (1989, p331), which differs slightly from Wedderburn's reported value.

###  Fit the biplot model as in Gabriel (1998, p694)
biplotModel <- gnm(y ~ -1 + instances(Mult(site, variety), 2),
                   family = wedderburn, data = barley)
barleySVD <- svd(matrix(biplotModel$predictors, 10, 9))
A <- sweep(barleySVD$v, 2, sqrt(barleySVD$d), "*")[, 1:2]
B <- sweep(barleySVD$u, 2, sqrt(barleySVD$d), "*")[, 1:2]
##  These are essentially A and B as in Gabriel (1998, p694), from which
##  the biplot is made by
plot(rbind(A, B), pch = c(LETTERS[1:9], as.character(1:9), "X"))

###  Fit the double-additive model as in Gabriel (1998, p697)
variety.binary <- factor(match(barley$variety, c(2,3,6), nomatch = 0) > 0,
                         labels = c("Rest", "2,3,6"))
doubleAdditive <- gnm(y ~ variety + Mult(site, variety.binary),
                      family = wedderburn, data = barley)
```

`wheat` *Wheat Yields from Mexican Field Trials*

Description

Data from a 10-year experiment at the CIMMYT experimental station located in the Yaqui Valley near Ciudad Obregon, Sonora, Mexico — factorial design using 24 treatments in all. In each of the 10 years the experiment was arranged in a randomized complete block design with three replicates.

Usage

```
data(wheat)
```

Format

A data frame with 240 observations on the following 33 variables.

yield numeric, mean yield in kg/ha for 3 replicates

year a factor with levels `1988:1997`

tillage a factor with levels `T t`

summerCrop a factor with levels `S s`

manure a factor with levels `M m`

N a factor with levels `0 N n`

MTD numeric, mean max temp sheltered (deg C) in December

MTJ same for January

MTF same for February

MTM same for March

MTA same for April

mTD numeric, mean min temp sheltered (deg C) in December

mTJ same for January

mTF same for February

mTM same for March

mTA same for April

mTUD numeric, mean min temp unsheltered (deg C)in December

mTUJ same for January

mTUF same for February

mTUM same for March

mTUA same for April

PRD numeric, total precipitation (mm) in December

PRJ same for January

PRF same for February

PRM same for March

SHD numeric, mean sun hours in December

SHJ same for January

SHF same for February

EVD numeric, total evaporation (mm) in December

EVJ same for January

EVF same for February

EVM same for March

EVA same for April

Source

Tables A1 and A3 of Vargas, M, Crossa, J, van Eeuwijk, F, Sayre, K D and Reynolds, M P (2001). Interpreting treatment by environment interaction in agronomy trials. *Agronomy Journal* **93**, 949–960.

Examples

```
set.seed(1)
data(wheat)

##  Scale yields to reproduce analyses reported in Vargas et al (2001)
yield.scaled <- wheat$yield * sqrt(3/1000)

##  Reproduce (up to error caused by rounding) Table 1 of Vargas et al (2001)
aov(yield.scaled ~ year*tillage*summerCrop*manure*N, data = wheat)
treatment <- interaction(wheat$tillage, wheat$summerCrop, wheat$manure,
                         wheat$N, sep = "")
mainEffects <- lm(yield.scaled ~ year + treatment, data = wheat)
svdStart <- residSVD(mainEffects, year, treatment, 3)
bilinear1 <- update(asGnm(mainEffects), . ~ . +
                    Mult(year, treatment),
                    start = c(coef(mainEffects), svdStart[,1]))
bilinear2 <- update(bilinear1, . ~ . +
                    Mult(year, treatment, inst = 2),
                    start = c(coef(bilinear1), svdStart[,2]))
bilinear3 <- update(bilinear2, . ~ . +
                    Mult(year, treatment, inst = 3),
                    start = c(coef(bilinear2), svdStart[,3]))
anova(mainEffects, bilinear1, bilinear2, bilinear3)

##  Examine the extent to which, say, mTF explains the first bilinear term
bilinear1mTF <- gnm(yield.scaled ~ year + treatment + Mult(1 + mTF, treatment),
                    family = gaussian, data = wheat)
anova(mainEffects, bilinear1mTF, bilinear1)

##  How to get the standard SVD representation of an AMMI-n model
##
##  We'll work with the AMMI-2 model, which here is called "bilinear2"
##
##  First, extract the contributions of the 5 terms in the model:
##
wheat.terms <- termPredictors(bilinear2)
##
##  That's a matrix, whose 4th and 5th columns are the interaction terms
##
##  Combine those two interaction terms, to get the total estimated
##  interaction effect:
##
wheat.interaction <- wheat.terms[, 4] + wheat.terms[, 5]
##
##  That's a vector, so we need to re-shape it as a 24 by 10 matrix
##  ready for calculating the SVD:
##
wheat.interaction <- matrix(wheat.interaction, 24, 10)
##
##  Now we can compute the SVD:
##
wheat.interaction.SVD <- svd(wheat.interaction)
```

```
##
##  Only the first two singular values are nonzero, as expected
##  (since this is an AMMI-2 model, the interaction has rank 2)
##
##  So the result object can be simplified by re-calculating the SVD with
##  just two dimensions:
##
wheat.interaction.SVD <- svd(wheat.interaction, nu = 2, nv = 2)
```

`yaish` *Class Mobility by Level of Education in Israel*

Description

A 3-way contingency table of father/son pairs, classified by father's social class (`orig`), son's social class (`dest`) and son's education level (`educ`).

Usage

```
data(yaish)
```

Format

A table of counts, with classifying factors `educ` (levels `1:5`), `orig` (levels `1:7`) and `dest` (levels `1:7`).

Author(s)

David Firth

Source

Originally in Yaish (1998), see also Yaish (2004, p316).

References

Yaish, M (1998). Opportunities, Little Change. Class Mobility in Israeli Society: 1974-1991. D.Phil. Thesis, Nuffield College, University of Oxford.

Yaish, M (2004). *Class Mobility Trends in Israeli Society, 1974-1991.* Lewiston: Edwin Mellen Press.

Examples

```
set.seed(1)

data(yaish)

## Fit the "UNIDIFF" mobility model across education levels, leaving out
## the uninformative subtable for dest == 7:
```

```
##
unidiff <- gnm(Freq ~ educ*orig + educ*dest +
                    Mult(Exp(educ), orig:dest), family = poisson,
                    data = yaish, subset = (dest != 7))
## Deviance should be 200.3, 116 d.f.
##
## Look at the multipliers of the orig:dest association:
ofInterest(unidiff) <- pickCoef(unidiff, "[.]educ")
coef(unidiff)
##
## Coefficients of interest:
## Mult(Exp(.), orig:dest).educ1 Mult(Exp(.), orig:dest).educ2
##                     -0.5513258                     -0.7766976
## Mult(Exp(.), orig:dest).educ3 Mult(Exp(.), orig:dest).educ4
##                     -1.2947494                     -1.5902644
## Mult(Exp(.), orig:dest).educ5
##                     -2.8008285
##
## Get standard errors for the contrasts with educ1:
##
getContrasts(unidiff, ofInterest(unidiff))
##                                 estimate        SE    quasiSE
## Mult(Exp(.), orig:dest).educ1  0.0000000 0.0000000 0.09757438
## Mult(Exp(.), orig:dest).educ2 -0.2253718 0.1611874 0.12885847
## Mult(Exp(.), orig:dest).educ3 -0.7434236 0.2335083 0.21182123
## Mult(Exp(.), orig:dest).educ4 -1.0389386 0.3434256 0.32609380
## Mult(Exp(.), orig:dest).educ5 -2.2495026 0.9453764 0.93560643
##                                 quasiVar
## Mult(Exp(.), orig:dest).educ1 0.00952076
## Mult(Exp(.), orig:dest).educ2 0.01660450
## Mult(Exp(.), orig:dest).educ3 0.04486823
## Mult(Exp(.), orig:dest).educ4 0.10633716
## Mult(Exp(.), orig:dest).educ5 0.87535940
##
## Table of model residuals:
##
residuals(unidiff)
```

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