Generalized nonlinear models in R: an overview of the *gnm* package

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Contents

1 Introduction **2**

2 Generalized Linear Models **2**
2.1 Preamble . . . 2
2.2 `Diag` and `Symm` . . . 2
2.3 `Topo` . . . 3
2.4 The `wedderburn` family . . . 4
2.5 `termPredictors` . . . 5

3 Nonlinear Terms **5**
3.1 Multiplicative Interaction Terms using `Mult` . . . 6
3.2 Other Nonlinear Terms using `Nonlin` . . . 6
3.2.1 `MultHomog` . . . 6
3.2.2 `Dref` . . . 7
3.2.3 Custom Plug-in Functions . . . 7

4 Controlling the Fitting Procedure **9**
4.1 Basic control parameters . . . 9
4.2 Using *start* . . . 9
4.3 Using *constrain* . . . 10
4.4 Using *eliminate* . . . 12

5 Methods and Accessor functions **14**
5.1 Methods . . . 14
5.2 `checkEstimable` . . . 15
5.3 `getContrasts`, `se` . . . 16
5.4 `residSVD` . . . 17

6 Examples **18**
6.1 Row-column Association Models . . . 18
6.1.1 RC(1) model . . . 18
6.1.2 RC(2) model . . . 20
6.1.3 Homogeneous effects . . . 21
6.2 Diagonal Reference Models . . . 22
6.3 Uniform Difference (UNIDIFF) Models . . . 30
6.4 Generalized Additive Main Effects and Multiplicative Interaction (GAMMI) Models . . . 31
6.5 Biplot Models . . . 32
6.6 Stereotype Model . . . 36
6.7 Exponential and sum-of-exponentials models for decay curves . . . 40
6.7.1 Example: single exponential decay term . . . 40
6.7.2 Example: sum of two exponentials . . . 41

A User-level Functions **44**

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1 Introduction

The *gnm* package provides facilities for fitting *generalized nonlinear models*, i.e., regression models in which the link-transformed mean is described as a sum of predictor terms, some of which may be non-linear in the unknown parameters. Linear and generalized linear models, as handled by the `lm` and `glm` functions in R, are included in the class of generalized nonlinear models, as the special case in which there is no nonlinear term.

This document gives an extended overview of the *gnm* package, with some examples of applications. The primary package documentation in the form of standard help pages, as viewed in R by, for example, `?gnm` or `help(gnm)`, is supplemented rather than replaced by the present document.

We begin below with a preliminary note (Section 2) on some ways in which the *gnm* package extends R's facilities for specifying, fitting and working with generalized *linear* models. Then (Section 3 onwards) the facilities for nonlinear terms are introduced, explained and exemplified.

The *gnm* package is installed in the standard way for CRAN packages, for example by using `install.packages`. Once installed, the package is loaded into an R session by

```
> library(gnm)
```

2 Generalized Linear Models

2.1 Preamble

Central to the facilities provided by the *gnm* package is the model-fitting function `gnm`, which interprets a model formula and returns a model object. The user interface of `gnm` is patterned after `glm` (which is included in R's standard *stats* package), and indeed `gnm` can be viewed as a replacement for `glm` for specifying and fitting generalized linear models. In general there is no reason to prefer `gnm` to `glm` for fitting generalized linear models, except perhaps when the model involves a large number of incidental parameters which are treatable by `gnm`'s *eliminate* mechanism (see Section 4.4).

While the main purpose of the *gnm* package is to extend the class of models to include nonlinear terms, some of the new functions and methods can be used also with the familiar `lm` and `glm` model-fitting functions. These are: three new data-manipulation functions `Diag`, `Symm` and `Topo`, for setting up structured interactions between factors; a new *family* function, `wedderburn`, for modelling a continuous response variable in [0, 1] with the variance function $V(\mu) = \mu^2(1-\mu)^2$ as in Wedderburn (1974); and a new generic function `termPredictors` which extracts the contribution of each term to the predictor from a fitted model object. These functions are briefly introduced here, before we move on to the main purpose of the package, nonlinear models, in Section 3.

2.2 `Diag` and `Symm`

When dealing with *homologous* factors, that is, categorical variables whose levels are the same, statistical models often involve structured interaction terms which exploit the inherent symmetry. The functions `Diag` and `Symm` facilitate the specification of such structured interactions.

As a simple example of their use, consider the log-linear models of *quasi-independence*, *quasi-symmetry* and *symmetry* for a square contingency table. Agresti (2002), Section 10.4, gives data on migration between regions of the USA between 1980 and 1985:

```
> count <- c(11607, 100, 366, 124, 87, 13677, 515, 302, 172, 225,
+     17819, 270, 63, 176, 286, 10192)
> region <- c("NE", "MW", "S", "W")
> row <- gl(4, 4, labels = region)
> col <- gl(4, 1, length = 16, labels = region)
```

The comparison of models reported by Agresti can be achieved as follows:

```
> independence <- glm(count ~ row + col, family = poisson)
> quasi.indep <- glm(count ~ row + col + Diag(row, col), family = poisson)
> symmetry <- glm(count ~ Symm(row, col), family = poisson)
> quasi.symm <- glm(count ~ row + col + Symm(row, col), family = poisson)
> comparison1 <- anova(independence, quasi.indep, quasi.symm)
> print(comparison1, digits = 7)
```

```
Analysis of Deviance Table

Model 1: count ~ row + col
Model 2: count ~ row + col + Diag(row, col)
Model 3: count ~ row + col + Symm(row, col)
  Resid. Df Resid. Dev Df  Deviance
1         9  125923.29
2         5      69.51  4 125853.78
3         3       2.99  2     66.52

> comparison2 <- anova(symmetry, quasi.symm)
> print(comparison2)

Analysis of Deviance Table

Model 1: count ~ Symm(row, col)
Model 2: count ~ row + col + Symm(row, col)
  Resid. Df Resid. Dev Df Deviance
1         6    243.550
2         3      2.986  3  240.564
```

The Diag and Symm functions also generalize the notions of diagonal and symmetric interaction to cover situations involving more than two homologous factors.

2.3 Topo

More general structured interactions than those provided by Diag and Symm can be specified using the function Topo. (The name of this function is short for 'topological interaction', which is the nomenclature often used in sociology for factor interactions with structure derived from subject-matter theory.)

The Topo function operates on any number (k, say) of input factors, and requires an argument named *spec* which must be an array of dimension $L_1 \times \ldots \times L_k$, where L_i is the number of levels for the ith factor. The *spec* argument specifies the interaction level corresponding to every possible combination of the input factors, and the result is a new factor representing the specified interaction.

As an example, consider fitting the 'log-multiplicative layer effects' models described in Xie (1992). The data are 7 by 7 versions of social mobility tables from Erikson et al. (1982):

```
> data(erikson)
> 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)
```

From sociological theory — for which see Erikson et al. (1982) or Xie (1992) — the log-linear interaction between origin and destination is assumed to have a particular structure:

```
> 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)
```

The models of table 3 of Xie (1992) can now be fitted as follows:

```
> ## Null association between origin and destination
> nullModel <- gnm(Freq ~ country:origin + country:destination,
+                  family = poisson, data = erikson)
Running main iterations.
Done
> ## Interaction specified by levelMatrix, common to all countries
> commonTopo <- update(nullModel, ~ . +
+                      Topo(origin, destination, spec = levelMatrix))
Running main iterations.
Done
> ## Interaction specified by levelMatrix, different multiplier for each country
> multTopo <- update(nullModel, ~ . + Mult(country, Topo(origin, destination,
+                                       spec = levelMatrix)))
Running start-up iterations..
Running main iterations.......
Done
> ## Interaction specified by levelMatrix, different effects for each country
> separateTopo <- update(nullModel, ~ . +
+                        country:Topo(origin, destination, spec = levelMatrix))
Running main iterations.
Done
>
> anova(nullModel, commonTopo, multTopo, separateTopo)
Analysis of Deviance Table

Model 1: Freq ~ country:origin + country:destination
Model 2: Freq ~ Topo(origin, destination, spec = levelMatrix) + country:origin +
    country:destination
Model 3: Freq ~ Mult(country, Topo(origin, destination, spec = levelMatrix)) +
    country:origin + country:destination
Model 4: Freq ~ country:origin + country:destination + country:Topo(origin,
    destination, spec = levelMatrix)
  Resid. Df Resid. Dev  Df Deviance
1       108     4860.0
2       103      244.3   5   4615.7
3       101      216.4   2     28.0
4        93      208.5   8      7.9
```

Here we have used `gnm` to fit all of these log-link models; the first, second and fourth are log-linear and could equally well have been fitted using `glm`.

2.4 The wedderburn family

In Wedderburn (1974) it was suggested to represent the mean of a continuous response variable in $[0, 1]$ using a quasi-likelihood model with logit link and the variance function $\mu^2(1-\mu)^2$. This is not one of the variance functions made available as standard in R's `quasi` family. The `wedderburn` family provides it. As an example, Wedderburn's analysis of data on leaf blotch on barley can be reproduced as follows:

```
> data(barley)
> logitModel <- glm(y ~ site + variety, family = wedderburn, data = barley)
> fit <- fitted(logitModel)
> print(sum((barley$y - fit)^2/(fit * (1 - fit))^2))

[1] 71.17401
```

This agrees with the chi-squared value reported on page 331 of McCullagh and Nelder (1989), which differs slightly from Wedderburn's own reported value.

2.5 termPredictors

The generic function `termPredictors` extracts a term-by-term decomposition of the predictor function in a linear, generalized linear or generalized nonlinear model.

As an illustrative example, we can decompose the linear predictor in the above quasi-symmetry model as follows:

```
> print(temp <- termPredictors(quasi.symm))

   (Intercept)       row      col Symm(row, col)
1   -0.2641848 0.0000000 0.000000     9.62354843
2   -0.2641848 0.0000000 4.918310    -0.09198126
3   -0.2641848 0.0000000 1.539852     4.63901793
4   -0.2641848 0.0000000 5.082641     0.00000000
5   -0.2641848 4.8693457 0.000000    -0.09198126
6   -0.2641848 4.8693457 4.918310     0.00000000
7   -0.2641848 4.8693457 1.539852     0.07295506
8   -0.2641848 4.8693457 5.082641    -3.94766844
9   -0.2641848 0.7465235 0.000000     4.63901793
10  -0.2641848 0.7465235 4.918310     0.07295506
11  -0.2641848 0.7465235 1.539852     7.76583039
12  -0.2641848 0.7465235 5.082641     0.00000000
13  -0.2641848 4.4109017 0.000000     0.00000000
14  -0.2641848 4.4109017 4.918310    -3.94766844
15  -0.2641848 4.4109017 1.539852     0.00000000
16  -0.2641848 4.4109017 5.082641     0.00000000

> rowSums(temp) - quasi.symm$linear.predictors

 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16
 0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
```

Such a decomposition might be useful, for example, in assessing the relative contributions of different terms or groups of terms.

3 Nonlinear Terms

The main purpose of the *gnm* package is to provide a flexible framework for the specification and estimation of generalized models with nonlinear terms. Multiplicative interaction terms can be estimated using the in-built capability of the `gnm` function and are specified in the model formula using the symbolic function `Mult`. Other nonlinear terms can be estimated using plug-in functions for `gnm` and are specified using `Nonlin`.

There are two plug-in functions currently made available in the *gnm* package: `MultHomog` for fitting multiplicative interaction terms with homogeneous effects and `Dref` for fitting diagonal reference terms. Users of *gnm* can define their own custom plug-in functions to specify other types of nonlinear term.

3.1 Multiplicative Interaction Terms using `Mult`

Multiplicative interaction terms can be included in the formula argument to `gnm` by using the symbolic wrapper function `Mult`. Constituent multipliers[1] in the interaction are passed as unspecified arguments to `Mult` and are expressed by symbolic linear formulae. An intercept is automatically added to each constituent multiplier unless otherwise specified. For example, to fit the row-column association model

$$\log \mu_{rc} = \alpha_r + \beta_c + \gamma_r \delta_c,$$

also known as the Goodman RC model (Goodman, 1979), the *formula* argument of `gnm` would be

```
mu ~ R + C + Mult(-1 + R, -1 + C)
```

where `R` and `C` are row and column factors respectively.

`Mult` has one specified argument *multiplicity*, which is `1` by default. This argument determines the number of times that the specified multiplicative structure appears in the model. For example,

```
mu ~ R + C + Mult(-1 + R, -1 + C, multiplicity = 2)
```

would give the RC(2) model (Goodman, 1979)

$$\log \mu_{rc} = \alpha_r + \beta_c + \gamma_r \delta_c + \theta_r \phi_c.$$

In some contexts, it may be desirable to constrain one or more of the constituent multipliers so that it is always nonnegative. This may be achieved by specifying the multiplier as an exponential, as in the following 'uniform difference' model (Xie, 1992; Erikson and Goldthorpe, 1992)

$$\log \mu_{rct} = \alpha_{rt} + \beta_{ct} + e^{\gamma_t} \delta_{rc}.$$

Exponentiated constituent multipliers are specified in *gnm* models using the symbolic function `Exp`; for example, the uniform difference model above would be specified by the formula

```
mu ~ R:T + C:T + Mult(Exp(-1 + T), R:C)
```

3.2 Other Nonlinear Terms using `Nonlin`

Nonlinear terms which can not be specified using `Mult` may be specified using `Nonlin`. This symbolic function indicates a term which requires a plug-in function to estimate the associated parameters. `Nonlin` takes a single argument, which is a call to the relevant plug-in function.

For example, in the formula

```
mu ~ x + A + B + Nonlin(PlugInFunction(A, B, arg1 = x, arg2 = C))
```

the call to `Nonlin` is used to specify a term that requires the plug-in function `PlugInFunction`.

The two plug-in functions already included in the *gnm* package are described below, followed by a guide to writing custom plug-in functions.

3.2.1 `MultHomog`

The `MultHomog` function provides the tools required to fit multiplicative interaction terms with one component 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. The arguments of `MultHomog` are the factors in the interaction, which are assumed to be objects of class *factor*.

As an example, consider the following association model with homogeneous row-column effects:

$$\log \mu_{rc} = \alpha_r + \beta_c + \theta_r I(r = c) + \gamma_r \gamma_c.$$

To fit this model, with response variable named `mu`, the formula argument to `gnm` would be

```
mu ~ R + C + Diag(R, C) + Nonlin(MultHomog(R, C))
```

If the factors passed to `MultHomog` do not have exactly the same levels, a common set of levels is obtained by taking the union of the levels of each factor, sorted into increasing order.

[1] A note on terminology: the rather cumbersome phrase 'constituent multiplier', or sometimes the abbreviation 'multiplier', will be used throughout this document in preference to the more elegant and standard mathematical term 'factor'. This will avoid possible confusion with the completely different meaning of the word 'factor' — that is, a categorical variable — in R.

3.2.2 Dref

`Dref` is a plug-in function to fit diagonal reference terms involving two or more factors with a common set of levels. A diagonal reference term comprises an additive component for each factor. The component for factor f, is given by

$$w_f \gamma_l$$

for an observation with level l of factor f, where w_f is the weight for factor f and γ_l is the "diagonal effect" for level l.

The weights are constrained to be nonnegative and to sum to one so that a "diagonal effect", say γ_l, is the value of the diagonal reference term for data points with level l across the factors. `Dref` constrains the weights by defining them as

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

and estimating the δ_f.

Factors defining the diagonal reference term are passed as unspecified arguments to `Dref`. For example, the following diagonal reference model for a contingency table classified by the row factor `R` and the column factor `C`,

$$\mu_{rc} = \frac{e^{\delta_1}}{e^{\delta_1} + e^{\delta_2}}\gamma_r + \frac{e^{\delta_2}}{e^{\delta_1} + e^{\delta_2}}\gamma_c,$$

would be specified by the formula

```
mu ~ -1 + Nonlin(Dref(R, C))
```

`Dref` has one specified argument, *formula*, which is a symbolic description of the dependence of δ_f on any covariates. For example, the formula

```
mu ~ -1 + x + Nonlin(Dref(R, C, formula = ~ 1 + x))
```

specifies the following diagonal reference model

$$\mu_{rc} = \beta_X x + \frac{e^{\xi_1+\beta_1 x}}{e^{\xi_1+\beta_1 x} + e^{\xi_2+\beta_2 x}}\gamma_r + \frac{e^{\xi_2+\beta_2 x}}{e^{\xi_1+\beta_x} + e^{\xi_2+\beta_2 x}}\gamma_c.$$

The default value of *formula* is `~1`, so that constant weights are estimated. The coefficients returned by `gnm` are those that are directly estimated, i.e. the δ_f or the ξ_f and β_f, rather than the implied weights w_f.

3.2.3 Custom Plug-in Functions

Custom plug-in functions may be written to enable `gnm` to fit nonlinear terms that can not be specified by `Mult` or through existing plug-in functions provided by the *gnm* package.

There are no constraints on the arguments that a plug-in function may take. However it is important that `Nonlin`, when given a call to the plug-in function, can determine the variables that are in the term, so that these variables can be added to the model frame. By default, expressions passed to unspecified arguments of the plug-in function are assumed to represent the variables in the term.

If the default action of `Nonlin` will not capture the required variables, a companion function must exist (in the environment of the plug-in function), which takes the same arguments as the plug-in function and returns deparsed expressions representing the necessary variables. The name of this function must be the name of the plug-in function suffixed with "Variables". For example, the (non-visible) companion function for `Dref` is defined as

```
DrefVariables <- function(..., formula = ~ 1) {
    as.character(c(match.call(expand.dots = FALSE)[[2]], formula[[2]]))
}
```

returning the expressions passed to unspecified arguments and the right-hand side of the formula passed to *formula*, as character strings. For instance

```
> gnm:::DrefVariables(A, B, formula = ~1 + C)

[1] "A"     "B"     "1 + C"
```

from which Nonlin will know that A, B and C need to be added to the model frame.

The call to the plug-in function is evaluated in the environment of the model frame and in the enclosing environment of the parent frame of the call to gnm. This should ensure that variables passed directly to the plug-in function can be found. However, to evaluate variables within the plug-in function, it may be necessary to access the model frame, which can be obtained using the function getModelFrame.

For example, the factors in a Dref term are passed directly to unspecified arguments, so the dummy variables for these factors can be found as follows:

```
# get design matrices for Dref factors
designList <- lapply(list(...), class.ind)
```

But any covariates on which the weights depend are only represented symbolically in the *formula* argument, so the design matrix for these variables must be found in the context of the model frame:

```
## get design matrix for local structure
gnmData <- getModelFrame()
local <- model.matrix(formula, data = gnmData)
```

The plug-in function should return a list with at least the following three components:

labels a character vector of labels for the parameters (to which gnm will prefix the call to the plug-in function).

predictor a function which takes a vector of parameter estimates and returns either a vector of fitted values or a matrix whose columns are additive components of the fitted values.

localDesignFunction a function which takes the specified arguments *coef* (a vector of parameter estimates) and *predictor* (the result of the predictor function), and returns the local design matrix. If the plug-in function does not return a start component (see below), the localDesignFunction must also take the argument *ind*, which specifies the index of a column to be returned instead of the full matrix.

and optionally one further component,

start a vector of default starting values for the parameters. NA may be used to indicate parameters which may be treated as linear for the purpose of finding starting values, given the non-NA values. See Section 4.2 for details of how these starting values will be used if provided and the starting procedure for nonlinear parameters that will be used otherwise.

As an example of a start component, Dref returns

```
c(runif(nLocal) - 0.5, rep(0.5, nGlobal))
```

where nLocal is the number of weight parameters (parameters which are "local" to a specific factor) and nGlobal is the number of diagonal effects ("global" level effects across factors). The randomness in the starting values for the weight parameters ensures that arbitrariness of the final parameterization is emphasised.

The MultHomog function provides a simple example of a predictor component:

```
predictor <- function(coef) {
    do.call("pprod", lapply(designList, "%*%", coef))
}
```

which computes the product of the vectors found by multiplying the design matrix for each factor in the interaction (held in designList) by the homogeneous coefficients (in coef). This function takes advantage of *lexical scoping*: designList is an object defined in MultHomog, which predictor is able to find because predictor is also defined in MultHomog and hence MultHomog is the enclosing environment of predictor.

The localDesignFunction created by MultHomog is slightly more complicated:

```
localDesignFunction <- function(coef, ind = NULL, ...) {
    X <- 0
    vList <- lapply(designList, "%*%", coef)
    for (i in seq(designList)) {
        if (is.null(ind))
```

```
            X <- X + designList[[*]] * drop(do.call("pprod", vList[-i]))
        else
            X <- X + designList[[]][, ind] *
                drop(do.call("pprod", vList[-i]))
    }
    X
}
```

Since the result of the predictor function is not needed here, the local design function does not have the specified argument *predictor*, but allows such an argument to be passed to the function by the use of the special argument '`...`'. Since `MultHomog` does not return a `start` component, the local design function can optionally return a single column of the local design matrix as specified by *ind*. This functionality is required by the default starting procedure for nonlinear parameters.

4 Controlling the Fitting Procedure

The `gnm` function has a number of arguments which affect the way a model will be fitted. Basic control parameters can be set using the arguments *tolerance*, *iterStart* and *iterMax*. Starting values for the parameter estimates can be set by *start* and parameters can be constrained to zero by specifying a *constrain* argument. Parameters of a stratification factor can be handled more efficiently by specifying the factor in an *eliminate* argument. These options are described in more detail below.

4.1 Basic control parameters

The arguments *iterStart* and *iterMax* control respectively the number of starting iterations (where applicable) and the number of main iterations used by the fitting algorithm. The progress of these iterations can be followed by setting either *verbose* or *trace* to `TRUE`. If *verbose* is `TRUE` and *trace* is `FALSE`, which is the default setting, progress is indicated by printing the character "." at the beginning of each iteration. If *trace* is `TRUE`, the deviance is printed at the beginning of each iteration (over-riding the printing of "." if necessary). Whenever *verbose* is `TRUE`, additional messages indicate each stage of the fitting process and diagnose any errors that cause that cause the algorithm to restart.

The fitting algorithm will terminate before the number of main iterations has reached *iterMax* if the convergence criteria have been met, with tolerance specified by *tolerance*. 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, the algorithm is deemed to have converged.

4.2 Using *start*

In some contexts, the default starting values may not be appropriate and the algorithm will fail to converge, or perhaps only converge after a large number of iterations. Alternative starting values may be passed on to `gnm` by specifying a *start* argument. This should be a numeric vector of length equal to the number of parameters (or possibly the non-eliminated parameters, see Section 4.4), however missing starting values (`NA`s) are allowed.

If there is no user-specified starting value for a parameter, the default value is used. This feature is particularly useful when adding terms to a model, since the estimates from the original model can be used as starting values, as in this example:

```
model1 <- gnm(mu ~ R + C + Mult(-1 + R, -1 + C))
model2 <- gnm(mu ~ R + C + Mult(-1 + R, -1 + C, multiplicity = 2),
              start = c(coef(model1), rep(NA, 10))
```

The `gnm` call can be made with `method = "coefNames"` to identify the parameters of a model prior to estimation, to assist with the specification of arguments such as *start*.

The starting procedure used by `gnm` is as follows

1. Generate starting values θ_i for all parameters $i = 1, \ldots, p$ from the Uniform(−0.1, 0.1) distribution. Shift these values away from zero as follows
$$\theta_i = \begin{cases} \theta_i - 0.1 & \text{if } \theta_i < 1 \\ \theta_i + 0.1 & \text{otherwise} \end{cases}$$
2. Replace generic starting values with default starting values set by plug-in functions, where applicable.
3. Replace default starting values with any starting values specified by the *start* argument of `gnm`.
4. Compute the `glm` estimate of any parameters that may be treated as linear (i.e. those in linear terms or those with a default starting value of `NA` set by a plug-in function), offsetting the contribution to the predictor of any terms specified by *start* or a plug-in function.
5. Run starting iterations: update one at a time any remaining nonlinear parameters not specified by *start* or a plug-in function, updating *all* parameters that may be treated as linear after each round of updates.

Note that no starting iterations (step 5) will be run if all parameters are linear, or if all nonlinear parameters are specified by *start* or a plug-in function.

4.3 Using *constrain*

By default, `gnm` only imposes identifiability constraints according to the general conventions used by `R` to handle linear aliasing. Therefore models that have any nonlinear terms will be usually be over-parameterized and `gnm` will return a random parameterization for unidentified coefficients.

To illustrate this point, consider the following application of `gnm`, discussed later in Section 6.1:

```
> data(occupationalStatus)
> set.seed(1)
> RChomog1 <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
+     Nonlin(MultHomog(origin, destination)), family = poisson,
+     data = occupationalStatus, verbose = FALSE)
```

Running the analysis again from a different seed

```
> set.seed(2)
> RChomog2 <- eval(RChomog1$call)
```

gives a different representation of the same model:

```
> compareCoef <- cbind(coef(RChomog1), coef(RChomog2))
> colnames(compareCoef) <- c("RChomog1", "RChomog2")
> round(compareCoef, 4)
```

```
                            RChomog1 RChomog2
(Intercept)                  -0.1304   0.1844
origin2                       0.5367   0.5143
origin3                       1.6920   1.6083
origin4                       2.0594   1.9158
origin5                       0.8415   0.6961
origin6                       2.9458   2.7480
origin7                       1.6538   1.4132
origin8                       1.4122   1.1466
destination2                  0.9557   0.9333
destination3                  2.0364   1.9527
destination4                  2.3478   2.2042
destination5                  1.7409   1.5955
destination6                  3.2493   3.0514
destination7                  2.4054   2.1648
destination8                  1.9875   1.7220
```

```
Diag(origin, destination)1         1.5267   1.5267
Diag(origin, destination)2         0.4560   0.4560
Diag(origin, destination)3        -0.0160  -0.0160
Diag(origin, destination)4         0.3892   0.3892
Diag(origin, destination)5         0.7385   0.7385
Diag(origin, destination)6         0.1347   0.1347
Diag(origin, destination)7         0.4576   0.4576
Diag(origin, destination)8         0.3885   0.3885
MultHomog(origin, destination).1  -1.5861  -1.4836
MultHomog(origin, destination).2  -1.3678  -1.2653
MultHomog(origin, destination).3  -0.7697  -0.6671
MultHomog(origin, destination).4  -0.1858  -0.0832
MultHomog(origin, destination).5  -0.1686  -0.0661
MultHomog(origin, destination).6   0.3431   0.4457
MultHomog(origin, destination).7   0.7593   0.8618
MultHomog(origin, destination).8   1.0029   1.1054
```

Even though the linear terms are constrained, the parameter estimates for the main effects of `origin` and `destination` still change, because these terms are aliased with the higher order multiplicative interaction, which is unconstrained.

Standard errors are only meaningful for identified parameters and hence the output of `summary.gnm` will show clearly which coefficients are estimable:

```
> summary(RChomog2)

Call:
gnm(formula = Freq ~ origin + destination + Diag(origin, destination) +
    Nonlin(MultHomog(origin, destination)), family = poisson,
    data = occupationalStatus, verbose = FALSE)


Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6588  -0.4297   0.0000   0.3862   1.7208

Coefficients:
                                Estimate Std. Error z value Pr(>|z|)
(Intercept)                      0.18438         NA      NA       NA
origin2                          0.51428         NA      NA       NA
origin3                          1.60827         NA      NA       NA
origin4                          1.91578         NA      NA       NA
origin5                          0.69610         NA      NA       NA
origin6                          2.74796         NA      NA       NA
origin7                          1.41323         NA      NA       NA
origin8                          1.14664         NA      NA       NA
destination2                     0.93329         NA      NA       NA
destination3                     1.95268         NA      NA       NA
destination4                     2.20421         NA      NA       NA
destination5                     1.59551         NA      NA       NA
destination6                     3.05143         NA      NA       NA
destination7                     2.16483         NA      NA       NA
destination8                     1.72201         NA      NA       NA
Diag(origin, destination)1       1.52667    0.44658   3.419  0.00063
Diag(origin, destination)2       0.45600    0.34595   1.318  0.18747
Diag(origin, destination)3      -0.01598    0.18098  -0.088  0.92965
Diag(origin, destination)4       0.38918    0.12748   3.053  0.00227
Diag(origin, destination)5       0.73852    0.23329   3.166  0.00155
```

```
Diag(origin, destination)6        0.13474    0.07934   1.698  0.08945
Diag(origin, destination)7        0.45764    0.15103   3.030  0.00245
Diag(origin, destination)8        0.38847    0.22172   1.752  0.07976
MultHomog(origin, destination).1 -1.48357         NA      NA       NA
MultHomog(origin, destination).2 -1.26527         NA      NA       NA
MultHomog(origin, destination).3 -0.66711         NA      NA       NA
MultHomog(origin, destination).4 -0.08323         NA      NA       NA
MultHomog(origin, destination).5 -0.06606         NA      NA       NA
MultHomog(origin, destination).6  0.44570         NA      NA       NA
MultHomog(origin, destination).7  0.86184         NA      NA       NA
MultHomog(origin, destination).8  1.10541         NA      NA       NA

(Dispersion parameter for poisson family taken to be 1)

Std. Error is NA where coefficient has been constrained or is unidentified

Residual deviance: 32.561 on 34 degrees of freedom
AIC: 414.9

Number of iterations: 7
```

Additional constraints may be specified through the *constrain* argument of gnm. This argument indicates parameters that are to be constrained to zero in the fitting process. Parameters can be indicated by a logical vector, a numeric vector of indices, a character vector of names or, if `constrain = "pick"` they can be selected through a *Tk* dialog.

In the case above, constraining one level of the homogeneous multiplicative factor is sufficient to make the parameters of the nonlinear term identifiable, and hence all parameters in the model identifiable. For example, setting the last level of the homogeneous multiplicative factor to zero,

```
> multCoef <- coef(RChomog1)[grep("Mult", names(coef(RChomog1)))]
> set.seed(1)
> RChomogConstrained1 <- update(RChomog1, constrain = 31, start = c(rep(NA,
+     23), multCoef - multCoef[8]))
> set.seed(2)
> RChomogConstrained2 <- eval(RChomogConstrained1$call)
> identical(coef(RChomogConstrained1), coef(RChomogConstrained2))

[1] TRUE
```

gives the same results regardless of the random seed set beforehand.

It is not usually so straightforward to constrain all the parameters in a generalized nonlinear model. However, the simple constraints imposed by *constrain* are often sufficient to make particular coefficients of interest identifiable. The functions `checkEstimable` or `getContrasts`, described in Section 5, may be used to check whether particular combinations of parameters are estimable.

4.4 Using *eliminate*

Sometimes a model will include a "stratification" factor which identifies units for which a unit-specific intercept should be estimated. It is often the case that such factors have a large number of levels and though they are required in the model, are not of direct interest in themselves.

The *eliminate* argument of gnm can be used to specify a stratification factor in a model, so that this factor can be handled more efficiently. The factor should be specified by an expression, which is interpreted as the first term in the model formula, replacing any intercept term. So in terms of the structure of the model,

```
gnm(mu ~ A + B + Mult(A, B), eliminate = strata1:strata2)
```

is equivalent to

```
gnm(mu ~ -1 + strata1:strata2 + A + B + Mult(A, B))
```

However specifying a stratification factor through *eliminate* has two advantages over the standard specification. First, the structure of the eliminated factor is exploited so that computational speed is improved — substantially so if the number of eliminated parameters is large. Second, the eliminated parameters are excluded from summaries of the model so that the focus is on the coefficients of interest.

The *eliminate* feature is useful, for example, when multinomial-response models are fitted by using the well known equivalence between multinomial and (conditional) Poisson likelihoods. In such situations the sufficient statistic involves a potentially large number of fixed multinomial row totals, and the corresponding parameters are of no substantive interest. For an application see Section 6.6 below. Here we give an artificial illustration: 500 randomly-generated trinomial responses, and a single predictor variable (whose effect on the data generation is null):

```
> set.seed(1)
> n <- 500
> x <- rep(rnorm(n), rep(3, n))
> counts <- as.vector(rmultinom(n, 10, c(0.7, 0.1, 0.2)))
> rowID <- factor(rep(1:n, rep(3, n)))
> resp <- factor(rep(1:3, n))
```

The logistic model for dependence on `x` can be fitted as a Poisson log-linear model[2], using either `glm` or `gnm`:

```
> system.time(temp.glm <- glm(counts ~ rowID + resp + resp:x, family = poisson))

[1] 10.05  0.17 14.30  0.00  0.00

> system.time(temp.gnm <- gnm(counts ~ resp + resp:x, eliminate = rowID,
+     family = poisson))

Initialising
Running main iterations...
Done
[1] 6.24 0.30 7.75 0.00 0.00

> c(deviance(temp.glm), deviance(temp.gnm))

[1] 1196.341 1196.341
```

Here the use of *eliminate* causes the `gnm` calculations to run more quickly than `glm`. The speed advantage[3] increases with the number of eliminated parameters (here 500). The eliminated parameters do not appear in printed model summaries:

```
> summary(temp.gnm)

Call:

gnm(formula = counts ~ resp + resp:x, eliminate = rowID, family = poisson)


Deviance Residuals:
      Min         1Q     Median         3Q        Max
-2.266771  -0.766713  -0.001797   0.375404   2.854789

Coefficients of interest:
         Estimate Std. Error z value Pr(>|z|)
resp2   -1.964709   0.047995  -40.94   <2e-16
resp3   -1.290139   0.036258  -35.58   <2e-16
resp1:x -0.009198         NA      NA       NA
resp2:x -0.017474         NA      NA       NA
```

[2]For this particular example, of course, it would be more economical to fit the model directly using `multinom` (from the recommended package *nnet*). But fitting as here via the 'Poisson trick' allows the model to be elaborated within the *gnm* framework using `Mult` or `Nonlin` terms.

[3]In fact *eliminate* is, in principle, capable of much bigger time savings than this: its implementation in the current version of *gnm* is really just a proof of concept, and it has not yet been optimized for speed.

```
resp3:x  0.045449         NA      NA       NA

(Dispersion parameter for poisson family taken to be 1)

Std. Error is NA where coefficient has been constrained or is unidentified

Residual deviance: 1196.3 on 996 degrees of freedom
AIC: 5982.5

Number of iterations: 3
```

As usual, gnm has worked here with an over-parameterized representation of the model. The parameterization used by glm can be seen from

```
> coef(temp.glm)[-(1:500)]

      resp2       resp3     resp1:x     resp2:x     resp3:x
-1.96470932 -1.29013922 -0.05464657 -0.06292256          NA
```

(we will not print the full summary of temp.glm here, since it gives details of all 505 parameters!), which easily can be obtained, if required, by using getContrasts:

```
> getContrasts(temp.gnm, 5:3)

rowID5 rowID4 rowID3
    NA  FALSE  FALSE
Note: not all of the specified contrasts in this set are estimable
[[1]]
       Estimate Std. Error
rowID5        0          0
```

The *eliminate* feature as implemented in *gnm* extends the earlier work of Hatzinger and Francis (2004) to a broader class of models and to over-parameterized model representations.

5 Methods and Accessor functions

5.1 Methods

The gnm function returns an object of class c("gnm", "glm", "lm"). There are several methods that have been written for objects of class *glm* or *lm* to facilitate inspection of fitted models. Out of the generic functions in the *base*, *stats* and *graphics* packages for which methods have been written for *glm* or *lm* objects, Figure 1 shows those that can be used to analyse *gnm* objects, whilst Figure 2 shows those that are not implemented for *gnm* objects.

anova	hatvalues	rstandard
case.names	labels	summary
coef	logLik	variable.names
cooks.distance	model.frame	vcov
deviance	model.matrix	weights
extractAIC	plot	
family	print	
formula	residuals	

Figure 1: Generic functions in the *base*, *stats* and *graphics* packages that can be used to analyse *gnm* objects.

In addition to the accessor functions shown in Figure 1, the *gnm* package provides a new generic function called termPredictors that has methods for objects of class *gnm*, *glm* and *lm*. This function returns the additive contribution of each term to the predictor. See Section 2 for an example of its use.

add1	dummy.coef
alias	effects
confint	influence
dfbeta	kappa
dfbetas	predict
drop1	proj

Figure 2: Generic functions in the *base*, *stats* and *graphics* packages for which methods have been written for *glm* or *lm* objects, but which are *not* implemented for *gnm* objects.

Most of the methods listed in Figure 1 can be used as they would be for *glm* or *lm* objects, however care must be taken with *vcov*, as the variance-covariance matrix will depend on the parameterization of the model. In particular, standard errors calculated using the variance-covariance matrix will only be valid for parameters or contrasts that are estimable!

5.2 checkEstimable

The checkEstimable function can be used to check the estimability of a linear combination of parameters. For non-linear combinations the same function can be used to check estimability based on the (local) vector of partial derivatives. The checkEstimable function provides a numerical version of the sort of algebraic test described in Catchpole and Morgan (1997).

Consider the following model, that is described later in Section 6.3:

```
> data(cautres)
> doubleUnidiff <- gnm(Freq ~ election:vote + election:class:religion +
+     Mult(Exp(election - 1), religion:vote - 1) + Mult(Exp(election -
+     1), class:vote - 1), family = poisson, data = cautres)

Initialising
Running start-up iterations..
Running main iterations.........
Done
```

The effects of the first constituent multiplier in the first multiplicative interaction are identified when the estimate of one of these effects is constrained to zero, say for the effect of the first level. The parameters to be estimated are then the differences between each effect and the effect of the first level. These differences can be represented by a contrast matrix as follows:

```
> coefs <- names(coef(doubleUnidiff))
> contrCoefs <- coefs[grep("Mult1.Factor1", coefs)]
> nContr <- length(contrCoefs)
> contrMatrix <- matrix(0, length(coefs), nContr, dimnames = list(coefs,
+     contrCoefs))
> contr <- contr.sum(contrCoefs)
> contr <- rbind(contr[nContr, ], contr[-nContr, ])
> contrMatrix[contrCoefs, 2:nContr] <- contr
> contrMatrix[contrCoefs, 2:nContr]

                      Mult1.Factor1.election2 Mult1.Factor1.election3
Mult1.Factor1.election1                      -1                      -1
Mult1.Factor1.election2                       1                       0
Mult1.Factor1.election3                       0                       1
Mult1.Factor1.election4                       0                       0
                      Mult1.Factor1.election4
Mult1.Factor1.election1                      -1
Mult1.Factor1.election2                       0
Mult1.Factor1.election3                       0
Mult1.Factor1.election4                       1
```

Then their estimability can be checked using `checkEstimable`

```
> checkEstimable(doubleUnidiff, contrMatrix)

Mult1.Factor1.election1 Mult1.Factor1.election2 Mult1.Factor1.election3
                     NA                    TRUE                    TRUE
Mult1.Factor1.election4
                   TRUE
```

which confirms that the effects for the other three levels are estimable when the parameter for the first level is set to zero.

However, applying the equivalent constraint to the second constituent multiplier in the interaction is not sufficient to make the parameters in that multiplier estimable:

```
> coefs <- names(coef(doubleUnidiff))
> contrCoefs <- coefs[grep("Mult1.Factor2", coefs)]
> nContr <- length(contrCoefs)
> contrMatrix <- matrix(0, length(coefs), length(contrCoefs), dimnames = list(coefs,
+     contrCoefs))
> contr <- contr.sum(contrCoefs)
> contrMatrix[contrCoefs, 2:nContr] <- rbind(contr[nContr, ], contr[-nContr,
+     ])
> checkEstimable(doubleUnidiff, contrMatrix)

Mult1.Factor2.religion1:vote1 Mult1.Factor2.religion2:vote1
                           NA                         FALSE
Mult1.Factor2.religion3:vote1 Mult1.Factor2.religion4:vote1
                        FALSE                         FALSE
Mult1.Factor2.religion1:vote2 Mult1.Factor2.religion2:vote2
                        FALSE                         FALSE
Mult1.Factor2.religion3:vote2 Mult1.Factor2.religion4:vote2
                        FALSE                         FALSE
```

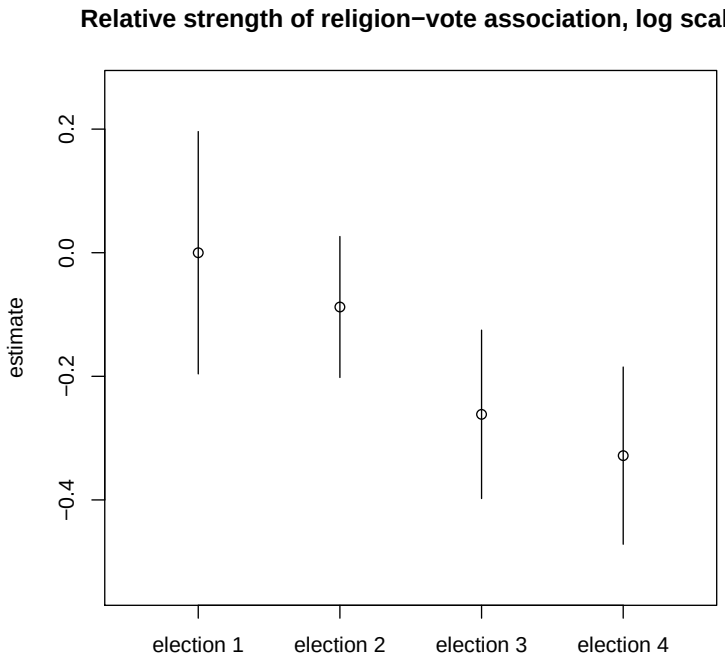
5.3 getContrasts, se

To investigate simple "sum to zero" contrasts such as those above, it is easiest to use the `getContrasts` function, which checks the estimability of the contrasts and returns the parameter estimates with their standard errors. Returning to the example of the first constituent multiplier in the first multiplicative interaction term, the differences between each election and the first can be obtained as follows:

```
> coefs.of.interest <- grep("Mult1.Factor1", names(coef(doubleUnidiff)))
> print(myContrasts <- getContrasts(doubleUnidiff, coefs.of.interest))

[[1]]
                          estimate        SE    quasiSE    quasiVar
Mult1.Factor1.election1  0.0000000 0.0000000 0.09803075 0.009610029
Mult1.Factor1.election2 -0.0878181 0.1136832 0.05702819 0.003252214
Mult1.Factor1.election3 -0.2615200 0.1184134 0.06812239 0.004640660
Mult1.Factor1.election4 -0.3283459 0.1221302 0.07168290 0.005138439
```

Visualization of estimated contrasts using 'quasi standard errors' (Firth, 2003; Firth and de Menezes, 2004) is achieved by plotting the resulting object:

```
> plot(myContrasts[[1]], levelNames = paste("election", c(1, 2,
+     3, 4)), main = "Relative strength of religion-vote association, log scale")
```



For more general linear combinations of parameters than contrasts, the lower-level `se` function (which is called internally by `getContrasts` and by the *summary* method) can be used directly. See `help(se)` for details.

5.4 residSVD

Sometimes it is useful to operate on the residuals of a model in order to create informative summaries of residual variation, or to obtain good starting values for additional parameters in a more elaborate model. The relevant arithmetical operations are weighted means of the so-called *working residuals*.

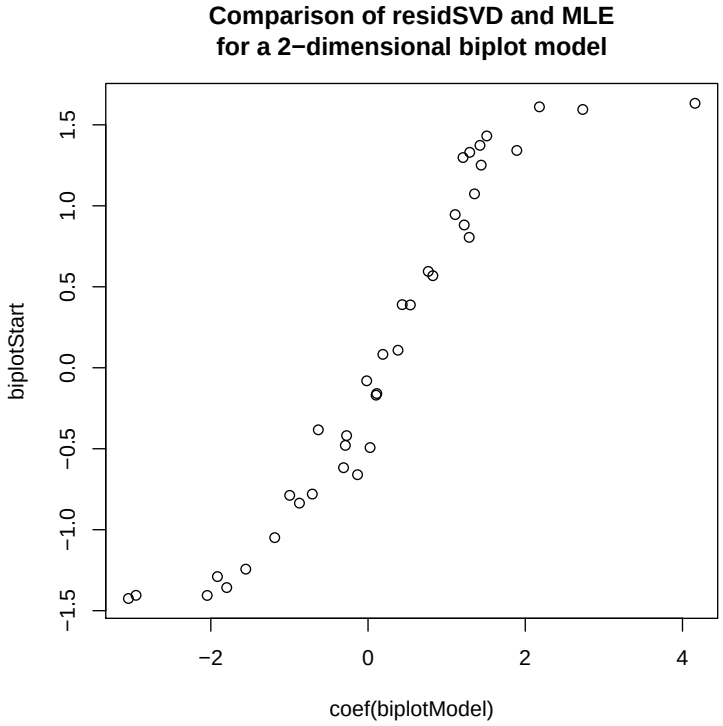
The `residSVD` function facilitates one particular residual analysis that is often useful when considering multiplicative interaction between factors as a model elaboration: in effect, `residSVD` provides a direct estimate of the parameters of such an interaction, by performing an appropriately weighted singular value decomposition on the working residuals.

As an illustration, consider the biplot model described in Section 6.5 below. We can proceed by fitting a smaller model, then use `residSVD` to obtain starting values for the parameters in the bilinear term:

```
> emptyModel <- gnm(y ~ -1, family = wedderburn, data = barley)
> biplotStart <- residSVD(emptyModel, barley$site, barley$variety,
+     d = 2)
> biplotModel <- gnm(y ~ -1 + Mult(-1 + site, -1 + variety, multiplicity = 2),
+     family = wedderburn, data = barley, start = biplotStart)

Running main iterations.....................................................
.....................................................................
..
Done
```

In this instance, the use of purposive (as opposed to the default, random) starting values had little effect: the fairly large number of iterations needed in this example is caused by a rather flat (quasi-)likelihood surface near the maximum, not by poor starting values. In other situations, the use of `residSVD` may speed the calculations dramatically (see for example Section 6.4), or it may be crucial to success in locating the MLE (for example see `help(House2001)`, where the number of multiplicative parameters is in the hundreds).

The `residSVD` result in this instance provides a crude approximation to the MLE of the enlarged model, as can be seen in the following plot:



6 Examples

This section provides some examples of the wide range of models that may be fitted using the *gnm* package. Sections 6.1, 6.2 and 6.3 consider various models for contingency tables; Section 6.4 considers AMMI and GAMMI models which are typically used in agricultural applications, and Section 6.6 considers the stereotype model, which is used to model an ordinal response.

6.1 Row-column Association Models

There are several models that have been proposed for modelling the relationship between the cell means of a contingency table and the cross-classifying factors. The following examples consider the row-column association models proposed by Goodman (1979). The examples shown use data from two-way contingency tables, but the *gnm* package can also be used to fit the equivalent models for higher order tables.

6.1.1 RC(1) model

The RC(1) model is a row and column association model with the interaction between row and column factors represented by one component of the multiplicative interaction. If the rows are indexed by r and the columns by c, then the log-multiplicative form of the RC(1) model for the cell means μ_{rc} is given by

$$\log \mu_{rc} = \alpha_r + \beta_c + \gamma_r \delta_c.$$

We shall fit this model to the `mentalHealth` data set taken from Agresti (2002) page 381, which is a two-way contingency table classified by the child's mental impairment (MHS) and the parents' socioeconomic status (SES). Although both of these factors are ordered, we do not wish to use polynomial contrasts in the model, so we begin by setting the contrasts attribute of these factors to "`treatment`":

```
> set.seed(1)
> data(mentalHealth)
> mentalHealth$MHS <- C(mentalHealth$MHS, treatment)
> mentalHealth$SES <- C(mentalHealth$SES, treatment)
```

The *gnm* model is then specified as follows, using the poisson family with a log link function:

```
> RC1model <- gnm(count ~ SES + MHS + Mult(-1 + SES, -1 + MHS),
+     family = poisson, data = mentalHealth)

Initialising
Running start-up iterations..
Running main iterations........
Done

> RC1model

Call:

gnm(formula = count ~ SES + MHS + Mult(-1 + SES, -1 + MHS), family = poisson,
    data = mentalHealth)


Coefficients:
              (Intercept)                      SESB
                 3.831281                 -0.067413
                     SESC                      SESD
                 0.109959                  0.404969
                     SESE                      SESF
                 0.025257                 -0.200685
                  MHSmild               MHSmoderate
                 0.712969                  0.204987
             MHSimpaired        Mult1.Factor1.SESA
                 0.251749                  0.340495
       Mult1.Factor1.SESB        Mult1.Factor1.SESC
                 0.343267                  0.114885
       Mult1.Factor1.SESD        Mult1.Factor1.SESE
                -0.006284                 -0.305574
       Mult1.Factor1.SESF     Mult1.Factor2.MHSwell
                -0.551460                  0.935600
    Mult1.Factor2.MHSmild  Mult1.Factor2.MHSmoderate
                 0.094793                 -0.056941
Mult1.Factor2.MHSimpaired
                -0.755299

Deviance:            3.570562
Pearson chi-squared: 3.568088
Residual df:         8
```

The row scores (parameters 10 to 15) and the column scores (parameters 16 to 19) of the multiplicative interaction 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))
> rowScores <- coef(RC1model)[10:15]
> colScores <- coef(RC1model)[16:19]
> rowScores <- rowScores - sum(rowScores * rowProbs)
> colScores <- colScores - sum(colScores * colProbs)
> beta1 <- sqrt(sum(rowScores^2 * rowProbs))
> beta2 <- sqrt(sum(colScores^2 * colProbs))
> assoc <- list(beta = beta1 * beta2, mu = rowScores/beta1, nu = colScores/beta2)
> assoc
```

```
$beta
[1] 0.1664874

$mu
Mult1.Factor1.SESA Mult1.Factor1.SESB Mult1.Factor1.SESC Mult1.Factor1.SESD
        1.11233090         1.12143715         0.37107612        -0.02702946
Mult1.Factor1.SESE Mult1.Factor1.SESF
       -1.01036153        -1.81823284

$nu
    Mult1.Factor2.MHSwell     Mult1.Factor2.MHSmild Mult1.Factor2.MHSmoderate
                1.6775144                 0.1403989                -0.1369924
Mult1.Factor2.MHSimpaired
               -1.4136910
```

6.1.2 RC(2) model

The RC(1) model can be extended to an RC(m) model with m components of the multiplicative interaction. For example, the RC(2) model is given by

$$\log \mu_{rc} = \alpha_r + \beta_c + \gamma_r \delta_c + \theta_r \phi_c.$$

Extra instances of the multiplicative interaction can be specified by the *multiplicity* argument of `Mult`, so the RC(2) model can be fitted to the `mentalHealth` data as follows

```
> RC2model <- gnm(count ~ SES + MHS + Mult(-1 + SES, -1 + MHS,
+     multiplicity = 2), family = poisson, data = mentalHealth)

Initialising
Running start-up iterations..
Running main iterations.....
Done

> RC2model

Call:

gnm(formula = count ~ SES + MHS + Mult(-1 + SES, -1 + MHS, multiplicity = 2),
    family = poisson, data = mentalHealth)


Coefficients:
              (Intercept)                      SESB
                  3.85530                   -0.06444
                     SESC                      SESD
                  0.11140                    0.38457
                     SESE                      SESF
                  0.01081                   -0.18462
                  MHSmild                MHSmoderate
                  0.69860                    0.16975
             MHSimpaired         Mult1.Factor1.SESA
                  0.22876                    0.95047
      Mult1.Factor1.SESB         Mult1.Factor1.SESC
                  0.99597                    0.33932
      Mult1.Factor1.SESD         Mult1.Factor1.SESE
                 -0.17292                   -0.91634
      Mult1.Factor1.SESF      Mult1.Factor2.MHSwell
                 -1.39376                    0.35782
```

```
    Mult1.Factor2.MHSmild  Mult1.Factor2.MHSmoderate
                  0.03795                   -0.02129
Mult1.Factor2.MHSimpaired         Mult2.Factor1.SESA
                 -0.28029                   -0.17762
       Mult2.Factor1.SESB         Mult2.Factor1.SESC
                 -0.25156                   -0.16614
       Mult2.Factor1.SESD         Mult2.Factor1.SESE
                  0.28993                    0.22675
       Mult2.Factor1.SESF      Mult2.Factor2.MHSwell
                 -0.45554                    0.30776
    Mult2.Factor2.MHSmild  Mult2.Factor2.MHSmoderate
                  0.09804                   -0.25536
Mult2.Factor2.MHSimpaired
                  0.06769

Deviance:            0.5225353
Pearson chi-squared: 0.523331
Residual df:         3
```

6.1.3 Homogeneous effects

If the row and column factors have the same levels, or perhaps some levels in common, then the row-column interaction could be modelled by a multiplicative interaction with homogeneous effects, that is

$$\log \mu_{rc} = \alpha_r + \beta_c + \gamma_r \gamma_c.$$

For example, the `occupationalStatus` data set from Goodman (1979) is a contingency table classified by the occupational status of fathers (origin) and their sons (destination). Goodman (1979) fits a row-column association model with homogeneous effects to these data after deleting the cells on the main diagonal. Equivalently we can account for the diagonal effects by a separate `Diag` term:

```
> data(occupationalStatus)
> RChomog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
+     Nonlin(MultHomog(origin, destination)), family = poisson,
+     data = occupationalStatus)

Initialising
Running start-up iterations..
Running main iterations........
Done

> RChomog

Call:
gnm(formula = Freq ~ origin + destination + Diag(origin, destination) +
    Nonlin(MultHomog(origin, destination)), family = poisson,
    data = occupationalStatus)


Coefficients:
                     (Intercept)                          origin2
                        -0.66871                          0.57191
                          origin3                          origin4
                          1.82383                          2.28549
                          origin5                          origin6
                          1.07035                          3.25732
                          origin7                          origin8
```

```
                      2.03247                       1.83018
                  destination2                   destination3
                      0.99093                       2.16824
                  destination4                   destination5
                      2.57393                       1.96977
                  destination6                   destination7
                      3.56080                       2.78406
                  destination8      Diag(origin, destination)1
                      2.40556                       1.52667
     Diag(origin, destination)2      Diag(origin, destination)3
                      0.45600                      -0.01598
     Diag(origin, destination)4      Diag(origin, destination)5
                      0.38918                       0.73852
     Diag(origin, destination)6      Diag(origin, destination)7
                      0.13474                       0.45764
     Diag(origin, destination)8 MultHomog(origin, destination).1
                      0.38847                      -1.74759
MultHomog(origin, destination).2 MultHomog(origin, destination).3
                     -1.52929                      -0.93113
MultHomog(origin, destination).4 MultHomog(origin, destination).5
                     -0.34725                      -0.33008
MultHomog(origin, destination).6 MultHomog(origin, destination).7
                      0.18168                       0.59782
MultHomog(origin, destination).8
                      0.84139

Deviance:            32.56098
Pearson chi-squared: 31.20716
Residual df:         34
```

To determine whether it would be better to allow for heterogeneous effects on the association of the fathers' occupational status and the sons' occupational status, we can compare this model to the RC(1) model for these data:

```
> data(occupationalStatus)
> RCheterog <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
+     Mult(origin, destination), family = poisson, data = occupationalStatus)

Initialising
Running start-up iterations..
Running main iterations...........
Done

> RChomog$dev - RCheterog$dev

[1] 3.411823

> RChomog$df.residual - RCheterog$df.residual

[1] 6
```

In this case there is little gain in allowing heterogeneous effects.

6.2 Diagonal Reference Models

Diagonal reference models, proposed by Sobel (1981, 1985), are designed for contingency tables classified by factors with the same levels. The cell means are modelled as a function of the diagonal effects, i.e., the mean responses of the 'diagonal' cells in which the levels of the row and column factors are the same.

`Dref` example 1: Political consequences of social mobility

To illustrate the use of diagonal reference models we shall use the `voting` data from Clifford and Heath (1993). The data come from the 1987 British general election and are the percentage voting Labour in groups cross-classified by the class of the head of household (`destination`) and the class of their father (`origin`). In order to weight these percentages by the group size, we first back-transform them to the counts of those voting Labour and those not voting Labour:

```
> set.seed(1)
> data(voting)
> count <- with(voting, percentage/100 * total)
> yvar <- cbind(count, voting$total - count)
```

The grouped percentages may be modelled by a basic diagonal reference model, that is, a weighted sum of the diagonal effects for the corresponding origin and destination classes. This model may be expressed as

$$\mu_{od} = \frac{e^{\delta_1}}{e^{\delta_1} + e^{\delta_2}}\gamma_o + \frac{e^{\delta_2}}{e^{\delta_1} + e^{\delta_2}}\gamma_d.$$

See Section 3.2.2 for more detail on the parameterization.

The basic diagonal reference model may be fitted using `gnm` as follows

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

Initialising
Running main iterations........
Done

> classMobility

Call:

gnm(formula = yvar ~ Nonlin(Dref(origin, destination)), family = binomial,
    data = voting)


Coefficients:
                          (Intercept)       Dref(origin, destination).origin
                              -1.34325                               -0.30736
Dref(origin, destination).destination           Dref(origin, destination).1
                              -0.05501                               -0.83455
          Dref(origin, destination).2           Dref(origin, destination).3
                               0.21066                               -0.61159
          Dref(origin, destination).4           Dref(origin, destination).5
                               0.76500                                1.38370

Deviance:            21.22093
Pearson chi-squared: 18.95311
Residual df:         19
```

and the origin and destination weights can be evaluated as below

```
> prop.table(exp(coef(classMobility)[2:3]))

     Dref(origin, destination).origin Dref(origin, destination).destination
                            0.4372469                              0.5627531
```

These results are slightly different from those reported by Clifford and Heath (1993). The reason for this is unclear: we are confident that the above results are correct for the data as given in Clifford and Heath (1993), but have not been able to confirm that the data as printed in the journal were exactly as used in Clifford and Heath's analysis.

Clifford and Heath (1993) suggest that movements in and out of the salariat (class 1) should be treated differently from movements between the lower classes (classes 2 - 5), since the former has a greater effect on social status. Thus they propose the following model

$$\mu_{od} = \begin{cases} \dfrac{e^{\delta_1}}{e^{\delta_1}+e^{\delta_2}}\gamma_o + \dfrac{e^{\delta_2}}{e^{\delta_1}+e^{\delta_2}}\gamma_d & \text{if } o = 1 \\ \dfrac{e^{\delta_3}}{e^{\delta_3}+e^{\delta_4}}\gamma_o + \dfrac{e^{\delta_4}}{e^{\delta_3}+e^{\delta_4}}\gamma_d & \text{if } d = 1 \\ \dfrac{e^{\delta_5}}{e^{\delta_5}+e^{\delta_6}}\gamma_o + \dfrac{e^{\delta_6}}{e^{\delta_5}+e^{\delta_6}}\gamma_d & \text{if } o \neq 1 \text{ and } d \neq 1 \end{cases}$$

To fit this model we define factors indicating movement in (upward) and out (downward) of the salariat

```
> upward <- with(voting, origin != 1 & destination == 1)
> downward <- with(voting, origin == 1 & destination != 1)
```

Then the diagonal reference model with separate weights for socially mobile groups can be estimated as follows

```
> socialMobility <- gnm(yvar ~ Nonlin(Dref(origin, destination,
+     formula = ~1 + downward + upward)), family = binomial, data = voting)

Initialising
Running main iterations..........
Done

> socialMobility

Call:
gnm(formula = yvar ~ Nonlin(Dref(origin, destination, formula = ~1 +
    downward + upward)), family = binomial, data = voting)


Coefficients:
                                                                                (Intercept)
                                                                                  -1.31739
      Dref(origin, destination, formula = ~1 + downward + upward).origin.(Intercept)
                                                                                  -0.39834
     Dref(origin, destination, formula = ~1 + downward + upward).origin.downwardTRUE
                                                                                   0.37858
       Dref(origin, destination, formula = ~1 + downward + upward).origin.upwardTRUE
                                                                                   0.06225
 Dref(origin, destination, formula = ~1 + downward + upward).destination.(Intercept)
                                                                                  -0.01158
Dref(origin, destination, formula = ~1 + downward + upward).destination.downwardTRUE
                                                                                  -0.43218
  Dref(origin, destination, formula = ~1 + downward + upward).destination.upwardTRUE
                                                                                   0.12247
                        Dref(origin, destination, formula = ~1 + downward + upward).1
                                                                                  -0.74021
                        Dref(origin, destination, formula = ~1 + downward + upward).2
                                                                                   0.20469
                        Dref(origin, destination, formula = ~1 + downward + upward).3
                                                                                  -0.67740
                        Dref(origin, destination, formula = ~1 + downward + upward).4
                                                                                   0.74824
                        Dref(origin, destination, formula = ~1 + downward + upward).5
```

```
                                                                    1.37497

Deviance:            18.97407
Pearson chi-squared: 17.07493
Residual df:         17
```

The weights for those moving into the salariat, those moving out of the salariat and those in any other group, can be evaluated as below

```
> prop.table(exp(coef(socialMobility)[c(4, 7)] + coef(socialMobility)[c(2,
+     5)]))

     Dref(origin, destination, formula = ~1 + downward + upward).origin.upwardTRUE
                                                                         0.3900792
Dref(origin, destination, formula = ~1 + downward + upward).destination.upwardTRUE
                                                                         0.6099208

> prop.table(exp(coef(socialMobility)[c(3, 6)] + coef(socialMobility)[c(2,
+     5)]))

     Dref(origin, destination, formula = ~1 + downward + upward).origin.downwardTRUE
                                                                           0.6044394
Dref(origin, destination, formula = ~1 + downward + upward).destination.downwardTRUE
                                                                           0.3955606

> prop.table(exp(coef(socialMobility)[c(2, 5)]))

     Dref(origin, destination, formula = ~1 + downward + upward).origin.(Intercept)
                                                                           0.4044959
Dref(origin, destination, formula = ~1 + downward + upward).destination.(Intercept)
                                                                           0.5955041
```

Again, the results differ slightly from those reported by Clifford and Heath (1993), but the essence of the results is the same: the origin weight is much larger for the downwardly mobile groups than for the other groups. The weights for the upwardly mobile groups are very similar to the base level weights, so the model may be simplified by only fitting separate weights for the downwardly mobile groups:

```
> downwardMobility <- gnm(yvar ~ Nonlin(Dref(origin, destination,
+     formula = ~1 + downward)), family = binomial, data = voting)

Initialising
Running main iterations.........
Done

> downwardMobility

Call:
gnm(formula = yvar ~ Nonlin(Dref(origin, destination, formula = ~1 +
    downward)), family = binomial, data = voting)


Coefficients:
                                                                  (Intercept)
                                                                     -1.30746
      Dref(origin, destination, formula = ~1 + downward).origin.(Intercept)
                                                                     -0.02851
     Dref(origin, destination, formula = ~1 + downward).origin.downwardTRUE
                                                                      0.37534
```

```
 Dref(origin, destination, formula = ~1 + downward).destination.(Intercept)
                                                                    0.38028
Dref(origin, destination, formula = ~1 + downward).destination.downwardTRUE
                                                                   -0.43540
                       Dref(origin, destination, formula = ~1 + downward).1
                                                                   -0.76241
                       Dref(origin, destination, formula = ~1 + downward).2
                                                                    0.20093
                       Dref(origin, destination, formula = ~1 + downward).3
                                                                   -0.68419
                       Dref(origin, destination, formula = ~1 + downward).4
                                                                    0.73438
                       Dref(origin, destination, formula = ~1 + downward).5
                                                                    1.36375

Deviance:            18.99389
Pearson chi-squared: 17.09981
Residual df:         18

> prop.table(exp(coef(downwardMobility)[c(3, 5)] + coef(downwardMobility)[c(2,
+     4)]))

     Dref(origin, destination, formula = ~1 + downward).origin.downwardTRUE
                                                                   0.5991571
Dref(origin, destination, formula = ~1 + downward).destination.downwardTRUE
                                                                   0.4008429

> prop.table(exp(coef(downwardMobility)[c(2, 4)]))

     Dref(origin, destination, formula = ~1 + downward).origin.(Intercept)
                                                                   0.3992031
Dref(origin, destination, formula = ~1 + downward).destination.(Intercept)
                                                                   0.6007969
```

`Dref` example 2: Conformity to parental rules

Another application of diagonal reference models is given by van der Slik et al. (2002). The data from this paper are not publicly available[4], but we shall show how the models presented in the paper may be estimated using `gnm`.

The data relate to the value parents place on their children conforming to their rules. There are two response variables: the mother's conformity score (MCFM) and the father's conformity score (FCFF). The data are cross-classified by two factors describing the education level of the mother (MOPLM) and the father (FOPLF), and there are six further covariates (AGEM, MRMM, FRMF, MWORK, MFCM and FFCF).

In their baseline model for the mother's conformity score, van der Slik et al. (2002) include five of the six covariates (leaving out the father's family conflict score, FCFF) and a diagonal reference term with constant weights based on the two education factors. This model may be expressed as

$$\mu_{rc} = \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5 + \frac{e^{\delta_1}}{e^{\delta_1} + e^{\delta_2}}\gamma_r + \frac{e^{\delta_2}}{e^{\delta_1} + e^{\delta_2}}\gamma_c.$$

The baseline model can be fitted as follows:

```
> set.seed(1)
>  A <- gnm(MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
+           Nonlin(Dref(MOPLM, FOPLF)), family = gaussian, data = conformity,
+           verbose = FALSE)
> A
```

[4] We thank Frans van der Slik for his kindness in sending us the data.

```
Call:
gnm(formula = MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
    Nonlin(Dref(MOPLM, FOPLF)), family = gaussian, data = conformity,
    verbose = FALSE)


Coefficients:
                    AGEM                     MRMM                     FRMF
                 0.06364                 -0.32425                 -0.25324
                   MWORK                     MFCM  Dref(MOPLM, FOPLF).MOPLM
                -0.06430                 -0.06043                 -0.33730
Dref(MOPLM, FOPLF).FOPLF      Dref(MOPLM, FOPLF).1      Dref(MOPLM, FOPLF).2
                -0.02507                  4.95123                  4.86328
    Dref(MOPLM, FOPLF).3      Dref(MOPLM, FOPLF).4      Dref(MOPLM, FOPLF).5
                 4.86458                  4.72343                  4.43516
    Dref(MOPLM, FOPLF).6      Dref(MOPLM, FOPLF).7
                 4.18873                  4.43379

Deviance:            425.3389
Pearson chi-squared: 425.3389
Residual df:         576
```

The coefficients of the covariates are not aliased with the parameters of the diagonal reference term and thus the basic identifiability constraints that have been imposed are sufficient for these parameters to be identified. The diagonal effects do not need to be constrained as they represent contrasts with the off-diagonal cells. Therefore the only unidentified parameters in this model are the weight parameters. This is confirmed in the summary of the model:

```
> summary(A)

Call:
gnm(formula = MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
    Nonlin(Dref(MOPLM, FOPLF)), family = gaussian, data = conformity,
    verbose = FALSE)


Deviance Residuals:
     Min        1Q    Median        3Q       Max
-3.63689  -0.50383   0.01714   0.56752   2.25140

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
AGEM                       0.06364    0.07375   0.863  0.38859
MRMM                      -0.32425    0.07766  -4.175 3.44e-05
FRMF                      -0.25324    0.07681  -3.297  0.00104
MWORK                     -0.06430    0.07431  -0.865  0.38727
MFCM                      -0.06043    0.07123  -0.848  0.39663
Dref(MOPLM, FOPLF).MOPLM -0.33730         NA      NA       NA
Dref(MOPLM, FOPLF).FOPLF -0.02507         NA      NA       NA
Dref(MOPLM, FOPLF).1       4.95123    0.16639  29.757  < 2e-16
Dref(MOPLM, FOPLF).2       4.86328    0.10436  46.601  < 2e-16
Dref(MOPLM, FOPLF).3       4.86458    0.12855  37.842  < 2e-16
Dref(MOPLM, FOPLF).4       4.72343    0.13523  34.928  < 2e-16
Dref(MOPLM, FOPLF).5       4.43516    0.19315  22.963  < 2e-16
Dref(MOPLM, FOPLF).6       4.18873    0.17142  24.435  < 2e-16
Dref(MOPLM, FOPLF).7       4.43379    0.16903  26.231  < 2e-16
```

```
(Dispersion parameter for gaussian family taken to be 0.7384355)

Std. Error is NA where coefficient has been constrained or is unidentified

Residual deviance: 425.34 on 576 degrees of freedom
AIC: 1507.8

Number of iterations: 10
```

The over-parameterization of the weights is immaterial, since the weights have been constrained to sum to one as described earlier, so the weights themselves are estimable. The weights may be evaluated as follows:

```
> prop.table(exp(coef(A)[6:7]))
Dref(MOPLM, FOPLF).MOPLM Dref(MOPLM, FOPLF).FOPLF
               0.4225701                0.5774299
```

giving the values reported by van der Slik et al. (2002). All the other coefficients of model A are the same as those reported by van der Slik et al. (2002) except the coefficients of the mother's gender role (MRMM) and the father's gender role (FRMF). van der Slik et al. (2002) reversed the signs of the coefficients of these factors since they were coded in the direction of liberal values, unlike the other covariates. However, simply reversing the signs of these coefficients does not give the same model, since the estimates of the diagonal effects depend on the estimates of these coefficients. For consistent interpretation of the covariate coefficients, it is better to recode the gender role factors as follows:

```
> MRMM2 <- as.numeric(!conformity$MRMM)
> FRMF2 <- as.numeric(!conformity$FRMF)
> A <- gnm(MCFM ~ -1 + AGEM + MRMM2 + FRMF2 + MWORK + MFCM +
+           Nonlin(Dref(MOPLM, FOPLF)), family = gaussian, data = conformity,
+           verbose = FALSE)
> A

Call:
gnm(formula = MCFM ~ -1 + AGEM + MRMM2 + FRMF2 + MWORK + MFCM +
    Nonlin(Dref(MOPLM, FOPLF)), family = gaussian, data = conformity,
    verbose = FALSE)


Coefficients:
                    AGEM                    MRMM2                    FRMF2
                 0.06364                  0.32425                  0.25324
                   MWORK                     MFCM  Dref(MOPLM, FOPLF).MOPLM
                -0.06430                 -0.06043                 -0.08270
Dref(MOPLM, FOPLF).FOPLF      Dref(MOPLM, FOPLF).1      Dref(MOPLM, FOPLF).2
                 0.22955                  4.37372                  4.28579
    Dref(MOPLM, FOPLF).3      Dref(MOPLM, FOPLF).4      Dref(MOPLM, FOPLF).5
                 4.28708                  4.14593                  3.85766
    Dref(MOPLM, FOPLF).6      Dref(MOPLM, FOPLF).7
                 3.61123                  3.85629

Deviance:            425.3389
Pearson chi-squared: 425.3389
Residual df:         576
```

The coefficients of the covariates are now as reported by van der Slik et al. (2002), but the diagonal effects have been adjusted appropriately.

van der Slik et al. (2002) compare the baseline model for the mother's conformity score to several other models in which the weights in the diagonal reference term are dependent on one of the covariates. One particular model they

consider incorporates an interaction of the weights with the mother's conflict score as follows:

$$\mu_{rc} = \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5 + \frac{e^{\xi_1+\beta_1 x}}{e^{\xi_1+\beta_1 x} + e^{\xi_2+\beta_2 x}}\gamma_r + \frac{e^{\xi_2+\beta_2 x}}{e^{\xi_1+\beta_1 x} + e^{\xi_2+\beta_2 x}}\gamma_c.$$

This model can be fitted as below, using the original coding for the gender role factors for ease of comparison to the results reported by van der Slik et al. (2002),

```
> F <- gnm(MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
+            Nonlin(Dref(MOPLM, FOPLF, formula = ~ 1 + MFCM)), family = gaussian,
+            data = conformity, verbose = FALSE)
> F

Call:
gnm(formula = MCFM ~ -1 + AGEM + MRMM + FRMF + MWORK + MFCM +
    Nonlin(Dref(MOPLM, FOPLF, formula = ~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, formula = ~1 + MFCM).MOPLM.(Intercept)
                                                 0.79413
       Dref(MOPLM, FOPLF, formula = ~1 + MFCM).MOPLM.MFCM
                                                -2.51751
Dref(MOPLM, FOPLF, formula = ~1 + MFCM).FOPLF.(Intercept)
                                                -0.27618
       Dref(MOPLM, FOPLF, formula = ~1 + MFCM).FOPLF.MFCM
                                                 2.03673
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).1
                                                 4.82477
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).2
                                                 4.88066
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).3
                                                 4.83969
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).4
                                                 4.74849
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).5
                                                 4.42019
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).6
                                                 4.17956
                Dref(MOPLM, FOPLF, formula = ~1 + MFCM).7
                                                 4.40819

Deviance:            420.9022
Pearson chi-squared: 420.9022
Residual df:         575
```

In this case there are two sets of weights, one for when the mother's conflict score is less than average (coded as zero) and one for when the score is greater than average (coded as one). These can be evaluated as follows:

```
> prop.table(exp(coef(F))[c(6,8)])
Dref(MOPLM, FOPLF, formula = ~1 + MFCM).MOPLM.(Intercept)
                                                0.7446574
Dref(MOPLM, FOPLF, formula = ~1 + MFCM).FOPLF.(Intercept)
                                                0.2553426
> prop.table(exp(coef(F)[c(7,9)] + coef(F)[c(6,8)]))
Dref(MOPLM, FOPLF, formula = ~1 + MFCM).MOPLM.MFCM
                                      0.02977308
Dref(MOPLM, FOPLF, formula = ~1 + MFCM).FOPLF.MFCM
                                      0.97022692
```

giving the same weights as in Table 4 of van der Slik et al. (2002).

6.3 Uniform Difference (UNIDIFF) Models

Uniform difference models (Xie, 1992; Erikson and Goldthorpe, 1992) use a simplified three-way interaction to provide an interpretable model of contingency tables classified by three or more variables. For example, the uniform difference model for a three-way contingency table, also known as the UNIDIFF model, is given by

$$\mu_{ijk} = \alpha_{ik} + \beta_{jk} + \exp(\delta_k)\gamma_{ij}.$$

The γ_{ij} represent a pattern of association that varies in strength over the dimension indexed by k, and $\exp(\delta_k)$ represents the relative strength of that association at level k.

This model can be applied to the `yaish` data set (Yaish, 1998, 2004), which is a contingency table cross-classified by father's social class (`orig`), son's social class (`dest`) and son's education level (`educ`). In this case, we can consider the importance of the association between the social class of father and son across the education levels. We omit the sub-table which corresponds to level 7 of `dest`, because its information content is negligible:

```
> set.seed(1)
> data(yaish)
> unidiff <- gnm(Freq ~ educ * orig + educ * dest + Mult(Exp(-1 +
+     educ), -1 + orig:dest), family = poisson, data = yaish, subset = (dest !=
+     7))

Initialising
Running start-up iterations..
Running main iterations.....................................
Done

> coefs.of.interest <- grep("Mult1.Factor1", names(coef(unidiff)))
> coef(unidiff)[coefs.of.interest]

Mult1.Factor1.educ1 Mult1.Factor1.educ2 Mult1.Factor1.educ3 Mult1.Factor1.educ4
         -0.8242687          -1.0496405          -1.5676923          -1.8632073
Mult1.Factor1.educ5
         -3.0737713
```

The `coefs.of.interest` are the multipliers of the association between the social class of father and son. We can contrast each multiplier to that of the lowest education level and obtain the standard errors for these parameters as follows:

```
> getContrasts(unidiff, coefs.of.interest)

[[1]]
                       estimate        SE    quasiSE   quasiVar
Mult1.Factor1.educ1  0.0000000 0.0000000 0.09757438 0.00952076
Mult1.Factor1.educ2 -0.2253718 0.1611874 0.12885847 0.01660450
```

```
Mult1.Factor1.educ3 -0.7434236 0.2335083 0.21182123 0.04486823
Mult1.Factor1.educ4 -1.0389386 0.3434256 0.32609379 0.10633716
Mult1.Factor1.educ5 -2.2495026 0.9453763 0.93560641 0.87535936
```

Four-way contingency tables may sometimes be described by a "double UNIDIFF" model

$$\mu_{ijkl} = \alpha_{il} + \beta_{jkl} + \exp(\delta_l)\gamma_{ij} + \exp(\phi_l)\theta_{ik},$$

where the strengths of two, two-way associations with a common variable are estimated across the levels of the fourth variable. The `cautres` data set, from Cautres et al. (1998), can be used to illustrate the application of the double UNIDIFF model. This data set is classified by the variables vote, class, religion and election. Using a double UNIDIFF model, we can see how the association between class and vote, and the association between religion and vote, differ between the most recent election and the other elections:

```
> set.seed(1)
> data(cautres)
> doubleUnidiff <- gnm(Freq ~ election * vote + election * class *
+     religion + Mult(Exp(-1 + election), religion:vote) + Mult(Exp(-1 +
+     election), class:vote), family = poisson, data = cautres)

Initialising
Running start-up iterations..
Running main iterations.........
Done

> getContrasts(doubleUnidiff, rev(grep("Mult1.Factor1", names(coef(doubleUnidiff)))))

[[1]]
                          estimate         SE    quasiSE    quasiVar
Mult1.Factor1.election4 0.00000000 0.00000000 0.07168290 0.005138439
Mult1.Factor1.election3 0.06682585 0.09906916 0.06812239 0.004640660
Mult1.Factor1.election2 0.24052778 0.09116479 0.05702819 0.003252214
Mult1.Factor1.election1 0.32834588 0.12213023 0.09803075 0.009610029

> getContrasts(doubleUnidiff, rev(grep("Mult2.Factor1", names(coef(doubleUnidiff)))))

[[1]]
                           estimate        SE    quasiSE    quasiVar
Mult2.Factor1.election4  0.00000000 0.0000000 0.10934798 0.011956980
Mult2.Factor1.election3  0.08754435 0.1446833 0.09475938 0.008979340
Mult2.Factor1.election2  0.31990726 0.1320022 0.07395886 0.005469913
Mult2.Factor1.election1 -0.36183013 0.2534754 0.22854400 0.052232362
```

6.4 Generalized Additive Main Effects and Multiplicative Interaction (GAMMI) Models

Generalized additive main effects and multiplicative interaction models, or GAMMI models, were motivated by two-way contingency tables and comprise the row and column main effects plus one or more components of the multiplicative interaction. The singular value corresponding to each multiplicative component is often factored out, as a measure of the strength of association between the row and column scores, indicating the importance of the component, or axis.

For cell means μ_{rc} a GAMMI-K model has the form

$$g(\mu_{rc}) = \alpha_r + \beta_c + \sum_{k=1}^{K} \sigma_k \gamma_{kr} \delta_{kc},$$

in which g is a link function, α_r and β_c are the row and column main effects, γ_{kr} and δ_{kc} are the row and column scores for multiplicative component k and σ_k is the singular value for component k. The number of multiplicative components, K, is less than or equal to the rank of the matrix of residuals from the main effects.

The row-column association models discussed in Section 6.1 are examples of GAMMI models, with a log link and poisson variance. Here we illustrate the use of an AMMI model, which is a GAMMI model with an identity link and a constant variance.

We shall use the `wheat` data set taken from Vargas et al. (2001), which gives wheat yields measured over ten years. First we scale these yields and create a new treatment factor, so that we can reproduce the analysis of Vargas et al. (2001):

```
> set.seed(1)
> data(wheat)
> yield.scaled <- wheat$yield * sqrt(3/1000)
> treatment <- interaction(wheat$tillage, wheat$summerCrop, wheat$manure,
+     wheat$N, sep = "")
```

Now we can fit the AMMI-1 model, to the scaled yields using the combined treatment factor and the year factor from the `wheat` dataset. We will proceed by first fitting the main effects model, then using `residSVD` (see Section 5.4) for the parameters of the multiplicative term:

```
> mainEffects <- gnm(yield.scaled ~ year + treatment, family = gaussian,
+     data = wheat)

Linear predictor - using glm.fit

> svdStart <- residSVD(mainEffects, year, treatment, 3)
> bilinear1 <- update(mainEffects, . ~ . + Mult(year - 1, treatment -
+     1), start = c(coef(mainEffects), svdStart[, 1]))

Running main iterations
Done
```

We can compare the AMMI-1 model to the main effects model,

```
> anova(mainEffects, bilinear1)

Analysis of Deviance Table

Model 1: yield.scaled ~ year + treatment
Model 2: yield.scaled ~ year + treatment + Mult(year - 1, treatment -
    1)
  Resid. Df Resid. Dev  Df Deviance
1       207     279515
2       176     128383  31   151133
```

giving the same results as in Table 1 of Vargas et al. (2001) (up to error caused by rounding).

6.5 Biplot Models

Biplots are used to display two-dimensional data transformed into a space spanned by linearly independent vectors, such as the principal components or singular vectors. The plot represents the levels of the two classifying factors by their scores on the two axes which show the most information about the data, for example the first two principal components.

A rank-n model is a model based on the first n components of the decomposition. In the case of a singular value decomposition, this is equivalent to a model with n components of the multiplicative interaction.

To illustrate the use of biplot models, we shall use the `barley` data set which describes the incidence of leaf blotch over ten varieties of barley grown at nine sites (Wedderburn, 1974; Gabriel, 1998). The biplot model is fitted as follows:

```
> data(barley)
> set.seed(1)
> biplotModel <- gnm(y ~ -1 + Mult(site, variety, multiplicity = 2),
+     family = wedderburn, data = barley)
```

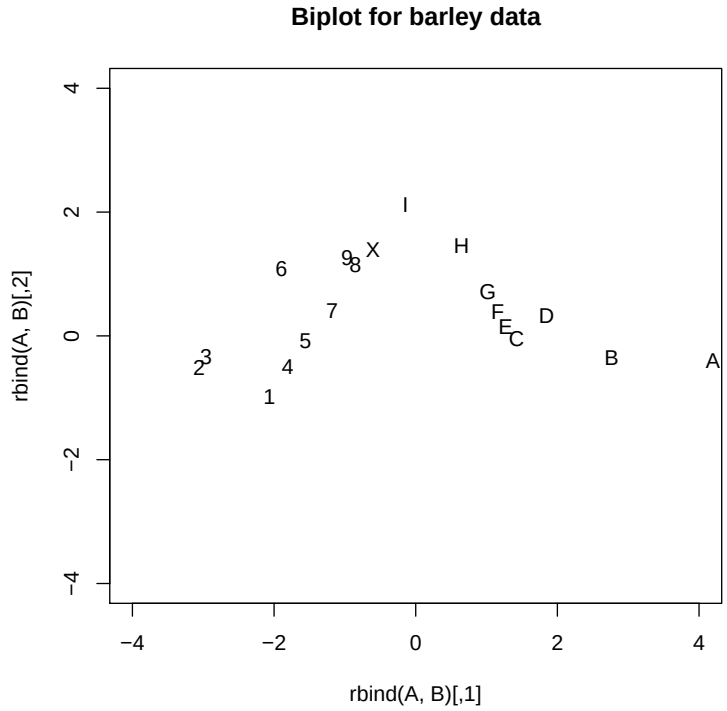
```
Initialising
Running start-up iterations..
Running main iterations.....................................................
.....................................................................
Done
```

using the wedderburn family function introduced in Section 2. Matrices of the row and column scores for the first two singular vectors can then be obtained by:

```
> 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]
> A

            [,1]        [,2]
 [1,]  4.1948212 -0.39186806
 [2,]  2.7642419 -0.33951298
 [3,]  1.4250456 -0.04654256
 [4,]  1.8463067  0.33365981
 [5,]  1.2704091  0.15776743
 [6,]  1.1562916  0.40048225
 [7,]  1.0172048  0.72727990
 [8,]  0.6451366  1.46162702
 [9,] -0.1470898  2.13234195

> B

            [,1]        [,2]
 [1,] -2.0673655 -0.97420449
 [2,] -3.0599788 -0.50683009
 [3,] -2.9598021 -0.33190618
 [4,] -1.8086251 -0.49758487
 [5,] -1.5579480 -0.08444513
 [6,] -1.8939998  1.08460534
 [7,] -1.1790432  0.40687015
 [8,] -0.8490092  1.14671353
 [9,] -0.9704664  1.26558193
[10,] -0.6036790  1.39655898
```

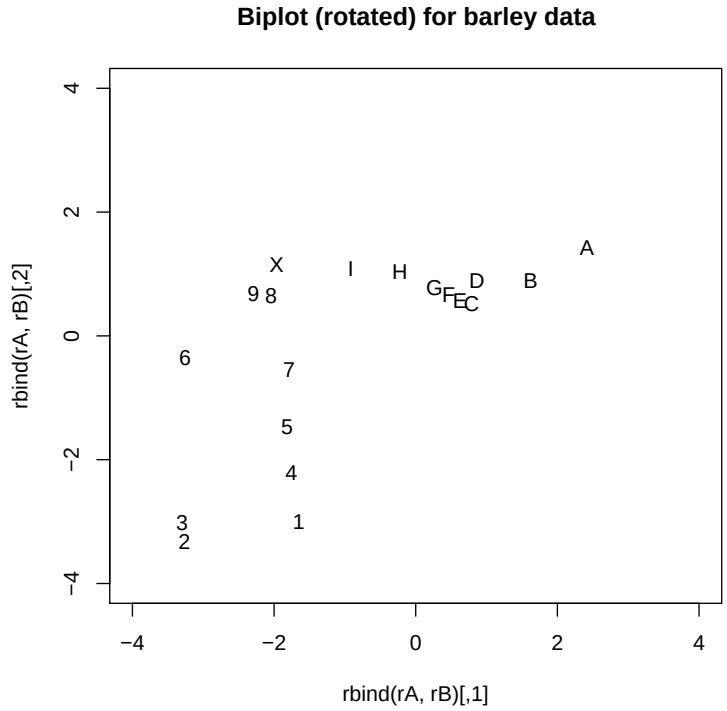
These matrices are essentially the same as in Gabriel (1998). From these the biplot can be produced, for sites $A \ldots I$ and varieties $1 \ldots 9, X$:

```
> plot(rbind(A, B), pch = c(levels(barley$site), levels(barley$variety)),
+     xlim = c(-4, 4), ylim = c(-4, 4), main = "Biplot for barley data")
```



The product of the matrices `A` and `B` is unaffected by rotation or reciprocal scaling along either axis, so we can rotate the data so that the points for the sites are roughly parallel to the horizontal axis and the points for the varieties are roughly parallel to the vertical axis. In addition, we can scale the data so that points for the sites are about the line one unit about the horizontal axis, roughly

```
> a <- pi/5
> rotation <- matrix(c(cos(a), sin(a), -sin(a), cos(a)), 2, 2,
+     byrow = TRUE)
> rA <- (2 * A/3) %*% rotation
> rB <- (3 * B/2) %*% rotation
> plot(rbind(rA, rB), pch = c(levels(barley$site), levels(barley$variety)),
+     xlim = c(-4, 4), ylim = c(-4, 4), main = "Biplot (rotated) for barley data")
```



In the original biplot, the co-ordinates for the sites and varieties were given by the rows of A and B respectively, i.e

$$\begin{aligned} \alpha_i^T &= \sqrt{(d)}(u_{1i}, u_{2i}) \\ \beta_j^T &= \sqrt{(d)}(v_{1j}, v_{2j}) \end{aligned}$$

The rotated and scaled biplot suggests the simpler model

$$\begin{aligned} \alpha_i^T &= (\gamma_i, 1) \\ \beta_j^T &= (\delta_j, \tau_j) \end{aligned}$$

which implies the following model for the logits of the leaf blotch incidence:

$$\alpha_i^T \beta_j = \gamma_i \delta_j + \tau_j.$$

Gabriel (1998) describes this as a double additive model, which we can fit as follows:

```
> 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)
```

```
Initialising
Running start-up iterations..
Running main iterations.....................
Done
```

Comparing the chi-squared statistics, we see that the double additive model is an adequate model for the leaf blotch incidence:

```
> biplotModChiSq <- sum(residuals(biplotModel, type = "pearson")^2)
> doubleAddChiSq <- sum(residuals(doubleAdditive, type = "pearson")^2)
> c(doubleAddChiSq - biplotModChiSq, doubleAdditive$df.residual -
+     biplotModel$df.residual)
```

```
[1]  9.513782 15.000000
```

6.6 Stereotype Model

The stereotype model was proposed by Anderson (1984) for ordered categorical data. It is a linear logistic model, in which there is assumed to be a common relationship between the response and the covariates in the model, but the scale of this association varies between categories and there is an additional category main effect or category-specific intercept:

$$\log \mu_{ic} = \beta_{0c} + \gamma_c \sum_r \beta_r x_{ir}.$$

This model can be estimated by re-expressing the categorical data as counts and using a *gnm* model with a log link and poisson variance function. The *gnm* package includes the utility function `expandCategorical` to facilitate the required data processing.

For example, the `backPain` data set from Anderson (1984) describes the progress of patients with back pain. The data set consists of an ordered factor quantifying the progress of each patient, and three prognostic variables. These data can be re-expressed as follows:

```
> set.seed(1)
> data(backPain)
> backPain[1:2, ]
```

```
  x1 x2 x3               pain
1  1  1  1               same
2  1  1  1 marked.improvement
```

```
> backPainLong <- expandCategorical(backPain, "pain")
> backPainLong[1:12, ]
```

```
    x1 x2 x3                 pain count id
1    1  1  1                worse     0  1
1.1  1  1  1                 same     1  1
1.2  1  1  1   slight.improvement     0  1
1.3  1  1  1 moderate.improvement     0  1
1.4  1  1  1   marked.improvement     0  1
1.5  1  1  1      complete.relief     0  1
2    1  1  1                worse     0  2
2.1  1  1  1                 same     0  2
2.2  1  1  1   slight.improvement     0  2
2.3  1  1  1 moderate.improvement     0  2
2.4  1  1  1   marked.improvement     1  2
2.5  1  1  1      complete.relief     0  2
```

We can now fit the stereotype model to these data:

```
> oneDimensional <- gnm(count ~ pain + Mult(pain - 1, x1 + x2 +
+     x3 - 1), eliminate = id, family = "poisson", data = backPainLong)
```

```
Initialising
Running start-up iterations..
Running main iterations.............
Done
```

```
> oneDimensional
```

```
Call:
gnm(formula = count ~ pain + Mult(pain - 1, x1 + x2 + x3 - 1),
    eliminate = id, family = "poisson", data = backPainLong)


Coefficients of interest:
```

```
                              painsame                   painslight.improvement
                               16.1578                                  15.6848
                painmoderate.improvement                   painmarked.improvement
                               12.4555                                  19.9140
                     paincomplete.relief                 Mult1.Factor1.painworse
                               21.6653                                  -0.2675
                  Mult1.Factor1.painsame    Mult1.Factor1.painslight.improvement
                                1.6657                                   1.5614
Mult1.Factor1.painmoderate.improvement    Mult1.Factor1.painmarked.improvement
                                1.1045                                   2.1356
     Mult1.Factor1.paincomplete.relief                       Mult1.Factor2.x1
                                2.5318                                  -1.9190
                        Mult1.Factor2.x2                       Mult1.Factor2.x3
                               -1.1007                                  -0.9691

Deviance:            303.1003
Pearson chi-squared: 433.3727
Residual df:         493
```

using *eliminate* to handle the `id` factor so that these structural parameters do not appear in the model summaries. This model is one dimensional since it involves only one function of $\mathbf{x} = (x1, x2, x3)$. We can compare this model to one with category-specific coefficents of the x variables, as may be used for a qualitative categorical response:

```
> threeDimensional <- gnm(count ~ pain + pain:(x1 + x2 + x3), eliminate = id,
+     family = "poisson", data = backPainLong)

Initialising
Running main iterations.....................................................
.....................................................
Done

> threeDimensional

Call:
gnm(formula = count ~ pain + pain:(x1 + x2 + x3), eliminate = id,
    family = "poisson", data = backPainLong)


Coefficients of interest:
                   painsame       painslight.improvement
                    31.3062                      30.9255
   painmoderate.improvement       painmarked.improvement
                    27.8080                      35.0086
        paincomplete.relief                  painworse:x1
                    37.4566                       8.2129
                painsame:x1    painslight.improvement:x1
                    -2.9470                      -2.6174
painmoderate.improvement:x1    painmarked.improvement:x1
                    -2.3539                      -4.1771
     paincomplete.relief:x1                  painworse:x2
                    -4.6890                       0.2552
                painsame:x2    painslight.improvement:x2
                    -2.4188                      -2.2961
painmoderate.improvement:x2    painmarked.improvement:x2
                    -1.4168                      -2.5886
     paincomplete.relief:x2                  painworse:x3
                    -3.0197                      -1.9924
```

```
               painsame:x3    painslight.improvement:x3
                   -3.1478                     -3.2844
painmoderate.improvement:x3    painmarked.improvement:x3
                   -2.7386                     -3.6838
     paincomplete.relief:x3
                   -4.9330

Deviance:            299.0153
Pearson chi-squared: 443.0034
Residual df:         485
```

This model has the maximum dimensionality of three (as determined by the number of covariates). To obtain the log-likelihoods as reported in Anderson (1984) we need to adjust for the extra parameters introduced to formulate the models as Poisson models. We write a simple function to do this and compare the log-likelihoods of the one dimensional model and the three dimensional model:

```
> logLikMultinom <- function(model) {
+     object <- get(model)
+     if (inherits(object, "gnm")) {
+         l <- logLik(object) + object$eliminate
+         c(nParameters = attr(l, "df") - object$eliminate, logLikelihood = l)
+     }
+     else c(nParameters = object$edf, logLikelihood = -deviance(object)/2)
+ }
> t(sapply(c("oneDimensional", "threeDimensional"), logLikMultinom))

                 nParameters logLikelihood
oneDimensional            12     -151.5501
threeDimensional          20     -149.5076
```

which show that the oneDimensional model is adequate.

To obtain estimates of the category-specific multipliers in the stereotype model, we need to constrain both the location and the scale of these parameters. The latter constraint can be imposed by fixing the slope of one of the covariates in the second multiplier to 1, which may be achieved by specifying the covariate as an offset:

```
> summary(oneDimensional)

Call:
gnm(formula = count ~ pain + Mult(pain - 1, x1 + x2 + x3 - 1),
    eliminate = id, family = "poisson", data = backPainLong)


Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9708  -0.6506  -0.4438  -0.1448   2.1385

Coefficients of interest:
                                      Estimate Std. Error z value Pr(>|z|)
painsame                               16.1578     6.5741   2.458 0.013980
painslight.improvement                 15.6848     6.5274   2.403 0.016265
painmoderate.improvement               12.4555     6.4312   1.937 0.052777
painmarked.improvement                 19.9140     6.4975   3.065 0.002178
paincomplete.relief                    21.6653     6.5571   3.304 0.000953
Mult1.Factor1.painworse                -0.2675         NA      NA       NA
Mult1.Factor1.painsame                  1.6657         NA      NA       NA
Mult1.Factor1.painslight.improvement    1.5614         NA      NA       NA
Mult1.Factor1.painmoderate.improvement  1.1045         NA      NA       NA
```

```
Mult1.Factor1.painmarked.improvement     2.1356         NA       NA       NA
Mult1.Factor1.paincomplete.relief        2.5318         NA       NA       NA
Mult1.Factor2.x1                        -1.9190         NA       NA       NA
Mult1.Factor2.x2                        -1.1007         NA       NA       NA
Mult1.Factor2.x3                        -0.9691         NA       NA       NA

(Dispersion parameter for poisson family taken to be 1)

Std. Error is NA where coefficient has been constrained or is unidentified

Residual deviance: 303.1 on 493 degrees of freedom
AIC: 731.1

Number of iterations: 15

> oneDimensional <- gnm(count ~ pain + Mult(pain - 1, offset(x1) +
+     x2 + x3 - 1), eliminate = id, family = "poisson", data = backPainLong)

Initialising
Running start-up iterations..
Running main iterations..............
Done

> summary(oneDimensional)

Call:
gnm(formula = count ~ pain + Mult(pain - 1, offset(x1) + x2 +
    x3 - 1), eliminate = id, family = "poisson", data = backPainLong)


Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9708  -0.6506  -0.4438  -0.1448   2.1385

Coefficients of interest:
                                     Estimate Std. Error z value Pr(>|z|)
painsame                              16.1578     6.5742   2.458 0.013980
painslight.improvement                15.6848     6.5274   2.403 0.016265
painmoderate.improvement              12.4556     6.4312   1.937 0.052777
painmarked.improvement                19.9140     6.4976   3.065 0.002178
paincomplete.relief                   21.6653     6.5571   3.304 0.000953
Mult1.Factor1.painworse                1.3644         NA      NA       NA
Mult1.Factor1.painsame                -2.3453         NA      NA       NA
Mult1.Factor1.painslight.improvement  -2.1453         NA      NA       NA
Mult1.Factor1.painmoderate.improvement -1.2685        NA      NA       NA
Mult1.Factor1.painmarked.improvement  -3.2472         NA      NA       NA
Mult1.Factor1.paincomplete.relief     -4.0074         NA      NA       NA
Mult1.Factor2.x2                       0.5736     0.2178   2.633 0.008451
Mult1.Factor2.x3                       0.5050     0.2431   2.077 0.037807

(Dispersion parameter for poisson family taken to be 1)

Std. Error is NA where coefficient has been constrained or is unidentified

Residual deviance: 303.1 on 493 degrees of freedom
AIC: 731.1
```

```
Number of iterations: 15
```

The location of the category-specific multipliers can constrained by setting one of the parameters to zero, either through the *constrain* argument of `gnm` or with `getContrasts`:

```
> getContrasts(oneDimensional, 6:11)

  id6   id7   id8   id9  id10  id11
   NA  TRUE FALSE FALSE FALSE FALSE
Note: not all of the specified contrasts in this set are estimable
[[1]]
    Estimate Std. Error
id6        0   0.000000
id7        0   1.414214
```

giving the required estimates.

6.7 Exponential and sum-of-exponentials models for decay curves

A class of nonlinear functions which arise in various application contexts — a notable one being pharmacokinetic studies – involves one or more *exponential decay* terms. For example, a simple decay model with additive error is

$$y = \alpha + \exp(\beta + \gamma x) + e \tag{1}$$

(with $\gamma < 0$), while a more complex ('sum of exponentials') model might involve two decay terms:

$$y = \alpha + \exp(\beta_1 + \gamma_1 x) + \exp(\beta_2 + \gamma_2 x) + e. \tag{2}$$

Estimation and inference with such models are typically not straightforward, partly on account of multiple local maxima in the likelihood (e.g., Seber and Wild, 1989, Ch.3). We illustrate the difficulties here, with a couple of artificial examples. These examples will make clear the value of making repeated calls to `gnm`, in order to use different, randomly-generated parameterizations and starting values and thus improve the chances of locating both the global maximum and all local maxima of the likelihood.

6.7.1 Example: single exponential decay term

Let us first construct some data from model (1). For our illustrative purposes here, we will use *noise-free* data, i.e., we fix the variance of e to be zero; for the other parameters we will use $\alpha = 0, \beta = 0, \gamma = -0.1$.

```
> x <- 1:100
> y <- exp(-x/10)
> set.seed(1)
> saved.fits <- list()
> for (i in 1:100) saved.fits[[i]] <- gnm(y ~ Mult(Exp(x)), verbose = FALSE)
> summary(sapply(saved.fits, deviance))

     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
7.795e-16 8.099e-16 9.753e-16 1.590e+00 3.613e+00 3.613e+00
```

The `saved.fits` object thus contains the results of 100 calls to `gnm`, each using a different, randomly-generated starting value for the vector of parameters (α, β, γ). The median deviance (in this case, residual sum of squares) among the 100 fits is essentially zero: in fact, 56 of these 100 fits reproduce the data exactly, to machine accuracy. The remaining 44 fits are all identical to one another, but they are far from globally optimal, with residual sum of squares 3.61: they result from divergence of $\hat{\gamma}$ to $+\infty$, and correspondingly of $\hat{\beta}$ to $-\infty$, such that the fitted 'curve' is in fact just a constant, with level equal to $\bar{y} = 0.09508$. For example, the very first of the 100 fits is of this kind:

```
> saved.fits[[1]]
```

```
Call:
gnm(formula = y ~ Mult(Exp(x)), verbose = FALSE)


Coefficients:
              (Intercept)  Mult1.Factor1.(Intercept)
                9.508e-02                 -7.527e+02
          Mult1.Factor1.x
               -1.073e+03

Deviance:            3.612654
Pearson chi-squared: 3.612654
Residual df:         99
```

The use of repeated calls to gnm, as here, allows the local and global maxima to be easily distinguished.

6.7.2 Example: sum of two exponentials

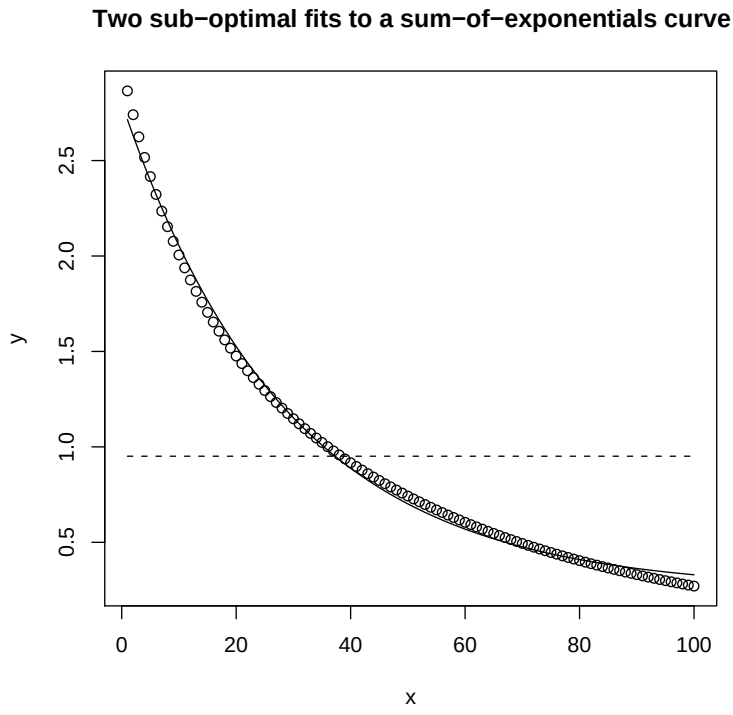
We can conduct a similar exercise based on the more complex model (2):

```
> x <- 1:100
> y <- exp(-x/10) + 2 * exp(-x/50)
> set.seed(1)
> saved.fits <- list()
> for (i in 1:100) saved.fits[[i]] <- gnm(y ~ Mult(Exp(x), multiplicity = 2),
+     verbose = FALSE)
> unlist(sapply(saved.fits, deviance))

 [1] 1.589496e-01 3.407062e-16 3.953716e-15 2.634119e-15 1.589496e-01
 [6] 4.164390e+01 4.093554e-13 4.285232e-16 3.155106e-15 8.427057e-15
[11] 8.471544e-15 1.589496e-01 1.589496e-01
```

In this instance, only 13 of the 100 calls to gnm have successfully located a local maximum of the likelihood: in the remaining 87 cases the starting values generated were such that numerical problems resulted, and the fitting algorithm was abandoned (giving a NULL result). Among the 13 'successful' fits, it is evident that there are three distinct solutions (with respective residual sums of squares equal to 0.1589, 41.6, and essentially zero — the last of these, the exact fit to the data, having been found 8 times out of the above 13). The two non-optimal local maxima here correspond to the best fit with a single exponential (which has residual sum of squares 0.1589) and to the fit with no dependence at all on x (residual sum of squares 41.6), as we can see by comparing with:

```
> singleExp <- gnm(y ~ Mult(Exp(x)), start = c(NA, NA, -0.1), verbose = FALSE)
> singleExp

Call:
gnm(formula = y ~ Mult(Exp(x)), start = c(NA, NA, -0.1), verbose = FALSE)


Coefficients:
              (Intercept)  Mult1.Factor1.(Intercept)
                  0.25007                    0.93664
          Mult1.Factor1.x
                 -0.03465

Deviance:            0.1589496
Pearson chi-squared: 0.1589496
Residual df:         97
```

```
> meanOnly <- gnm(y ~ 1, verbose = FALSE)
> meanOnly

Call:
gnm(formula = y ~ 1, verbose = FALSE)


Coefficients:
(Intercept)
     0.9511

Deviance:            41.6439
Pearson chi-squared: 41.6439
Residual df:         99

> plot(x, y, main = "Two sub-optimal fits to a sum-of-exponentials curve")
> lines(x, fitted(singleExp))
> lines(x, fitted(meanOnly), lty = "dashed")
```



In this example, it is clear that even a small amount of noise in the data would make it practically impossible to distinguish between competing models containing one and two exponential-decay terms.

In summary: the default gnm setting of randomly-chosen starting values is useful for identifying multiple local maxima in the likelihood; and reasonably good starting values are needed if the global maximum is to be found. In the present example, knowing that γ_1 and γ_2 should both be small and negative, we might perhaps have tried

```
> gnm(y ~ Mult(Exp(x), multiplicity = 2), start = c(NA, NA, -0.1,
+     NA, -0.1), verbose = FALSE)

Call:
gnm(formula = y ~ Mult(Exp(x), multiplicity = 2), start = c(NA,
    NA, -0.1, NA, -0.1), verbose = FALSE)
```

```
Coefficients:
              (Intercept)  Mult1.Factor1.(Intercept)
                1.773e-07                 -4.064e-07
          Mult1.Factor1.x  Mult2.Factor1.(Intercept)
               -1.000e-01                  6.931e-01
          Mult2.Factor1.x
               -2.000e-02

Deviance:            6.690625e-15
Pearson chi-squared: 6.690625e-15
Residual df:         95
```

which reliably yields the (globally optimal) perfect fit to the data.

A User-level Functions

We list here, for easy reference, all of the user-level functions in the *gnm* package. For full documentation see the package help pages.

Model Fitting	
`gnm`	fit generalized nonlinear models
Model Specification	
`Diag`	create factor differentiating diagonal elements
`Symm`	create symmetric interaction of factors
`Topo`	create 'topological' interaction factors
`Mult`	specify a multiplicative interaction in a `gnm` formula
`Exp`	specify an exponentiated constituent multiplier in a `Mult` term
`Nonlin`	specify a special nonlinear term in a `gnm` formula
`Dref`	gnm plug-in function to fit diagonal reference terms
`MultHomog`	gnm plug-in function to fit multiplicative interactions with homogeneous effects
`wedderburn`	specify the Wedderburn quasi-likelihood family
Methods and Accessor Functions	
summary.gnm	summarize *gnm* fits
`getContrasts`	estimate contrasts and their standard errors for parameters in a gnm model
`checkEstimable`	check whether one or more parameter combinations in a *gnm* model is identified
`exitInfo`	print numerical details of last iteration when `gnm` has not converged
`residSVD`	multiplicative approximation of model residuals
`se`	get standard errors of linear parameter combinations in *gnm* models
`termPredictors`	(*generic*) extract term contributions to predictor
Auxiliary Functions	
`asGnm`	coerce an object of class *lm* or *glm* to class *gnm*
`expandCategorical`	expand a data frame by re-expressing categorical data as counts
`getModelFrame`	get the model frame in use by `gnm`
`MPinv`	Moore-Penrose pseudoinverse of a real-valued matrix
`qrSolve`	Minimum-length solution of a linear system

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