

# Generalized Nonlinear Models in R

Heather Turner

RSE Fellow/Associate Professor  
Department of Statistics, University of Warwick, UK

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# Preface

Generalized linear models (logit/probit regression, log-linear models, etc.) are now part of the standard empirical toolkit.

Sometimes the assumption of a *linear* predictor is unduly restrictive.

This short course shows how *generalized nonlinear models* may be viewed as a unified class, and how to work with such models in R.

# Plan

Getting Started

Association Models

Other Multiplicative Models

Other Specialized Models

# Section 1

## Getting Started

## Linear models:

e.g.,

$$E(y_i) = \beta_0 + \beta_1 x_i + \beta_2 z_i$$

$$E(y_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2$$

$$E(y_i) = \beta_0 + \gamma_1 \delta_1 x_i + \exp(\theta_2) z_i$$

In general:

$$E(y_i) = \eta_i(\beta) = \text{linear function of unknown parameters}$$

Also assumes variance essentially constant:

$$\text{var}(y_i) = \phi a_i$$

with  $a_i$  known (often  $a_i \equiv 1$ ).

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# Generalized linear models

Problems with linear models in many applications:

- ▶ range of  $y$  is restricted (e.g.,  $y$  is a count, or is binary, or is a duration)
- ▶ effects are not additive
- ▶ variance depends on mean (e.g., large mean  $\Rightarrow$  large variance)

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## └ Getting Started

## └ Linear and generalized linear models

Generalized linear model:

$$g[E(y_i)] = \eta_i = \text{linear function of unknown parameters}$$

$$\text{var}(y_i) = \phi a_i V(\mu_i)$$

with the functions  $g$  (link function) and  $V$  (variance function) known.

## └ Getting Started

## └ Linear and generalized linear models

## Examples:

- ▶ binary logistic regressions
- ▶ rate models for event counts
- ▶ log-linear models for contingency tables (including multinomial logit models)
- ▶ multiplicative models for durations and other positive measurements
- ▶ hazard models for event history data

etc., etc.

## └ Getting Started

## └ Linear and generalized linear models

e.g., binary logistic regression:

$$y_i = \begin{cases} 1 & \text{event happens} \\ 0 & \text{otherwise} \end{cases}$$

$\mu_i = E(y_i)$  = probability that event happens

$$\text{var}(y_i) = \mu_i(1 - \mu_i)$$

Variance is completely determined by mean.

Common link functions are logit, probit, and (complementary) log-log, all of which transform constrained  $\mu$  into unconstrained  $\eta$ .

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e.g., multiplicative (i.e., log-linear) rate model for event counts.

‘Exposure’ for observation  $i$  is a fixed, known quantity  $t_i$ .

Rate model:

$$E(y_i) = t_i \exp(\beta_0) \exp(\beta_1 x_i) \exp(\beta_2 z_i)$$

i.e.,

$$\log E(y_i) = \log t_i + \beta_0 + \beta_1 x_i + \beta_2 z_i$$

— effects are rate multipliers.

Variance is typically taken as the Poisson-like function  $V(\mu) = \mu$   
(variance is equal to, or is proportional to, the mean).



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## └ Getting Started

## └ Generalized nonlinear models

Generalized linear:  $\eta = g(\mu)$  is a linear function of the unknown parameters. Variance depends on mean through  $V(\mu)$ .

Generalized *nonlinear*: still have  $g$  and  $V$ , but now relax the linearity assumption.

Many important aspects remain unchanged:

- ▶ fitting by maximum likelihood or quasi-likelihood
- ▶ analysis of deviance to assess significance of effects
- ▶ diagnostics based on residuals, etc.

But technically more difficult [essentially because  $\partial\eta/\partial\beta = X$  becomes  $\partial\eta/\partial\beta = X(\beta)$ ].

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But technically more difficult [essentially because  $\partial\eta/\partial\beta = X$  becomes  $\partial\eta/\partial\beta = X(\beta)$ ].

Some practical consequences of the technical difficulties:

- ▶ automatic detection and elimination of redundant parameters is very difficult — it's no longer just a matter of linear algebra
- ▶ automatic generation of good starting values for ML fitting algorithms is hard
- ▶ great care is needed in cases where the likelihood has more than one maximum (which cannot happen in the linear case).

## Some motivation: structured interactions

GNMs are not exclusively about structured interactions, but many applications are of this kind.

A classic example is log-linear models for structurally-square contingency tables (e.g., pair studies, before-after studies, etc.).

Pairs are classified twice, into row and column of a table of counts.

The independence model is

$$\log E(y_{rc}) = \theta + \beta_r + \gamma_c$$

or with **glm**

```
glm(y ~ row + col, family = poisson)
```

Some standard (generalized linear) models for departure from independence are

- ▶ quasi-independence,

```
y ~ row + col + Diag(row, col)
```

- ▶ quasi-symmetry,

```
y ~ row + col + Symm(row, col)
```

- ▶ symmetry,

```
y ~ Symm(row, col)
```

Functions **Diag** and **Symm** are provided by the **gnm** package along with the function **Topo** for fully-specified *topological* association structures, see ?Topo.

## Row-column association

The uniform association model (for ordered categories) has

$$\log E(y_{rc}) = \beta_r + \gamma_c + \delta u_r v_c$$

with the  $u_r$  and  $v_c$  defined as fixed, equally-spaced scores for the rows and columns.

A natural generalization is to allow the *data* to determine the scores (Goodman, 1979). This can be done either heterogeneously,

$$\log E(y_{rc}) = \beta_r + \gamma_c + \phi_r \psi_c$$

or (in the case of a structurally square table) homogeneously,

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## Introduction to the **gnm** package

The **gnm** package aims to provide a unified computing framework for specifying, fitting and criticizing generalized nonlinear models in R.

The central function is **gnm**, which is designed with the same interface as **glm**.

Since generalized linear models are included as a special case, the **gnm** function can be used in place of **glm**, and will give equivalent results.

For the special case  $g(\mu) = \mu$  and  $V(\mu) = 1$ , the **gnm** fit is equivalent to an **nls** fit.

## Nonlinear model terms

Nonlinear model terms are specified in model formulae using functions of class `"nonlin"`.

These functions specify the term structure, possibly also labels and starting values.

There are a number of `"nonlin"` functions provided by **gnm**. Some of these specify basic mathematical functions of predictors, e.g. heterogeneous row and column scores

$$\phi_r \psi_c$$

are specified as `Mult(row, col)`.

Other basic `"nonlin"` functions include **Exp** and **Inv**.

## Specialized "nonlin" functions

There are two specialized "nonlin" functions provided by **gnm**

**MultHomog**: for homogeneous row and column scores, as in

$$\phi_r \phi_c$$

specified as `MultHomog(row, col)`

**Dref**: 'diagonal reference' dependence on a square classification,

$$w_1 \gamma_r + w_2 \gamma_c$$

(Sobel, 1981, 1985) specified as `Dref(row, col)`

Any (differentiable) nonlinear term can be specified by nesting existing "nonlin" functions or writing a custom "nonlin" function.

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## Over-parameterization

The `gnm` function makes no attempt to remove redundant parameters from nonlinear terms. This is deliberate.

As a consequence, fitted models are typically represented in a way that is *over-parameterized*: not all of the parameters are 'estimable' (i.e., 'identifiable', 'interpretable').

A simple example:

$$\phi_r \psi_c$$

is equivalent to

$$\phi_r^* \psi_c^* = (2\phi_r)(\psi_c/2)$$

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## Practical I

1. Load the **gnm** package. This provides the `occupationalStatus` data set, which is a contingency table classified by the occupational status of fathers (`origin`) and their sons (`destination`).
2. Use the generic function `plot` to create a mosaic plot of the table. Print `occupationalStatus` to see the cell frequencies represented by the plot.
3. If a table is passed to the `data` argument of `gnm`, it will be converted to a data frame with a column for each of the row and column factors and a column for the frequencies named `Freq`.  
  
Use `gnm` to fit an independence model to these data (see p13), assigning the result to a suitable name. Print this object.

4. Type `?plot.gnm` to open the help page on the `gnm` method for the `plot` function. Find out how to use `plot` to create a plot of residuals vs. fitted values and do this for the independence model. The poor fit should be very apparent!
5. Load the **vcdExtra** package. This provides the generic function `mosaic`, which has a method for `"gnm"` objects. Use this to visualize the goodness-of-fit of the independence model across the contingency table.
6. Fit a row-column association model with a homogeneous multiplicative interaction between origin and destination (see p15, p18). Check the fit with `mosaic`. Investigate the effect of modelling the diagonal elements separately, by adding `Diag(origin, destination)`.

7. Keeping the Diag term in the model, use `coef` to access the coefficients and assign the result. Re-run the model fit and assign the coefficients of the re-fitted model to another name. Compare the coefficients side-by-side using `cbind`. Which parameters have been automatically constrained to zero? Which coefficients are the same in both models?
8. Standard errors can only be obtained for estimable parameters. Use `summary` to confirm which parameters are estimable in the current model. The homogeneous scores can be identified by setting one of them to zero. Re-fit the model using the argument `constrain = "MultHomog(origin, destination)1"`. Compare the summary of the constrained model to the summary of the unconstrained model.

## Section 2

### Association Models

## RC(M) Models

The row-column association models introduced in Section I are special cases of the RC(M) model:

$$\log(\mu_{rc}) = \alpha_r + \beta_c + \sum_{k=1}^K \sigma_k \phi_{kr} \psi_{kc},$$

We will use this class of models to further explore the issues of identifiability, parameterization and obtaining standard errors.

## RC(1) with Homogeneous Scores

For the RC(1) model with homogeneous scores, we have

$$\begin{aligned}\alpha_r + \beta_c + \phi_r \phi_c &= -k^2 + (\alpha_r - k\phi_r) + (\beta_c - k\phi_c) + (\phi_r + k)(\phi_c + k) \\ &= \alpha_r^* + \beta_c^* + \phi_r^* \phi_c^*\end{aligned}$$

Constraining one of the  $\phi_r$  to a constant fixes the location of the homogeneous scores so the parameterization is unique.

Let  $k = -\phi_1$ , then

$$\begin{aligned}\phi_1^* &= \phi_1 - \phi_1 = 0 \\ \phi_r^* &= \phi_r - \phi_1 \quad r \neq 1\end{aligned}$$

So constraining one parameter to zero is equivalent to fitting the unconstrained model, then estimating simple contrasts.



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So constraining one parameter to zero is equivalent to fitting the unconstrained model, then estimating simple contrasts.

## Example: Occupational Status Data

As in Practical I, we fit a homogeneous row-column association model, separating out the diagonal effects, then use `getContrasts`

```
RCh <- gnm(Freq ~ origin + destination + Diag(origin, destination) +
            MultHomog(origin, destination), family = poisson,
            data = occupationalStatus, verbose = FALSE)
getContrasts(RCh, pickCoef(RCh, "MultHomog"))
```

##	estimate	SE	quasiSE	quasiVar
## MultHomog(origin, destination)1	0.000	0.000	0.1573	0.02473
## MultHomog(origin, destination)2	0.218	0.235	0.1190	0.01416
## MultHomog(origin, destination)3	0.816	0.167	0.0611	0.00374
## MultHomog(origin, destination)4	1.400	0.160	0.0518	0.00269
## MultHomog(origin, destination)5	1.418	0.172	0.0798	0.00637
## MultHomog(origin, destination)6	1.929	0.157	0.0360	0.00129
## MultHomog(origin, destination)7	2.345	0.173	0.0796	0.00634
## MultHomog(origin, destination)8	2.589	0.189	0.1095	0.01200

## └ Association Models

## └ RC(1) with Homogeneous Scores

Standard errors will change depending on the reference category:

```
getContrasts(RCh, pickCoef(RCh, "MultHomog"), ref = "last")
```

##		estimate	SE	quasiSE	quasiVar
##	MultHomog(origin, destination)1	-2.589	0.189	0.1573	0.02473
##	MultHomog(origin, destination)2	-2.371	0.158	0.1190	0.01416
##	MultHomog(origin, destination)3	-1.773	0.120	0.0611	0.00374
##	MultHomog(origin, destination)4	-1.189	0.116	0.0518	0.00269
##	MultHomog(origin, destination)5	-1.171	0.131	0.0798	0.00637
##	MultHomog(origin, destination)6	-0.660	0.116	0.0360	0.00129
##	MultHomog(origin, destination)7	-0.244	0.158	0.0796	0.00634
##	MultHomog(origin, destination)8	0.000	0.000	0.1095	0.01200

*Quasi standard errors* allow the calculation of an approximate standard error for *any* contrast; they are independent of the choice of reference category. For the theory see Firth and de Menezes (2004).

## RC(1) with Heterogeneous Scores

Now since, for example,

$$\begin{aligned}\alpha_r + \beta_r + \phi_r \psi_c &= \alpha_r + (\beta_r - \psi_c) + (\phi_r + 1) \psi_c \\ &= \alpha_r + \beta_r + (2\phi_r)(\psi_c/2)\end{aligned}$$

we need to constrain both the location and scale.

A standard convention is to constrain the scores so that

$$\begin{aligned}\sum_r \phi_r \pi_r &= \sum_c \psi_c \pi_c = 0 \\ \text{and } \sum_r \phi_r^2 \pi_r &= \sum_c \psi_c^2 \pi_c = 1\end{aligned}$$

where  $\pi_r$  and  $\pi_c$  are the row and column probabilities respectively. The full interaction is then given by  $\sigma \phi_r \psi_c$ , where  $\sigma > 0$  is the *intrinsic association parameter*.

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## Example: Mental Health Data

1660 residents of Manhattan cross-classified by child's mental impairment and parents' socioeconomic status (Agresti, 2013).

```
xtabs(count ~ SES + MHS, mentalHealth)
```

```
##      MHS
## SES well mild moderate impaired
##  A   64   94      58      46
##  B   57   94      54      40
##  C   57  105      65      60
##  D   72  141      77      94
##  E   36   97      54      78
##  F   21   71      54      71
```

We require treatment contrasts for the RC(1) model

```
mentalHealth$MHS <- C(mentalHealth$MHS, treatment)
mentalHealth$SES <- C(mentalHealth$SES, treatment)
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## └ Association Models

## └ RC(1) with Heterogeneous Scores

We fit the RC(1) using the `ofInterest` argument to specify that only the parameters of the multiplicative interaction should be shown in model summaries.

```
RC <- gnm(count ~ SES + MHS + Mult(SES, MHS), family = poisson,
          data = mentalHealth, verbose = FALSE, ofInterest = "Mult")
coef(RC)
```

```
## Coefficients of interest:
##           Mult(., MHS).SESA           Mult(., MHS).SESB
##           -0.38132           -0.38444
##           Mult(., MHS).SESC           Mult(., MHS).SESD
##           -0.12790           0.00821
##           Mult(., MHS).SESE           Mult(., MHS).SESF
##           0.34440           0.62060
##           Mult(SES, .).MHSwell       Mult(SES, .).MHSmild
##           -0.82733           -0.07881
##           Mult(SES, .).MHSmoderate Mult(SES, .).MHSimpaired
##           0.05627           0.67798
```

## └ Association Models

## └ RC(1) with Heterogeneous Scores

The constraints that the weighted sum of column scores should sum to zero and the weighted sum of squares should sum to one are met by the scaled contrasts

$$\frac{\psi_c - \sum_c \psi_c \pi_c}{\sqrt{\sum_c \pi_c (\psi_c - \sum_c \psi_c \pi_c)^2}}$$

These contrasts can be obtained with `getContrasts` as follows:

```
colProbs <- with(mentalHealth, tapply(count, MHS, sum) / sum(count))
colScores <- getContrasts(RC, pickCoef(RC, "[.]MHS"), ref = colProbs,
                          scaleRef = colProbs, scaleWeights = colProbs)

colScores
```

##	Estimate	Std. Error
## Mult(SSES, .).MHSwell	-1.678	0.194
## Mult(SSES, .).MHSmild	-0.140	0.200
## Mult(SSES, .).MHSmoderate	0.137	0.280
## Mult(SSES, .).MHSimpaired	1.414	0.172

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## └ Association Models

## └ RC(1) with Heterogeneous Scores

The row scores are computed in a similar way

```
rowProbs <- with(mentalHealth, tapply(count, SES, sum) / sum(count))
rowScores <- getContrasts(RC, pickCoef(RC, "[.]SES"), ref = rowProbs,
                          scaleRef = rowProbs, scaleWeights = rowProbs)
```

Then the intrinsic association parameter can be computed directly

```
phi <- pickCoef(RC, "[.]SES", value = TRUE)
psi <- pickCoef(RC, "[.]MHS", value = TRUE)
sqrt(sum(rowProbs*(phi - sum(rowProbs*phi))^2)) *
  sqrt(sum(colProbs*(psi - sum(colProbs*psi))^2))

## [1] 0.166
```

Since this value depends on the particular scaling used for the contrasts, it typically not of interest to conduct inference on this parameter directly. The standard error could be obtained, if desired, via the delta method.

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- └ Association Models

- └ RC(2), RC(3), ...

## RC(2), RC(3), ...

Additional multiplicative terms can be added via **instances**, e.g.

```
RC2 <- update(RC, count ~ SES + MHS + instances(Mult(SES, MHS), 2))
```

The sum of the multiplicative terms is a low rank approximation to the full interaction matrix. For the parameters to be identified, the multiplicative terms must be orthogonal to each other. This means constraining the rotation as well as the location and scale.

Decomposing a matrix into a sum of separable matrices (where a separable matrix can be written as the outer product of two vectors) is equivalent to singular value decomposition. Incorporating marginal probability weights is tricky. Furthermore, standard errors can not be directly computed. The **logmult** package helps with both these issues.

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Decomposing a matrix into a sum of separable matrices (where a separable matrix can be written as the outer product of two vectors) is equivalent to singular value decomposition. Incorporating marginal probability weights is tricky. Furthermore, standard errors can not be directly computed. The **logmult** package helps with both these issues.

## Introduction to the `logmult` package

The **logmult** package enhances the **gnm** package by providing a number of functions to support analyses involving log-multiplicative models.

Particular features include

- ▶ wrapper functions for fitting common models, including RC(M)
- ▶ specialized print and plot methods
- ▶ jackknife and bootstrap standard errors

## Example: Mental Health Data Revisited

```
MHtab <- xtabs(count ~ SES + MHS, data = mentalHealth)
rc(MHtab, verbose = FALSE)
```

```
## Call:
## rc(tab = MHtab, verbose = FALSE)
##
## Intrinsic association coefficients:
##   Dim1
## 0.166
##
## Normalized row scores (SES):
##      A      B      C      D      E      F
## 1.112  1.121  0.371 -0.027 -1.010 -1.818
##
## Normalized column scores (MHS):
##      well      mild moderate impaired
## 1.678    0.140   -0.137   -1.414
##
## Normalization weights: marginal
## Dim1 0.57
```

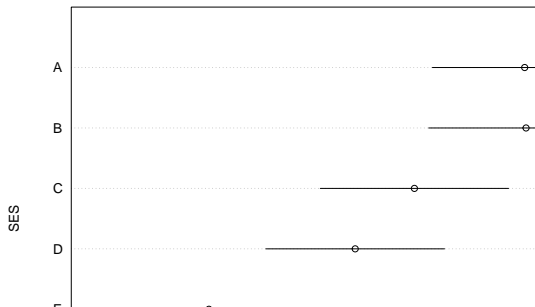
## └ Association Models

## └ Introduction to the logmult package

```

RC <- rc(MHtab, se = "jackknife", verbose = FALSE, ncpus = 1)
# plot(RC, what = "rows", conf.int = 0.95)
row <- RC$assoc$row[1:6,,] * sqrt(RC$assoc$phi[1])
se <- sqrt(diag(RC$assoc$adj.covmats[,1])[1:6])
dotchart(rev(row), xlab = "Row scores", ylab = "SES")
for (i in 1:6){
  segments(x0 = rev(row)[i] + 1.96 * rev(se)[i],
           x1 = rev(row)[i] - 1.96 * rev(se)[i],
           y0 = i, y1 = i)
}

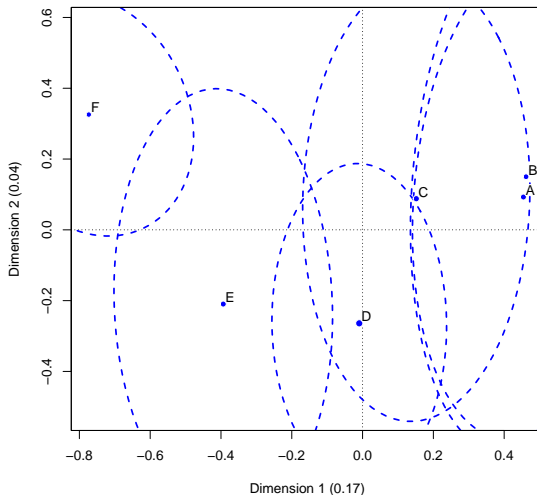
```



## └ Association Models

## └ Introduction to the logmult package

```
RC2 <- rc(MHtab, nd = 2, se = "jackknife", verbose = FALSE, ncpus = 1)
plot(RC2, what = "rows", conf.int = 0.95)
```



## Analysis of Association

An analysis of association compares successive RC(M) models to the independence model.

```
anoas(MHtab, nd=2, verbose = FALSE)
```

```
## Fitting independence model...
```

```
## Fitting model with 1 dimension...
```

```
## Fitting model with 2 dimensions...
```

##	Res.	Df	Res. Dev	Dev./Indep.	(%)	Dissim.	(%)	BIC	AIC	Dev.	Df
## Indep.	15		47.4		100		5.5	-64	17	NA	NA
## RC(1)	8		3.6		8		1.8	-56	-12	-44	-7
## RC(2)	3		0.5		1		0.7	-22	-5	-3	-5

## Other Multiplicative Association Models

The **logmult** package also provides facilities for the following:

- ▶ Models with skew-symmetric terms, either **HMSkew**:

$$\nu_r \omega_c - \omega_r \nu_c$$

or **YMSkew**:

$$\delta_{r < c} \omega_r (\omega_c - \omega_r) - \delta_{c > r} \omega_c (\omega_r - \omega_c)$$

which can replace or supplement RC(M) association terms.

- ▶ RC(M)-L models, an extension of RC(M) to three-way tables
- ▶ The UNIDIFF model, also for three-way tables

Of these, the UNIDIFF model is most commonly used in practice.

## UNIDIFF Model

UNIDIFF models postulate a simplified three-way interaction as follows:

$$\log(\mu_{rct}) = \alpha_{rt} + \beta_{ct} + \exp(\gamma_t)\delta_{rc}$$

This implies a common pattern of log ratios, modulated by a positive constant that is specific to the two-way table at each value of  $t$ .

This model can be specified in `gnm` via

```
unidiff <- gnm(y ~ row:table + col:table + Mult(Exp(table), row:col),  
              family = poisson)
```

Interest focuses of the  $\gamma_t$  parameters, for which simple contrasts are estimable.



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```

Interest focuses of the  $\gamma_t$  parameters, for which simple contrasts are estimable.

## Practical II

1. The `yaish` data set from `gnm` is a 3-way contingency table classified by father's social class (`orig`), son's social class (`dest`) and son's education (`educ`). Remove the last level of `dest` (due to low counts), then put `educ` as the third dimension (as required by `unidiff`).

```
yaish <- as.table(yaish[,,-7])  
yaish <- aperm(yaish, c("orig", "dest", "educ"))
```

2. Fit the UNIDIFF model using the `unidiff` function from `logmult` and print the result. The *layer coefficients* are  $\exp(\gamma_t)$ , with  $\gamma_1$  constrained to zero. The two-way interaction has been constrained s.t.

$$\sum_r \delta_{rc} \pi_r = \sum_c \delta_{rc} \pi_c = 0$$

where  $\pi_r$  and  $\pi_c$  are the marginal probabilities, factoring out an intrinsic association coefficient  $\phi$ . The *layer intrinsic association coefficients* are  $\phi \exp(\gamma_t)$ .

### 3. Plot the layer coefficients with confidence intervals, using

```
plot(model, se.type = "se")
```

This computes confidence intervals for the  $\gamma_t$  parameters, then exponentiates to give the displayed result.

4. Re-fit the UNIDIFF model using `gnm`, setting  $\gamma_1$  to zero with `constrain = "[.]educ1"` (see p40). Use `pickCoef` to select all the  $\gamma_t$  parameters. Exponentiate the result to obtain the layer coefficients returned by `unidiff`.

5. The confidence intervals produced in step 3 assume that the likelihood surface is approximately quadratic around the maximum likelihood solution. We can check if this is the case by profiling the likelihood. Use `profile` to profile the  $\gamma_t$  parameters, assigning the result. Plot this result using `plot`: if the likelihood surface is quadratic, the profile plot will show a straight line.

6. Obtain confidence intervals based on the profile likelihood by passing the profile object to `confint`, assigning the result. Re-plot the layer coefficients as in step 3. Add the confidence intervals based on profile likelihood via

```
segments(1:5+0.1, exp(conf[,1]), 1:5+0.1, exp(conf[,2]), col = "red")
```

and compare.

## Section 3

### Other Multiplicative Models

Several models with multiplicative terms have been proposed outside of the context of association modelling.

Prominent examples include

- ▶ the stereotype model (Anderson, 1984), for ordered categorical response
- ▶ certain Rasch models, for item responses
- ▶ the Lee-Carter model (Lee and Carter, 1992) for mortality data

In some cases the multiplicative term provides a simpler, more interpretable structure, whilst in other cases it provides a simple extension to a more flexible model.

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In some cases the multiplicative term provides a simpler, more interpretable structure, whilst in other cases it provides a simple extension to a more flexible model.



## Stereotype Models

The stereotype model (Anderson, 1984) is suitable for ordered categorical data. It is a special case of the multinomial logistic model:

$$pr(y_i = c | \mathbf{x}_i) = \frac{\exp(\beta_{0c} + \boldsymbol{\beta}_c^T \mathbf{x}_i)}{\sum_r \exp(\beta_{0r} + \boldsymbol{\beta}_r^T \mathbf{x}_i)}$$

in which only the *scale* of the relationship with the covariates changes between categories:

$$pr(y_i = c | \mathbf{x}_i) = \frac{\exp(\beta_{0c} + \gamma_c \boldsymbol{\beta}^T \mathbf{x}_i)}{\sum_r \exp(\beta_{0r} + \gamma_r \boldsymbol{\beta}^T \mathbf{x}_i)}$$

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

## Poisson Trick

The stereotype model can be fitted as a GNM by re-expressing the categorical data as category counts  $Y_i = (Y_{i1}, \dots, Y_{ik})$ .

Assuming a Poisson distribution for  $Y_{ic}$ , the joint distribution of  $Y_i$  is Multinomial( $N_i, p_{i1}, \dots, p_{ik}$ ) conditional on the total count  $N_i$ .

The expected counts are then  $\mu_{ic} = N_i p_{ic}$  and the parameters of the stereotype model can be estimated through fitting

$$\begin{aligned}\log \mu_{ic} &= \log(N_i) + \log(p_{ic}) \\ &= \alpha_i + \beta_{0c} + \gamma_c \sum_r \beta_r x_{ir}\end{aligned}$$

where the “nuisance” parameters  $\alpha_i$  ensure that the multinomial denominators are reproduced exactly, as required.

## └ Other Multiplicative Models

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## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

## Example: Back Pain Data

The backPain data are from an example in Anderson (1984). For 101 patients, 3 prognostic variables are recorded at baseline and their level of back pain is recorded again after 3 weeks.

```
backPain[1:5,]
```

```
##      x1 x2 x3                pain
## 1    1  1  1                same
## 2    1  1  1 marked.improvement
## 3    1  1  1  complete.relief
## 4    1  2  1                same
## 5    1  2  1 slight.improvement
```

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

The function `expandCategorical` converts the categorical data into sets of counts, by default grouping individuals with common covariates.

```
backPainLong <- expandCategorical(backPain, "pain", group = TRUE)
head(backPainLong)
```

##	x1	x2	x3	pain	id	count
## 1	1	1	1	worse	1	0
## 2	1	1	1	same	1	1
## 3	1	1	1	slight.improvement	1	0
## 4	1	1	1	moderate.improvement	1	0
## 5	1	1	1	marked.improvement	1	2
## 6	1	1	1	complete.relief	1	4

Grouping individuals reduces the size of the data set and does not affect comparisons between models.

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Grouping individuals reduces the size of the data set and does not affect comparisons between models.

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

The stereotype model can be fitted to these data as follows

```
stereotype <- gnm(count ~ pain + Mult(pain, x1 + x2 + x3),  
                  eliminate = id, family = poisson,  
                  data = backPainLong, verbose = FALSE)
```

The `eliminate` argument of `gnm` is used to specify that the `id` parameters replace the intercept in the model. This has two benefits:

- ▶ `gnm` exploits the structure of these parameters to estimate them more efficiently
- ▶ these nuisance parameters are excluded from summaries of the model object



## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

We can compare the stereotype model to the multinomial logistic model:

```
logistic <- gnm(count ~ pain + pain:(x1 + x2 + x3),  
                eliminate = id, family = poisson, data = backPainLong)  
anova(stereotype, logistic)
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: count ~ pain + Mult(pain, x1 + x2 + x3) - 1
```

```
## Model 2: count ~ pain + pain:x1 + pain:x2 + pain:x3 - 1
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
```

```
## 1         48         55.9
```

```
## 2         40         51.8   8      4.09    0.85
```

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

In order to make the category-specific multipliers identifiable, we must constrain both the location and scale.

One way to do this is to set the last multiplier to one and fix the coefficient of the first covariate to one. We can do this using `offset` along with the `constrain` and `constrainTo` arguments of `gnm`:

```
stereotype <- update(stereotype,  
  . ~ pain + Mult(pain, offset(x1) + x2 + x3),  
  constrain = "[.]paincomplete.relief",  
  constrainTo = 1)
```

We can (re-)define the coefficients of interest after fitting the model

```
ofInterest(stereotype) <- pickCoef(stereotype, "Mult")
```

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

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```

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

```
parameters(stereotype)
```

```
## Coefficients of interest:
##           Mult(., x2 + x3 + offset(x1)).painworse
##                                     6.372
##           Mult(., x2 + x3 + offset(x1)).painsame
##                                     2.662
##   Mult(., x2 + x3 + offset(x1)).painslight.improvement
##                                     2.862
## Mult(., x2 + x3 + offset(x1)).painmoderate.improvement
##                                     3.739
##   Mult(., x2 + x3 + offset(x1)).painmarked.improvement
##                                     1.760
##           Mult(., x2 + x3 + offset(x1)).paincomplete.relief
##                                     1.000
##           Mult(pain, . + x3 + offset(x1)).x2
##                                     0.574
##           Mult(pain, x2 + . + offset(x1)).x3
##                                     0.505
```

- Other Multiplicative Models

- Stereotype model for ordinal response

Is the scale of the relationship with the covariates really different for each category?

Consider common multiplier for same and `slight.improvement`

```
.pain <- backPainLong$pain
levels(.pain)[2:3] <- paste(levels(.pain)[2:3], collapse = " | ")
stereotype5 <- update(stereotype,
                      ~ pain + Mult(.pain, x1 + x2 + x3))
anova(stereotype, stereotype5)

## Analysis of Deviance Table
##
## Model 1: count ~ pain + Mult(pain, offset(x1) + x2 + x3) - 1
## Model 2: count ~ pain + Mult(.pain, x1 + x2 + x3) - 1
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         48         55.9
## 2         49         56.0 -1    -0.118    0.73
```

## └ Other Multiplicative Models

## └ Stereotype model for ordinal response

In fact, only three different multipliers are necessary

```
## Analysis of Deviance Table
##
## Model 1: count ~ pain + Mult(pain, offset(x1) + x2 + x3) - 1
## Model 2: count ~ pain + Mult(.pain, x1 + x2 + x3) - 1
## Model 3: count ~ pain + Mult(.pain, x1 + x2 + x3) - 1
## Model 4: count ~ pain + Mult(.pain, x1 + x2 + x3) - 1
## Model 5: count ~ pain + Mult(.pain, x1 + x2 + x3) - 1
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         48         55.9
## 2         49         56.0 -1      -0.12    0.731
## 3         50         58.4 -1      -2.35    0.126
## 4         51         61.6 -1      -3.19    0.074
## 5         52         83.4 -1     -21.79   3e-06
```

## Rasch Models

Rasch models are used in Item Response Theory to model the binary responses of *subjects* over a set of *items*.

The simplest one parameter logistic (1PL) model has the form

$$\log \frac{\pi_{is}}{1 - \pi_{is}} = \alpha_i + \gamma_s$$

The one-dimensional Rasch model extends the 1PL as follows:

$$\log \frac{\pi_{is}}{1 - \pi_{is}} = \alpha_i + \beta_i \gamma_s$$

where  $\beta_i$  measures the discrimination of item  $i$ : the larger  $\beta_i$  the steeper the item-response function that maps  $\gamma_s$  to  $\pi_{is}$ .

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$$\log \frac{\pi_{is}}{1 - \pi_{is}} = \alpha_i + \gamma_s$$

The one-dimensional Rasch model extends the 1PL as follows:

$$\log \frac{\pi_{is}}{1 - \pi_{is}} = \alpha_i + \beta_i \gamma_s$$

where  $\beta_i$  measures the discrimination of item  $i$ : the larger  $\beta_i$  the steeper the item-response function that maps  $\gamma_s$  to  $\pi_{is}$ .



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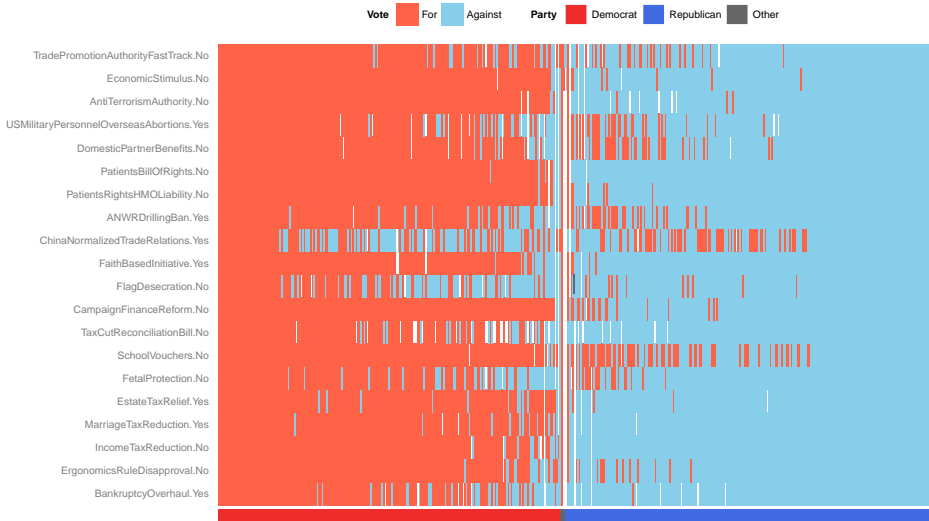
where  $\beta_i$  measures the discrimination of item  $i$ : the larger  $\beta_i$  the steeper the item-response function that maps  $\gamma_s$  to  $\pi_{is}$ .

## Other Multiplicative Models

## Rasch Models

## Example: US House of Representatives

Votes on 20 roll calls selected by Americans for Democratic Action (ADA)



## └ Other Multiplicative Models

## └ Rasch Models

The data are prepared for modelling as shown in ?House2001, specifically

- ▶ removing uninformative House members (too many NAs)
- ▶ creating a data frame with factors `member` and `rollCall`.

For representatives that always vote “For” or “Against” the ADA position, maximum likelihood will produce infinite  $\gamma_s$  estimates, so that the fitted probabilities are 0 or 1 (*complete separation*).

To mitigate this, the response is “flattened”: 0 becomes 0.03 and 1 becomes 0.97.

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To mitigate this, the response is “flattened”: 0 becomes 0.03 and 1 becomes 0.97.

## └ Other Multiplicative Models

## └ Rasch Models

For a large model such as this, we need good starting values. The utility function `residSVD` can be used to decompose multiplicatively the residuals from a smaller model:

```
baseModel <- glm(vote ~ -1 + rollCall,  
                 family = binomial, data = House2001f)  
Start <- residSVD(baseModel, rollCall, member)
```

The one-dimensional Rasch model is then fitted via

```
rasch1 <- gnm(voteAdj ~ Mult(rollCall, member),  
              eliminate = rollCall,  
              family = binomial, data = House2001f,  
              na.action = na.exclude, tolerance = 1e-03,  
              start = -Start, verbose = FALSE)
```

## └ Other Multiplicative Models

## └ Rasch Models

For a large model such as this, we need good starting values. The utility function `residSVD` can be used to decompose multiplicatively the residuals from a smaller model:

```
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```

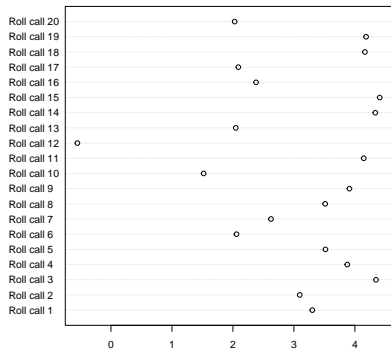
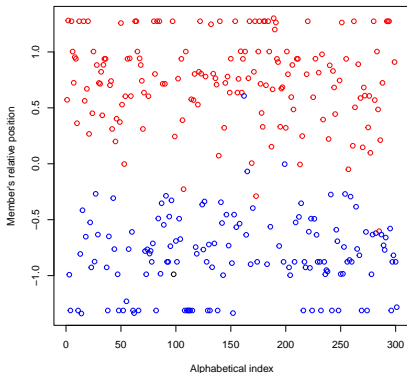
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              eliminate = rollCall,  
              family = binomial, data = House2001f,  
              na.action = na.exclude, tolerance = 1e-03,  
              start = -Start, verbose = FALSE)
```

## Other Multiplicative Models

## Rasch Models

```
plot(pickCoef(rasch1, "[.]member", value = TRUE),
     col = c("red", "black", "black", "blue")[parties],
     xlab = "Alphabetical index", ylab = "Member's relative position")
dotchart(pickCoef(rasch1, "[.]rollCall", value = TRUE),
         paste0("Roll call ", 1:20))
```



## Lee-Carter model for mortality trends

For the study and projection of age-specific population mortality rates, Lee and Carter (1992) proposed a model that has been the basis of many subsequent analyses.

Suppose that death count  $D_{ay}$  for individuals of age  $a$  in year  $y$  has mean  $\mu_{ay}$  and *quasi-Poisson* variance  $\phi\mu_{ay}$ .

*Lee-Carter model:*

$$\begin{aligned}\log(\mu_{ay}/e_{ay}) &= \alpha_a + \beta_a\gamma_y, \\ \Rightarrow \log(\mu_{ay}) &= \log(e_{ay}) + \alpha_a + \beta_a\gamma_y\end{aligned}$$

where  $e_{ay}$  is the *exposure* (number of lives at risk).



## └ Other Multiplicative Models

## └ Lee-Carter models for mortality trends

The Lee-Carter model can be fitted with `gnm` as follows

```
LCmodel <- gnm(Deaths ~ Mult(Exp(Age), Year),  
               eliminate = Age, offset = log(Exposure),  
               family = "quasipoisson")
```

where

- ▶ `Exp(Age)` is used to constrain the parameters representing the “sensitivity” of age group  $a$  to have the same sign,
- ▶ Age is “eliminated” since it will typically have many levels,
- ▶ `offset` is used to add the log exposure with a coefficient of 1,
- ▶ the `quasipoisson` family is used so that the dispersion parameter  $\phi$  is estimated rather than fixed to 1.

## Practical III

1. Use `read.table` to read the file `Canada.txt` provided on your USB stick: data from the Human Mortality Database on male deaths in Canada between 1921 and 2003. Convert Year and Age to factors and fit a simplified version of the Lee-Carter model in which the multiplicative term is replaced by a linear Year effect. Eliminate Age as on p62.
2. Extract the eliminated age coefficients via

```
AgeCoef <- attr(coef(model1), "eliminated")
```

Fit the Lee-Carter model using `update`, specifying the new formula and

```
start = c(AgeCoef, rep(0, length(AgeCoef)), 0, coef(model1))
```

This starts the `gnm` with the linear effects of age set to their estimates from the first model, the age multipliers set to one ( $= \exp(0)$ ), and the year multipliers set to their linear effects from the first model, including the effect for the first year which was constrained to zero by default.

3. Use `deviance` and `df.residual` to compare the deviance of the Lee-Carter model relative to the degrees of freedom. You should notice severe overdispersion ( $\text{deviance} \gg \text{df}$ ).
4. Use `residuals` to obtain the Pearson residuals from the Lee-Carter model. Plot the residuals vs. Age. The overdispersion is not evenly spread through the data, but is largely concentrated in two age groups, roughly ages 25–35 and 50–65. Plot the residuals vs. Year for each of these subgroups, in separate windows. There is a clear (and roughly cancelling) dependence on year, indicating that the assumed bilinear interaction between age and year does not hold for the full range of ages and years considered here.

5. Use `update` to re-fit the Lee-Carter model for males aged 45 or over. Look at the deviance and degrees of freedom: the over-dispersion should be much reduced. Plot the residuals against Age and Year to look for departures from the assumed bilinear structure.
6. Use `getContrasts` to compute quasi-standard errors for the logarithms of  $\beta_a$  – this takes several seconds! Use `plot` to plot the resulting qv object, using `levelNames = 45:98` to name the levels (the parameter for age 99 is unestimable). Consider the expected and unexpected features of this plot.

## Section 4

### Other Specialized Models

## Other Specialized Models

We have already seen an example of a specialized "**nonlin**" term, `MultHomog`. A specialized term is required if it

- ▶ requires common parameters to be estimated across different factors,
- ▶ cannot be expressed as a function of existing "**nonlin**" terms.

In this section we look at the other specialized "**nonlin**" term provided by `gnm`, `Dref`, and some examples of custom "**nonlin**" functions encountered in practice.

## Diagonal Reference Terms

Diagonal reference terms model the effect of factors with common levels. For factors indexed by  $i(f)$ , the term is defined as

$$\sum_f w_f \gamma_{i(f)}$$

where  $w_f$  is a weight for factor  $f$  and  $\gamma_l$  is the *diagonal effect* for level  $l$ .

The weights are constrained to be non-negative and to sum to one so that  $\gamma_l$  is the value for observations with level  $l$  across all the factors.

Unlike the GNM models considered so far, which structure interaction terms, this structures the main effects of the corresponding factors.

**Dref** specifies the constraints on the weights by defining them as

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

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## Example: Conformity to parental rules

Data from van der Slik et al. (2002).

An analysis of the value that parents place on their children conforming to their rules.

Two response variables: mother's conformity score (MCFM), father's (FCFF).

Covariates are education level of mother and of father (MOPLM, FOPLF) plus 5 others.

## └ Other Specialized Models

## └ Diagonal Reference Model

Basic diagonal reference model for MCFM:

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

Note that including an intercept in the model would require one of the diagonal effects to be set to zero for identifiability – the intercept would then be  $\gamma_1$  and the other diagonal effects would be  $\gamma_r - \gamma_1$ .

If the model included another factor, say nationality, a reference level must be set, e.g.

- ▶ setting first level of nationality to zero
- ▶ setting first diagonal effect to zero
- ▶ adding intercept and setting first diagonal effect to zero

## └ Other Specialized Models

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- ▶ setting first diagonal effect to zero
- ▶ adding intercept and setting first diagonal effect to zero

## └ Other Specialized Models

## └ Diagonal Reference Model

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

In order for the diagonal weights to be identified, one of the  $\delta_f$  must be constrained to zero. `DrefWeights` computes the weights  $w_f$ , re-fitting the model constraining  $\delta_1 = 0$  if necessary:

```
w <- DrefWeights(A)
```

```
w
```

```
## $MOPLM
```

```
## weight      se
```

```
##  0.423  0.144
```

```
##
```

```
## $FOPLF
```

```
## weight      se
```

```
##  0.577  0.144
```

- Other Specialized Models

- Diagonal Reference Model

## Inference on the Weights

If the diagonal weights are near to 0.5, then a Normal approximation can be use to obtain a confidence interval, e.g.

```
w$MOPLM["weight"] + qnorm(c(0.025, 0.975)) * w$MOPLM["se"]

## [1] 0.140 0.705
```

Since  $0 < w_f < 1$ , a t-test is not a valid test of  $H_0 : w_1 = 0$ . Instead use **anova** to compare against the implied GLM, e.g.

```
## Analysis of Deviance Table
##
## Model 1: MCFM ~ AGEM + MRMM + FRMF + MWORK + MFCM + FOPLF - 1
## Model 2: MCFM ~ AGEM + MRMM + FRMF + MWORK + MFCM + Dref(MOPLM, FOPLF)
##      1
##      Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1          577          428
## 2          576          425   1         2.9    0.048
```

- Other Specialized Models

- Diagonal Reference Model

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## 2      576      425   1      2.9    0.048
```

## └ Other Specialized Models

## └ Diagonal Reference Model

The **Dref** function allows dependence of the weights on other variables. van der Slik et al. (2002) consider weights dependent upon mother's conflict score (MFCM), as in

$$\delta_k = \xi_k + \phi_k x_5 \quad (k = 1, 2)$$

which can be specified in R as

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

## └ Other Specialized Models

## └ Diagonal Reference Model

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).

DrefWeights(F)

```
## $MOPLM
##      MFCM weight      se
## 1      1 0.0297 0.228
## 2      0 0.7447 0.201
##
## $FOPLF
##      MFCM weight      se
## 1      1 0.970 0.228
## 2      0 0.255 0.201
```



## Custom "nonlin" Functions

A `"nonlin"` function creates a list of arguments for the internal function `nonlinTerms`.

The term is viewed as a function of

- `predictors` linear predictors with coefficients to be estimated, including the special case of single parameters

- `variables` variables included in the term with a coefficient of 1

## Example: Modelling Prey Consumption

A ecology student wished to use the Holling Type II function to model the number of prey eaten by a certain predator in a given time period:

$$y(x) = \frac{ax}{1 + ahx}$$

where  $x$  is the number of prey at the start of the experiment,  $a$  is the attack rate and  $h$  is the time the predator spends handling the prey.

In addition, she wished to allow the parameters to depend on a factor specifying the catchment.

We consider the simpler model first.

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We consider the simpler model first.

## └ Other Specialized Models

## └ Custom "nonlin" Functions

The model can be broken down into **predictors** and **variables** as follows

$$\frac{ax}{1 + \{a\}\{h\}x}$$

We start to build our **nonlin** function as follows:

```
TypeII <- function(x){  
  list(predictors = list(a = 1, h = 1),  
        variables = list(substitute(x)))  
}  
class(TypeII) <- "nonlin"
```

## └ Other Specialized Models

## └ Custom "nonlin" Functions

The `term` argument of `nonlinTerms` takes labels for the predictors and variables and returns a deparsed expression of the term:

```
term = function(predLabels, varLabels){  
  paste0(predLabels[1], "*", varLabels[1], "/(1 + ",  
         predLabels[1], "*", predLabels[2], "*", varLabels[1], ")")  
}  
term(c("a", "h"), "x")  
  
## [1] "a*x/(1 + a*h*x)"
```

Or using `sprintf`

```
term = function(predLabels, varLabels){  
  sprintf("%s * %s / (1 + %s * %s * %s)",  
         predLabels[1], varLabels[1],  
         predLabels[1], predLabels[2], varLabels[1])  
}
```

## └ Other Specialized Models

## └ Custom "nonlin" Functions

# Complete Function

```
TypeII <- function(x){  
  list(predictors = list(a = 1, h = 1),  
        variables = list(substitute(x)),  
        term = function(predLabels, varLabels){  
          sprintf("%s * %s / (1 + %s * %s * %s)",  
                  predLabels[1], varLabels[1],  
                  predLabels[1], predLabels[2], varLabels[1])  
        })  
}  
class(TypeII) <- "nonlin"
```

## └ Other Specialized Models

## └ Custom "nonlin" Functions

Some test data were provided:

```
Density <- rep(c(2,5,10,15,20,30), each = 4)
Eaten <- c(1,1,0,0,2,2,1,1,1,2,3,2,2,2,3,3,3,3,4,3,3,3,4,3)
```

The counts are expected to be underdispersed so we use the `quasipoisson` family with `link = "identity"`. Both  $a$  and  $h$  should be positive, so we provide starting values

```
mod1 <- gnm(Eaten ~ -1 + TypeII(Density), start = c(a = 0.1, h = 0.1),
            family = quasipoisson(link = "identity"))

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

## └ Other Specialized Models

## └ Custom "nonlin" Functions

```
##
## Call:
##
## gnm(formula = Eaten ~ -1 + TypeII(Density), family = quasipoisson(link
##      start = c(a = 0.1, h = 0.1))
##
## Deviance Residuals:
##      Min        1Q    Median        3Q        Max
## -1.1154  -0.2854  -0.0166   0.3345   0.5938
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## a    0.3546     0.0778    4.56 0.00016
## h    0.1975     0.0415    4.76 9.5e-05
##
## (Dispersion parameter for quasipoisson family taken to be 0.208)
##
## Residual deviance: 5.7279 on 22 degrees of freedom
## AIC: NA
##
## Number of iterations: 7
```



- Other Specialized Models
  - Custom "nonlin" Functions

## Incorporating dependence

The parameters  $a$  and  $h$  can be allowed to depend on a factor as follows

```
TypeII <- function(C, x){  
  list(predictors = list(a = substitute(C), h = substitute(C)),  
        variables = list(substitute(x)),  
        term = function(predLabels, varLabels){  
          sprintf("%s * %s / (1 + %s * %s * %s)",  
                  predLabels[1], varLabels[1],  
                  predLabels[1], predLabels[2], varLabels[1])  
        })  
}  
  
class(TypeII) <- "nonlin"
```

## └ Other Specialized Models

## └ Custom "nonlin" Functions

```
Catchment <- factor(rep(1:2, 6, each = 2))
mod2 <- gnm(Eaten ~ -1 + TypeII(Catchment, Density),
            start = rep(0.2, 4),
            family = quasipoisson(link = "identity"))

## Running main iterations.....
## Done

coef(mod2)

## Coefficients:
## aCatchment1 aCatchment2 hCatchment1 hCatchment2
##          0.697          0.246          0.318          0.107
```

## └ Other Specialized Models

## └ Custom "nonlin" Functions

If instead we wanted to allow a general predictor to be supplied by the user as a formula we would use

```
TypeII <- function(f, x){  
  list(predictors = list(a = f, h = f),  
        variables = list(substitute(x)),  
        term = function(predLabels, varLabels){  
          sprintf("(%s) * (%s)/ (1 + (%s) * (%s) * %s)",  
                  predLabels[1], varLabels[1],  
                  predLabels[1], predLabels[2], varLabels[1])  
        })  
}  
class(TypeII) <- "nonlin"
```

Note additional parentheses!

## └ Other Specialized Models

## └ Custom "nonlin" Functions

```
mod2 <- gnm(Eaten ~ -1 + TypeII(~ 1 + Catchment, Density),  
            start = c(0.2, -0.1, 0.2, -0.1),  
            family = quasipoisson(link = "identity"))  
  
## Running main iterations.....  
## Done  
  
coef(mod2)  
  
## Coefficients:  
## a(Intercept)  aCatchment2 h(Intercept)  hCatchment2  
##           0.697        -0.451         0.318        -0.211
```

## More Complex "nonlin" Terms

The "nonlin" features introduced in the last example will be sufficient in many cases. The **gnm** vignette gives further details on

- ▶ specifying homologous parameters
- ▶ implementing *dot-style* parameter labelling
- ▶ implementing term-specific starting values
- ▶ enabling multiple instances

## Practical IVa

1. The voting data in `gnm` are from the 1987 British general election. The data frame comprises the percentage voting Labour (percentage), the total number of people (total), the class of the head of household (destination) and the class of their father (origin). We shall fit a diagonal reference model to these data.

First we want to convert percentage into a binomial response. So that `gnm` will automatically weight the proportion of successes by the group size, we choose to do this by creating a two-column matrix with the columns giving the number of households voting Labour ('success') and the number of households voting otherwise ('failure'):

```
count <- with(voting, percentage/100 * total)
yvar <- cbind(count, voting$total - count)
```

2. Use `gnm` to model `yvar` by a diagonal reference term based on `origin` and `destination` (see p71), with `family = binomial`. Look at the summary - does the model fit well? Use the `mosaic` function from `vcdExtra` to examine the residuals over the `origin` by `destination` table. Since the data were not provided to `gnm` as a table, you will need to provide a formula with the cross-classifying factors.
3. It could be that the diagonal weights should be different for the upwardly mobile. Define a variable to indicate this group as follows:

```
origin <- as.numeric(as.character(voting$origin))
destination <- as.numeric(as.character(voting$destination))
upward <- origin > destination
```

Using this variable, refit the diagonal reference model to have separate weights for the upwardly and downwardly mobile (note the stable are modelled by the diagonal effects). Do the weights differ between the two groups?

4. It could be that individuals which have come into or out of the salariat (class 1) vote differently from other individuals. Define variables indicating movement in and out of class 1 as follows:

```
in1 <- origin != 1 & destination == 1  
out1 <- origin == 1 & destination != 1
```

Re-fit the diagonal reference model, specifying  $\sim 1 + \text{in1} + \text{out1}$  as the **formula** argument of **Dref**, so the weights are parameterized by a main effect with additional effects for **in1** and **out1**.

5. Evaluate the weights under the new model. The weights for groups that have moved in to the salariat are similar to the general weights. Fit a model that only has separate weights for the groups moving out of the salariat. Is this model a significant improvement on the standard diagonal reference model?



## Practical IVb

1. The generalized logistic function or Richard's curve is defined as

$$y(t) = A + \frac{K - A}{(1 + \exp(-B(t - M)))^{1/v}}$$

where

**A** is the lower asymptote

**K** is the upper asymptote

**B** is the growth rate

**v** affects near which asymptote the growth rate is at its maximum

**M** is the time at which the growth rate is at its maximum

Create a custom `nonlin` function to fit this model.

2. Some test data are provided in the file `Richard.txt` on your USB stick. Plot  $y$  against  $t$ . Since  $y$  decreases as  $t$  increases (i.e. the growth rate is negative) the upper asymptote is the value as  $t \rightarrow -\infty$  and the lower asymptote is the value as  $t \rightarrow \infty$ . Given that if  $v = 1$ ,  $M$  is the value of  $t$  at which  $y$  is half-way between the lower and upper asymptotes, make reasonable guesses for starting values of  $A$ ,  $K$ ,  $B$ ,  $v$  and  $M$ . Use `gnm` to fit the Richard's curve to these data, with `family = gaussian` and `start` set to your guessed values. Note the starting values must be in the same order as specified by the `predictors` element of your `"nonlin"` term.

3. Add the fitted line to your plot. Does the model fit well? Look at the summary for your fitted model. Are all the parameters significant? Investigate whether one or more of the following simplifications is reasonable:

- ▶  $v = 1$
- ▶  $A = 0$
- ▶  $K = 100$

## Concluding Remarks

Many frequently-used GNM models can be handled by `gnm` and convenience functions for association models are available in `logmult`.

Other examples in the `gnm` vignette/documentation include

- ▶ GAMMI models (RC(M) models for a general response)
- ▶ biplot models for two-way data
- ▶ compound exponential decay curves
- ▶ double UNIDIFF model for 4-way table ?cautres

Formula interface to `gnm` encourages experimentation and uninhibited modelling.

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