Package 'MCMCglmm'

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Title MCMC Generalised Linear Mixed Models

Depends Matrix, coda, ape

Imports corpcor, tensorA, cubature, methods

Suggests rgl, combinat, mvtnorm, orthopolynom

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Description MCMC Generalised Linear Mixed Models.

License GPL (>= 2)

SystemRequirements C++11

NeedsCompilation yes

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R topics documented:

`MCMCglmm-package` *Multivariate Generalised Linear Mixed Models*

Description

MCMCglmm is a package for fitting Generalised Linear Mixed Models using Markov chain Monte Carlo techniques (Hadfield 2009). Most commonly used distributions like the normal and the Poisson are supported together with some useful but less popular ones like the zero-inflated Poisson and the multinomial. Missing values and left, right and interval censoring are accommodated for all traits. The package also supports multi-trait models where the multiple responses can follow different types of distribution. The package allows various residual and random-effect variance structures

to be specified including heterogeneous variances, unstructured covariance matrices and random regression (e.g. random slope models). Three special types of variance structure that can be specified are those associated with pedigrees (animal models), phylogenies (the comparative method) and measurement error (meta-analysis).

The package makes heavy use of results in Sorensen & Gianola (2002) and Davis (2006) which taken together result in what is hopefully a fast and efficient routine. Most small to medium sized problems should take seconds to a few minutes, but large problems (> 20,000 records) are possible. My interest is in evolutionary biology so there are also several functions for applying Rice's (2004) tensor analysis to real data and functions for visualising and comparing matrices.

Please read the tutorial `vignette("Tutorial", "MCMCglmm")` or the course notes `vignette("CourseNotes", "MCMCglmm"`

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Hadfield, J.D. (2009) MCMC methods for Multi-response Generalised Linear Mixed Models: The MCMCglmm R Package, *submitted*

Sorensen, D. & Gianola, D. (2002) Likelihood, Bayesian and MCMC Methods in Quantitative Genetics, Springer

Davis, T.A. (2006) Direct Methods for Sparse Linear Systems, SIAM

Rice (2004) Evolutionary Theory: Mathematical and Conceptual Foundations, Sinauer

---

at.level *Incidence Matrix of Levels within a Factor*

Description

Incidence matrix of levels within a factor

Usage

```
at.level(x, level)
```

Arguments

x	factor
level	factor level

Value

incidence matrix for level in x

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

at.set

Examples

```
fac<-gl(3,10,30, labels=letters[1:3])
x<-rnorm(30)
model.matrix(~at.level(fac,"b"):x)
```

---

at.set *Incidence Matrix of Combined Levels within a Factor*

Description

Incidence Matrix of Combined Levels within a Factor

Usage

```
at.set(x, level)
```

Arguments

x	factor
level	set of factor levels

Value

incidence matrix for the set `level` in x

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

at.level

Examples

```
fac<-gl(3,10,30, labels=letters[1:3])
x<-rnorm(30)
model.matrix(~at.set(fac,2:3):x)
```

BTdata — *Blue Tit Data for a Quantitative Genetic Experiment*

Description

Blue Tit (*Cyanistes caeruleus*) Data for a Quantitative Genetic Experiment

Usage

```
BTdata
```

Format

a data frame with 828 rows and 7 columns, with variables tarsus length (`tarsus`) and colour (`back`) measured on 828 individuals (`animal`). The mother of each is also recorded (`dam`) together with the foster nest (`fosternest`) in which the chicks were reared. The date on which the first egg in each nest hatched (`hatchdate`) is recorded together with the sex (`sex`) of the individuals.

References

Hadfield, J.D. et. al. 2007 Journal of Evolutionary Biology 20 549-557

See Also

BTped

BTped — *Blue Tit Pedigree*

Description

Blue Tit (*Cyanistes caeruleus*) Pedigree

Usage

```
BTped
```

Format

a data frame with 1040 rows and 3 columns, with individual identifier (`animal`) mother identifier (`dam`) and father identifier (`sire`). The first 212 rows are the parents of the 828 offspring from 106 full-sibling families. Parents are assumed to be unrelated to each other and have NA's in the `dam` and `sire` column.

References

Hadfield, J.D. et. al. 2007 Journal of Evolutionary Biology 20 549-557

See Also

BTped

---

buildV *Forms expected (co)variances for GLMMs fitted with MCMCglmm*

Description

Forms the expected covariance structure of link-scale observations for GLMMs fitted with MCMCglmm

Usage

```
buildV(object, marginal=object$Random$formula, diag=TRUE, it=NULL, posterior="mean", ...)
```

Arguments

object	an object of class "MCMCglmm"
marginal	formula defining random effects to be maginalised
diag	logical; if TRUE the covariances betwween observations are not calculated
it	integer; optional, MCMC iteration on which covariance structure should be based
posterior	character; if it is NULL should the covariance structure be based on the marginal posterior means ('mean') of the VCV parameters, or the posterior modes ('mode'), or a random draw from the posterior with replacement ('distribution'). If posterior=="all" the posterior distribution of observation variances is returned
...	Further arguments to be passed

Value

If diag=TRUE an n by n covariance matrix. If diag=FALSE and posterior!="all" an 1 by n matrix of variances. If posterior=="all" an nit by n matrix of variances (where nit is the number of saved MCMC iterations).

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

MCMCglmm

commutation *Commutation Matrix*

Description

Forms an mn x mn commutation matrix which transforms $vec(\mathbf{A})$ into $vec(\mathbf{A}')$, where $\mathbf{A}$ is an m x n matrix

Usage

```
commutation(m, n)
```

Arguments

m	integer; number of rows of A
n	integer; number of columns of A

Value

Commutation Matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Magnus, J. R. & Neudecker, H. (1979) Annals of Statistics 7 (2) 381-394

Examples

```
commutation(2,2)
```

dcmvnorm *Density of a (conditional) multivariate normal variate*

Description

Density of a (conditional) multivariate normal variate

Usage

```
dcmvnorm(x, mean = 0, V = 1, keep=1, cond=(1:length(x))[-keep], log=FALSE)
```

Arguments

x	vector of observations
mean	vector of means
V	covariance matrix
keep	vector of integers: observations for which density is required
cond	vector of integers: observations to condition on
log	if TRUE, density p is given as log(p)

Value

numeric

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
V1<-cbind(c(1,0.5), c(0.5,1))
dcmvnorm(c(0,2), c(0,0), V=V1, keep=1, cond=2)
# density of x[1]=0 conditional on x[2]=2 given
# x ~ MVN(c(0,0), V1)

dcmvnorm(c(0,2), c(0,0), V=V1, keep=1, cond=NULL)
# density of x[1]=0 marginal to x[2]
dnorm(0,0,1)
# same as univariate density

V2<-diag(2)
dcmvnorm(c(0,2), c(0,0), V=V2, keep=1, cond=2)
# density of x[1]=0 conditional on x[2]=2 given
# x ~ MVN(c(0,0), V2)
dnorm(0,0,1)
# same as univariate density because V2 is diagonal
```

Ddivergence *d-divergence*

Description

Calculates Ovaskainen's (2008) d-divergence between 2 zero-mean multivariate normal distributions.

Usage

```
Ddivergence(CA=NULL, CB=NULL, n=10000)
```

Arguments

CA	Matrix A
CB	Matrix B
n	number of Monte Carlo samples for approximating the integral

Value

d-divergence

Note

In versions of MCMCglmm <2.26 Ovaskainen's (2008) d-divergence was incorrectly calculated.

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Ovaskainen, O. et. al. (2008) Proc. Roy. Soc - B (275) 1635 593-750

Examples

```
CA<-rIW(diag(2),10, n=1)
CB<-rIW(diag(2),10, n=1)
Ddivergence(CA, CB)
```

Dexpressions *List of unevaluated expressions for (mixed) partial derivatives of fitness with respect to linear predictors.*

Description

Unevaluated expressions for (mixed) partial derivatives of fitness with respect to linear predictors for survival and fecundity.

Usage

```
Dexpressions
```

Value

PW.d0W	Fitness (W) function for the Poisson-Weibull (PW) model.
PW.d1Wds	First Partial derivative of fitness (d1W) with respect to survival (d1s) linear predictor for the Poisson-Weibull (PW) model.
PW.d1Wdf	First Partial derivative of fitness (d1W) with respect to fecundity (d1f) linear redictor for the Poisson-Weibull (PW) model.
PW.d3Wd2sd1f	Mixed third partial derivative of fitness (d3W) with 2nd derivative of survival linear predictor (d2s) and first derivative of fecundity linear predictor (d1f) from the Poisson-Weibull (PW) model.
PW.d3Wdsd2f	and so on ...
PW.d2Wd2f	
PW.d2Wd2s	
PW.d3Wd3s	
PW.d3Wd3f	

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

Dtensor

Dtensor *Tensor of (mixed) partial derivatives*

Description

Forms tensor of (mixed) partial derivatives

Usage

```
Dtensor(expr, name=NULL, mu = NULL, m=1, evaluate = TRUE)
```

Arguments

expr	'expression'
name	character vector, giving the variable names with respect to which derivatives will be computed. If NULL all variables in the expression will be used
mu	optional: numeric vector, at which the derivatives are evaluated
m	order of derivative
evaluate	logical; if TRUE the derivatives are evaluated at mu, if FALSE the derivatives are left unevaluated

Value

`Dtensor` (list) of unevaluated expression(s) if `evaluate=FALSE` or a tensor if `evaluate=TRUE`

Author(s)

Jarrod Hadfield j.hadfield@ed.ac.uk

References

Rice, S.H. (2004) Evolutionary Theory: Mathematical and Conceptual Foundations. Sinauer (MA) USA.

See Also

`evalDtensor`, `Dexpressions`, `D`

Examples

```
f<-expression(beta_1 + time * beta_2 + u)
Dtensor(f,eval=FALSE)
```

---

evalDtensor *Evaluates a list of (mixed) partial derivatives*

Description

Evaluates a list of (mixed) partial derivatives

Usage

```
evalDtensor(x, mu, m=1)
```

Arguments

`x`	unevaluated (list) of expression(s)
`mu`	values at which the derivatives are evaluated: names need to match terms in x
`m`	order of derivative

Value

tensor

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

Dtensor, D

Examples

```
f<-expression(beta_1 + time*beta_2+u)
Df<-Dtensor(f, eval=FALSE, m=2)
evalDtensor(Df, mu=data.frame(beta_1=0.5, beta_2=1, time=3, u=2.3))
Dtensor(f, mu=c(1,3,1,2.3), m=2)
```

---

gelman.prior *Prior Covariance Matrix for Fixed Effects.*

Description

Prior Covariance Matrix for Fixed Effects.

Usage

```
gelman.prior(formula, data, scale=1, intercept=scale, singular.ok=FALSE)
```

Arguments

formula	formula for the fixed effects.
data	data.frame.
intercept	prior standard deviation for the intercept
scale	prior standard deviation for regression parameters
singular.ok	logical: if FALSE linear dependencies in the fixed effects are removed. if TRUE they are left in an estimated, although all information comes form the prior

Details

Gelman et al. (2008) suggest that the input variables of a categorical regression are standardised and that the associated regression parameters are assumed independent in the prior. Gelman et al. (2008) recommend a scaled t-distribution with a single degree of freedom (scaled Cauchy) and a scale of 10 for the intercept and 2.5 for the regression parameters. If the degree of freedom is infinity (i.e. a normal distribution) then a prior covariance matrix B$V can be defined for the regression parameters without input standardisation that corresponds to a diagonal prior $\mathbf{D}$ for the regression parameters had the inputs been standardised. The diagonal elements of $\mathbf{D}$ are set to scale^2 except the first which is set to intercept^2. With logistic regression $D = \pi^2/3 + \sigma^2$ gives a prior that is approximately flat on the probability scale, where σ^2 is the total variance due to the random effects. For probit regression it is $D = 1 + \sigma^2$.

Value

prior covariance matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Gelman, A. et al. (2008) The Annals of Appled Statistics 2 4 1360-1383

Examples

```
dat<-data.frame(y=c(0,0,1,1), x=gl(2,2))
# data with complete separation

#####################
# probit regression #
#####################

prior1<-list(
  B=list(mu=c(0,0), V=gelman.prior(~x, data=dat, scale=sqrt(1+1))),
  R=list(V=1,fix=1))

m1<-MCMCglmm(y~x, prior=prior1, data=dat, family="ordinal", verbose=FALSE)

c2<-1
p1<-pnorm(m1$Sol[,1]/sqrt(1+c2)) # marginal probability when x=1

######################
# logistic regression #
######################

prior2<-list(B=list(mu=c(0,0), V=gelman.prior(~x, data=dat, scale=sqrt(pi^2/3+1))),
             R=list(V=1,fix=1))

m2<-MCMCglmm(y~x, prior=prior2, data=dat, family="categorical", verbose=FALSE)

c2 <- (16 * sqrt(3)/(15 * pi))^2
p2<-plogis(m2$Sol[,1]/sqrt(1+c2)) # marginal probability when x=1

plot(mcmc.list(p1,p2))
```

---

inverseA *Inverse Relatedness Matrix and Phylogenetic Covariance Matrix*

Description

Henderson (1976) and Meuwissen and Luo (1992) algorithm for inverting relatedness matrices, and Hadfield and Nakagawa (2010) algorithm for inverting phylogenetic covariance matrices.

Usage

```
inverseA(pedigree=NULL, nodes="ALL", scale=TRUE, reduced=FALSE,
   tol = .Machine$double.eps^0.5)
```

Arguments

pedigree	ordered pedigree with 3 columns: id, dam and sire, or a phylo object.
nodes	"ALL" calculates the inverse for all individuals/nodes. For phylogenies "TIPS" calculates the inverse for the species tips only, and for pedigrees a vector of id's can be passed which inverts the relatedness matrix for that subset.
scale	logical: should a phylogeny (needs to be ultrametric) be scaled to unit length (distance from root to tip)?
reduced	logical: should childless nodes be dropped from the inverse and the pedigree/phylogeny representation be reduced?
tol	numeric: differences in branch length smaller than this are ignored when assessing whether a tree is ultrametric.

Value

Ainv	inverse as sparseMatrix
inbreeding	inbreeding coefficients/branch lengths
pedigree	pedigree/pedigree representation of phylogeny

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Henderson, C.R. (1976) Biometrics 32 (1) 69:83

Quaas, R. L. and Pollak, E. J. (1980) Journal of Animal Science 51:1277-1287.

Meuwissen, T.H.E and Luo, Z. (1992) Genetic Selection Evolution 24 (4) 305:313

Hadfield, J.D. and Nakagawa, S. (2010) Journal of Evolutionary Biology 23 494-508

Examples

```
data(bird.families)
Ainv<-inverseA(bird.families)
```

knorm *(Mixed) Central Moments of a Multivariate Normal Distribution*

Description

Forms a tensor of (mixed) central moments of a multivariate normal distribution

Usage

```
knorm(V, k)
```

Arguments

V	(co)variance matrix
k	kth central moment, must be even

Value

tensor

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Schott, J.R.(2003) Journal of Multivariate Analysis 87 (1) 177-190

See Also

dnorm

Examples

```
V<-diag(2)
knorm(V,2)
knorm(V,4)
```

KPPM *Kronecker Product Permutation Matrix*

Description

Forms an mk x mk Kronecker Product Permutation Matrix

Usage

```
KPPM(m, k)
```

Arguments

m	integer
k	integer

Value

Matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Schott, J.R.(2003) Journal of Multivariate Analysis 87 (1) 177-190

Examples

```
KPPM(2,3)
```

krzanowski.test *Krzanowski's Comparison of Subspaces*

Description

Calculates statistics of Krzanowski's comparison of subspaces.

Usage

```
krzanowski.test(CA, CB, vecsA, vecsB, corr = FALSE, ...)
```

Arguments

CA	Matrix A
CB	Matrix B
vecsA	Vector of integers indexing the eigenvectors determining the subspace of A
vecsB	Vector of integers indexing the eigenvectors determining the subspace of B
corr	logical; if TRUE the variances of A and B are standardised
...	further arguments to be passed

Value

sumofS	metric for overall similarity with 0 indicting no similarity and a value of length(vecsA) for identical subspaces
angles	angle in degrees between each best matched pair of vectors
bisector	vector that lies between each best matched pair of vectors

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Krzanowski, W.J. (2000) Principles of Multivariate Analysis. OUP

Examples

```
CA<-rIW(diag(5),10, n=1)
CB<-rIW(diag(5),10, n=1)
krzanowski.test(CA, CB, vecsA=1:2, vecsB=1:2)
krzanowski.test(CA, CA, vecsA=1:2, vecsB=1:2)
```

---

kunif *Central Moments of a Uniform Distribution*

Description

Returns the central moments of a uniform distribution

Usage

```
kunif(min, max, k)
```

Arguments

min, max	lower and upper limits of the distribution. Must be finite.
k	k central moment, must be even

Value

kth central moment

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

dunif

Examples

```
kunif(-1,1,4)
y<-runif(1000,-1,1)
mean((y-mean(y))^4)
```

`list2bdiag` *Forms the direct sum from a list of matrices*

Description

Forms a block-diagonal matrix from a list of matrices

Usage

```
list2bdiag(x)
```

Arguments

x	list of square matrices

Value

matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
M<-list(rIW(diag(3), 10), rIW(diag(2), 10))
list2bdiag(M)
```

MCMCglmm *Multivariate Generalised Linear Mixed Models*

Description

Markov chain Monte Carlo Sampler for Multivariate Generalised Linear Mixed Models with special emphasis on correlated random effects arising from pedigrees and phylogenies (Hadfield 2010). Please read the course notes: `vignette("CourseNotes","MCMCglmm")` or the overview `vignette("Overview", "MCMCglm`

Usage

```
MCMCglmm(fixed, random=NULL, rcov=~units, family="gaussian", mev=NULL,
    data,start=NULL, prior=NULL, tune=NULL, pedigree=NULL, nodes="ALL",
    scale=TRUE, nitt=13000, thin=10, burnin=3000, pr=FALSE,
    pl=FALSE, verbose=TRUE, DIC=TRUE, singular.ok=FALSE, saveX=TRUE,
    saveZ=TRUE, saveXL=TRUE, slice=FALSE, ginverse=NULL, trunc=FALSE)
```

Arguments

`fixed`	formula for the fixed effects, multiple responses are passed as a matrix using cbind
`random`	formula for the random effects. Multiple random terms can be passed using the + operator, and in the most general case each random term has the form `variance.function(formula):linking.function(random.terms)`. Currently, the only `variance.functions` available are `idv`, `idh`, `us`, `cor[]` and `ante[]`. `idv` fits a constant variance across all components in `formula`. Both `idh` and `us` fit different variances across each component in `formula`, but `us` will also fit the covariances. `corg` fixes the variances along the diagonal to one and `corgh` fixes the variances along the diagonal to those specified in the prior. `cors` allows correlation submatrices. `ante[]` fits ante-dependence structures of different order (e.g ante1, ante2), and the number can be prefixed by a `c` to hold all regression coefficients of the same order equal. The number can also be suffixed by a `v` to hold all innovation variances equal (e.g `antec2v` has 3 parameters). The `formula` can contain both factors and numeric terms (i.e. random regression) although it should be noted that the intercept term is suppressed. The (co)variances are the (co)variances of the `random.terms` effects. Currently, the only `linking.functions` available are `mm` and `str`. `mm` fits a multimembership model where multiple random terms are separated by the + operator. `str` allows covariances to exist between multiple random terms that are also separated by the + operator. In both cases the levels of all multiple random terms have to be the same. For simpler models the `variance.function(formula)` and `linking.function(random.terms)` can be omitted and the model syntax has the simpler form `~random1+random2+...`. There are two reserved variables: `units` which index rows of the response variable and `trait` which index columns of the response variable

rcov — formula for residual covariance structure. This has to be set up so that each data point is associated with a unique residual. For example a multi-response model might have the R-structure defined by ~us(trait):units

family — optional character vector of trait distributions. Currently, "gaussian", "poisson", "categorical", "multinomial", "ordinal", "threshold", "exponential", "geometric", "cengaussian", "cenpoisson", "cenexponential", "zipoisson", "zapoisson", "ztpoisson", "hupoisson", "zibinomial", "threshold" and nzbinom are supported, where the prefix "cen" means censored, the prefix "zi" means zero inflated, the prefix "za" means zero altered, the prefix "zt" means zero truncated and the prefix "hu" means hurdle. If NULL, data needs to contain a family column.

mev — optional vector of measurement error variances for each data point for random effect meta-analysis.

data — data.frame

start — optional list having 4 possible elements: R (R-structure) G (G-structure) and liab (latent variables or liabilities) should contain the starting values where G itself is also a list with as many elements as random effect components. The fourth element QUASI should be logical: if TRUE starting latent variables are obtained heuristically, if FALSE then they are sampled from a Z-distribution

prior — optional list of prior specifications having 3 possible elements: R (R-structure) G (G-structure) and B (fixed effects). B is a list containing the expected value (mu) and a (co)variance matrix (V) representing the strength of belief: the defaults are B$mu=0 and B$V=I*1e+10, where where I is an identity matrix of appropriate dimension. The priors for the variance structures (R and G) are lists with the expected (co)variances (V) and degree of belief parameter (nu) for the inverse-Wishart, and also the mean vector (alpha.mu) and covariance matrix (alpha.V) for the redundant working parameters. The defaults are nu=0, V=1, alpha.mu=0, and alpha.V=0. When alpha.V is non-zero, parameter expanded algorithms are used.

tune — optional (co)variance matrix defining the proposal distribution for the latent variables. If NULL an adaptive algorithm is used which ceases to adapt once the burn-in phase has finished.

pedigree — ordered pedigree with 3 columns id, dam and sire or a phylo object. This argument is retained for back compatibility - see ginverse argument for a more general formulation.

nodes — pedigree/phylogeny nodes to be estimated. The default, "ALL" estimates effects for all individuals in a pedigree or nodes in a phylogeny (including ancestral nodes). For phylogenies "TIPS" estimates effects for the tips only, and for pedigrees a vector of ids can be passed to nodes specifying the subset of individuals for which animal effects are estimated. Note that all analyses are equivalent if omitted nodes have missing data but by absorbing these nodes the chain max mix better. However, the algorithm may be less numerically stable and may iterate slower, especially for large phylogenies.

scale — logical: should the phylogeny (needs to be ultrametric) be scaled to unit length (distance from root to tip)?

nitt — number of MCMC iterations

thin	thinning interval
burnin	burnin
pr	logical: should the posterior distribution of random effects be saved?
pl	logical: should the posterior distribution of latent variables be saved?
verbose	logical: if TRUE MH diagnostics are printed to screen
DIC	logical: if TRUE deviance and deviance information criterion are calculated
singular.ok	logical: if FALSE linear dependencies in the fixed effects are removed. if TRUE they are left in an estimated, although all information comes form the prior
saveX	logical: save fixed effect design matrix
saveZ	logical: save random effect design matrix
saveXL	logical: save structural parameter design matrix
slice	logical: should slice sampling be used? Only applicable for binary traits with independent residuals
ginverse	a list of sparse inverse matrices ($\mathbf{A^{-1}}$) that are proportional to the covariance structure of the random effects. The names of the matrices should correspond to columns in data that are associated with the random term. All levels of the random term should appear as rownames for the matrices.
trunc	logical: should latent variables in binary models be truncated to prevent under/overflow (+/-20 for categorical/multinomial models and +/-7 for threshold/probit models)?

Value

Sol	Posterior Distribution of MME solutions, including fixed effects
VCV	Posterior Distribution of (co)variance matrices
CP	Posterior Distribution of cut-points from an ordinal model
Liab	Posterior Distribution of latent variables
Fixed	list: fixed formula and number of fixed effects
Random	list: random formula, dimensions of each covariance matrix, number of levels per covariance matrix, and term in random formula to which each covariance belongs
Residual	list: residual formula, dimensions of each covariance matrix, number of levels per covariance matrix, and term in residual formula to which each covariance belongs
Deviance	deviance -2*log(p(yl...))
DIC	deviance information criterion
X	sparse fixed effect design matrix
Z	sparse random effect design matrix
XL	sparse structural parameter design matrix
error.term	residual term for each datum
family	distribution of each datum
Tune	(co)variance matrix of the proposal distribution for the latent variables
meta	logical; was mev passed?

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

General analyses: Hadfield, J.D. (2010) Journal of Statistical Software 33 2 1-22

Phylogenetic analyses: Hadfield, J.D. & Nakagawa, S. (2010) Journal of Evolutionary Biology 23 494-508

Background Sorensen, D. & Gianola, D. (2002) Springer

See Also

mcmc

Examples

```
# Example 1: univariate Gaussian model with standard random effect

data(PlodiaPO)
model1<-MCMCglmm(PO~1, random=~FSfamily, data=PlodiaPO, verbose=FALSE,
 nitt=1300, burnin=300, thin=1)
summary(model1)

# Example 2: univariate Gaussian model with phylogenetically correlated
# random effect

data(bird.families)

phylo.effect<-rbv(bird.families, 1, nodes="TIPS")
phenotype<-phylo.effect+rnorm(dim(phylo.effect)[1], 0, 1)

# simulate phylogenetic and residual effects with unit variance

test.data<-data.frame(phenotype=phenotype, taxon=row.names(phenotype))

Ainv<-inverseA(bird.families)$Ainv

# inverse matrix of shared phyloegnetic history

prior<-list(R=list(V=1, nu=0.002), G=list(G1=list(V=1, nu=0.002)))

model2<-MCMCglmm(phenotype~1, random=~taxon, ginverse=list(taxon=Ainv),
 data=test.data, prior=prior, verbose=FALSE, nitt=1300, burnin=300, thin=1)

plot(model2$VCV)
```

mult.memb *Design Matrices for Multiple Membership Models*

Description

Forms design matrices for multiple membership models

Usage

```
mult.memb(formula)
```

Arguments

formula	formula

Details

Currently mult.memb can only usefully be used inside an idv variance function. The formula usually contains serveral factors that have the same factor levels.

Value

design matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
fac1<-factor(sample(letters[1:3], 5, TRUE), levels=letters[1:3])
fac2<-factor(sample(letters[1:3], 5, TRUE), levels=letters[1:3])
cbind(fac1, fac2)
mult.memb(~fac1+fac2)
```

path *Design Matrix for Path Analyses*

Description

Forms design matrix for path analyses that involve paths within residual blocks

Usage

```
path(cause=NULL, effect=NULL, k)
```

Arguments

cause	integer; index of predictor 'trait' within residual block
effect	integer; index of response 'trait' within residual block
k	integer; dimension of residual block

Value

design matrix

Note

For more general path anlaytic models see sir which allows paths to exist between responses that are not in the same residual block. However, sir does not handle non-Gaussian or missing responses. Note that path models involving non-Gaussian data are defined on the link scale which may not always be appropriate.

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

sir

Examples

```
path(1, 2,2)
```

PlodiaPO *Phenoloxidase measures on caterpillars of the Indian meal moth.*

Description

Phenoloxidase measures on caterpillars of the Indian meal moth (*Plodia interpunctella*).

Usage

```
PlodiaPO
```

Format

a data frame with 511 rows and 3 columns, with variables indicating full-sib family (FSfamily), phenoloxidase measures (PO), and plate (plate). PO has undergone a Box-Cox power transformation of 0.141

Source

Tidbury H & Boots M (2007) University of Sheffield

See Also

PlodiaR, PlodiaRB

`PlodiaR` *Resistance of Indian meal moth caterpillars to the granulosis virus PiGV.*

Description

Resistance of Indian meal moth (*Plodia interpunctella*) caterpillars to the granulosis virus PiGV.

Usage

```
PlodiaR
```

Format

a data frame with 50 rows and 5 columns, with variables indicating full- sib family (`FSfamly`), date of egg laying (`date_laid`) and assaying (`date_Ass`), and the number of individuals from the family that were experimentally infected with the virus `Infected` and the number of those that pupated `Pupated`. These full-sib family identifiers also relate to the full-sib family identifiers in PlodiaPO

Source

Tidbury H & Boots M (2007) University of Sheffield

See Also

PlodiaRB, PlodiaPO

`PlodiaRB` *Resistance (as a binary trait) of Indian meal moth caterpillars to the granulosis virus PiGV.*

Description

Resistance (as a binary trait) of Indian meal moth (*Plodia interpunctella*) caterpillars to the granulosis virus PiGV.

Usage

```
PlodiaRB
```

Format

a data frame with 784 rows and 4 columns, with variables indicating full- sib family (FSfamly), date of egg laying (date_laid) and assaying (date_Ass), and a binary variable indicating whether an individual was resistant (Pupated) to an experimental infection of the virus. These data are identical to those in the data.frame PlodiaR except each family-level binomial variable has been expanded into a binary variable for each individual.

Source

Tidbury H & Boots M (2007) University of Sheffield

See Also

PlodiaR, PlodiaPO

---

plot.MCMCglmm *Plots MCMC chains from MCMCglmm using plot.mcmc*

Description

plot method for class "MCMCglmm".

Usage

```
## S3 method for class 'MCMCglmm'
plot(x, random=FALSE, ...)
```

Arguments

x	an object of class "MCMCglmm"
random	logical; should saved random effects be plotted
...	Further arguments to be passed

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

plot.mcmc, MCMCglmm

plotsubspace *Plots covariance matrices*

Description

Represents covariance matrices as 3-d ellipsoids using the rgl package. Covariance matrices of dimension greater than 3 are plotted on the subspace defined by the first three eigenvectors.

Usage

```
plotsubspace(CA, CB=NULL, corr = FALSE, shadeCA = TRUE,
    shadeCB = TRUE, axes.lab = FALSE, ...)
```

Arguments

CA	Matrix
CB	Optional second matrix
corr	If TRUE the covariance matrices are transformed into correlation matrices
shadeCA	If TRUE the ellipsoid is solid, if FALSE the ellipsoid is wireframe
shadeCB	If TRUE the ellipsoid is solid, if FALSE the ellipsoid is wireframe
axes.lab	If TRUE the axes are labelled with the eigenvectors
...	further arguments to be passed

Details

The matrix CA is always red, and the matrix CB if given is always blue. The subspace is defined by the first three eigenvectors of CA, and the percentage of variance for each matrix along these three dimensions is given in the plot title.

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk> with code taken from the rgl package

See Also

rgl

Examples

```
if(requireNamespace("rgl")!=FALSE){
  G1<-rIW(diag(4),10)
  G2<-G1*1.2
#  plotsubspace(G1, G2, shadeCB=FALSE)
# commented out because of problems with rgl
}
```

posterior.ante *Posterior distribution of ante-dependence parameters*

Description

Posterior distribution of ante-dependence parameters

Usage

```
posterior.ante(x,k=1)
```

Arguments

x	mcmc object of (co)variances stacked column-wise
k	order of the ante-dependence structure

Value

posterior ante-dependence parameters (innovation variances followed by regression ceofficients)

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

posterior.cor, posterior.evals, posterior.inverse

Examples

```
v<-rIW(diag(2),10, n=1000)
plot(posterior.ante(mcmc(v),1))
```

posterior.cor *Transforms posterior distribution of covariances into correlations*

Description

Transforms posterior distribution of covariances into correlations

Usage

```
posterior.cor(x)
```

Arguments

x	mcmc object of (co)variances stacked column-wise

Value

posterior correlation matrices

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

posterior.evals, posterior.inverse, posterior.ante

Examples

```
v<-rIW(diag(2),3, n=1000)
hist(posterior.cor(mcmc(v))[,2])
```

---

posterior.evals *Posterior distribution of eigenvalues*

Description

Posterior distribution of eigenvalues

Usage

```
posterior.evals(x)
```

Arguments

x	mcmc object of (co)variances stacked column-wise

Value

posterior eigenvalues

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

posterior.cor, posterior.inverse, posterior.ante

Examples

```
v<-rIW(diag(2),3, n=1000)
hist(posterior.evals(mcmc(v))[,2])
```

posterior.inverse *Posterior distribution of matrix inverse*

Description

Posterior distribution of matrix inverse

Usage

```
posterior.inverse(x)
```

Arguments

x	mcmc object of (co)variances stacked column-wise

Value

posterior of inverse (co)variance matrices

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

posterior.cor, posterior.evals, posterior.ante

Examples

```
v<-rIW(diag(2),3, n=1000)
plot(posterior.inverse(mcmc(v)))
```

posterior.mode *Estimates the marginal parameter modes using kernel density estimation*

Description

Estimates the marginal parameter modes using kernel density estimation

Usage

```
posterior.mode(x, adjust=0.1, ...)
```

Arguments

x	mcmc object
adjust	numeric, passed to density to adjust the bandwidth of the kernal density
...	other arguments to be passed

Value

modes of the kernel density estimates

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

density

Examples

```
v<-rIW(as.matrix(1),10, n=1000)
hist(v)
abline(v=posterior.mode(mcmc(v)), col="red")
```

---

predict.MCMCglmm *Predict method for GLMMs fitted with MCMCglmm*

Description

Predicted values for GLMMs fitted with MCMCglmm

Usage

```
## S3 method for class 'MCMCglmm'
predict(object, newdata=NULL, marginal=object$Random$formula,
        type="response", interval="none", level=0.95, it=NULL,
        posterior="all", verbose=FALSE, approx="numerical", ...)
```

Arguments

object	an object of class "MCMCglmm"
newdata	An optional data frame in which to look for variables with which to predict
marginal	formula defining random effects to be maginalised
type	character; either "terms" (link scale) or "response" (data scale)
interval	character; either "none", "confidence" or "prediction"
level	A numeric scalar in the interval (0,1) giving the target probability content of the intervals.

it	integer; optional, MCMC iteration on which predictions should be based
posterior	character; if it is NULL should marginal posterior predictions be calculated ("all"), or should they be made conditional on the marginal posterior means ("mean") of the parameters, the posterior modes ("mode"), or a random draw from the posterior ("distribution").
verbose	logical; if TRUE, warnings are issued with newdata when the original model has fixed effects that do not appear in newdata and/or newdata has random effects not present in the original model.
approx	character; for distributions for which the mean cannot be calculated analytically what approximation should be used: numerical integration (numerical; slow), second order Taylor expansion (taylor2) and for logistic models approximations presented in Diggle (2004) (diggle) and McCulloch and Searle (2001) (mcculloch)
...	Further arguments to be passed

Value

Expectation and credible interval

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Diggle P, et al. (2004). Analysis of Longitudinal Data. 2nd Edition. Oxford University Press.

McCulloch CE and Searle SR (2001). Generalized, Linear and Mixed Models. John Wiley & Sons, New York.

See Also

MCMCglmm

---

prunePed *Pedigree pruning*

Description

Creates a subset of a pedigree by retaining the ancestors of a specified subset of individuals

Usage

```
prunePed(pedigree, keep, make.base=FALSE)
```

Arguments

pedigree	pedigree with id in column 1 dam in column 2 and sire in column 3
keep	individuals in pedigree for which the ancestors should be retained
make.base	logical: should ancestors that do not provide additional information be discarded?

Value

subsetted pedigree

Note

If the individuals in keep are the only phenotyped individuals for some analysis then some non-phenotyped individuals can often be discarded if they are not responsible for pedigree links between phenotyped individuals. In the simplest case (make.base=FALSE) all ancestors of phenotyped individuals will be retained, although further pruning may be possible using make.base=TRUE. In this case all pedigree links that do not connect phenotyped individuals are discarded resulting in some individuals becoming part of the base population. In terms of variance component and fixed effect estimation pruning the pedigree should have no impact on the target posterior distribution, although convergence and mixing may be better because there is less missing data.

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk> + Michael Morrissey

Ptensor *Tensor of Sample (Mixed) Central Moments*

Description

Forms a tensor of sample (mixed) central moments

Usage

```
Ptensor(x, k)
```

Arguments

x	matrix; traits in columns samples in rows
k	kth central moment

Value

tensor

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
n<-1000
y<-matrix(rnorm(n), n/2, 2)
Ptensor(y,2)
cov(y)*((n-1)/n)
```

---

rbv *Random Generation of MVN Breeding Values and Phylogenetic Effects*

Description

Random Generation of MVN Breeding Values and Phylogenetic Effects

Usage

```
rbv(pedigree, G, nodes="ALL", scale=TRUE, ggroups=NULL, gmeans=NULL)
```

Arguments

pedigree	ordered pedigree with 3 columns id, dam and sire or a phylo object.
G	(co)variance matrix
nodes	effects for pedigree/phylogeny nodes to be returned. The default, nodes="ALL" returns effects for all individuals in a pedigree or nodes in a phylogeny (including ancestral nodes). For phylogenies nodes="TIPS" returns effects for the tips only, and for pedigrees a vector of ids can be passed to nodes specifying the subset of individuals for which animal effects are returned.
scale	logical: should a phylogeny (needs to be ultrametric) be scaled to unit length (distance from root to tip)?
ggroups	optional; vector of genetic groups
gmeans	matrix of mean breeding value for genetic groups (rows) by traits (columns)

Value

matrix of breeding values/phylogenetic effects

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
data(bird.families)
bv<-rbv(bird.families, diag(2))
```

residuals.MCMCglmm *Residuals form a GLMM fitted with MCMCglmm*

Description

`residuals` method for class "MCMCglmm".

Usage

```
## S3 method for class 'MCMCglmm'
residuals(object, type = c("deviance", "pearson", "working",
                                "response", "partial"), ...)
```

Arguments

object	an object of class "MCMCglmm"
type	the type of residuals which should be returned. The alternatives are: "deviance" (default), "pearson","working", "response", and "partial".
...	Further arguments to be passed

Value

vector of residuals

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

residuals, MCMCglmm

rIW *Random Generation from the Conditional Inverse Wishart Distribution*

Description

Samples from the inverse Wishart distribution, with the possibility of conditioning on a diagonal submatrix

Usage

```
rIW(V, nu, fix=NULL, n=1, CM=NULL)
```

Arguments

V	Expected (co)varaince matrix as nu tends to infinity
nu	degrees of freedom
fix	optional integer indexing the partition to be conditioned on
n	integer: number of samples to be drawn
CM	matrix: optional matrix to condition on. If not given, and fix!=NULL, V_22 is conditioned on

Details

If $\mathbf{W^{-1}}$ is a draw from the inverse Wishart, fix indexes the diagonal element of $\mathbf{W^{-1}}$ which partitions $\mathbf{W^{-1}}$ into 4 submatrices. fix indexes the upper left corner of the lower diagonal matrix and it is this matrix that is conditioned on.

For example partioning $\mathbf{W^{-1}}$ such that

$$\mathbf{W^{-1}} = \begin{bmatrix} \mathbf{W^{-1}}_{11} & \mathbf{W^{-1}}_{12} \\ \mathbf{W^{-1}}_{21} & \mathbf{W^{-1}}_{22} \end{bmatrix}$$

fix indexes the upper left corner of $\mathbf{W^{-1}}_{22}$. If CM!=NULL then $\mathbf{W^{-1}}_{22}$ is fixed at CM, otherwise $\mathbf{W^{-1}}_{22}$ is fixed at V_{22}. For example, if dim(V)=4 and fix=2 then $\mathbf{W^{-1}}_{11}$ is a 1X1 matrix and $\mathbf{W^{-1}}_{22}$ is a 3X3 matrix.

Value

if n = 1 a matrix equal in dimension to V, if n>1 a matrix of dimension n x length(V)

Note

In versions of MCMCglmm >1.10 the arguments to rIW have changed so that they are more intuitive in the context of MCMCglmm. Following the notation of Wikipedia (http://en.wikipedia.org/wiki/Inverse-Wishart_distribution) the inverse scale matrix $\mathbf{\Psi} = (V*nu)$. In earlier versions of MCMCglmm (<1.11) $\mathbf{\Psi} = V^{-1}$. Although the old parameterisation is consistent with the riwish function in MCMCpack and the rwishart function in bayesm it is inconsistent with the prior definition for MCMCglmm. The following pieces of code are sampling from the same distributions:

```
riwish(nu, nu*V)                  from MCMCpack
rwishart(nu, solve(nu*V))$IW      from bayesm
rIW(nu, solve(nu*V))              from MCMCglmm <1.11
rIW(V, nu)                        from MCMCglmm >=1.11
```

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Korsgaard, I.R. et. al. 1999 Genetics Selection Evolution 31 (2) 177:181

See Also

rwishart, rwish

Examples

```
nu<-10
V<-diag(4)
rIW(V, nu, fix=2)
```

`rtcmvnorm` *Random Generation from a Truncated Conditional Normal Distribution*

Description

Samples from the Truncated Conditional Normal Distribution

Usage

```
rtcmvnorm(n = 1, mean = 0, V = 1, x=0, keep=1, lower = -Inf, upper = Inf)
```

Arguments

`n`	integer: number of samples to be drawn
`mean`	vector of means
`V`	covariance matrix
`x`	vector of observations to condition on
`keep`	element of x to be sampled
`lower`	left truncation point
`upper`	right truncation point

Value

vector

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
par(mfrow=c(2,1))
V1<-cbind(c(1,0.5), c(0.5,1))
x1<-rtcmvnorm(10000, c(0,0), V=V1, c(0,2), keep=1, lower=-1, upper=1)
x2<-rtnorm(10000, 0, 1, lower=-1, upper=1)
plot(density(x1), main="Correlated conditioning observation")
lines(density(x2), col="red")
# denisties of conditional (black) and unconditional (red) distribution
# when the two variables are correlated (r=0.5)

V2<-diag(2)
x3<-rtcmvnorm(10000, c(0,0), V=V2, c(0,2), keep=1, lower=-1, upper=1)
x4<-rtnorm(10000, 0, 1, lower=-1, upper=1)
plot(density(x3), main="Uncorrelated conditioning observation")
lines(density(x4), col="red")
# denisties of conditional (black) and unconditional (red) distribution
# when the two variables are uncorrelated (r=0)
```

---

rtnorm *Random Generation from a Truncated Normal Distribution*

Description

Samples from the Truncated Normal Distribution

Usage

```
rtnorm(n = 1, mean = 0, sd = 1, lower = -Inf, upper = Inf)
```

Arguments

n	integer: number of samples to be drawn
mean	vector of means
sd	vector of standard deviations
lower	left truncation point
upper	right truncation point

Value

vector

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

References

Robert, C.P. (1995) Statistics & Computing 5 121-125

See Also

rtnorm

Examples

```
hist(rtnorm(100, lower=-1, upper=1))
```

---

simulate.MCMCglmm *Simulate method for GLMMs fitted with MCMCglmm*

Description

Simulated response vectors for GLMMs fitted with MCMCglmm

Usage

```
## S3 method for class 'MCMCglmm'
simulate(object, nsim = 1, seed = NULL, newdata=NULL, marginal = object$Random$formula,
          type = "response", it=NULL, posterior = "all", verbose=FALSE, ...)
```

Arguments

object	an object of class "MCMCglmm"
nsim	number of response vectors to simulate. Defaults to 1.
seed	Either NULL or an integer that will be used in a call to set.seed before simulating the response vectors. The default, NULL will not change the random generator state.
newdata	An optional data frame for which to simulate new observations
marginal	formula defining random effects to be maginalised
type	character; either "terms" (link scale) or "response" (data scale)
it	integer; optional, MCMC iteration on which predictions should be based
posterior	character; if it is NULL should the response vector be simulated using the marginal posterior means ("mean") of the parameters, or the posterior modes ("mode"), random draws from the posterior with replacement ("distribution") or without replacement ("all")
verbose	logical; if TRUE, warnings are issued with newdata when the original model has fixed effects that do not appear in newdata and/or newdata has random effects not present in the original model.
...	Further arguments to be passed

Value

A matrix (with nsim columns) of simulated response vectors

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

MCMCglmm

`sir` *Design Matrix for Simultaneous and Recursive Relationships between Responses*

Description

Forms design matrix for simultaneous and recursive relationships between responses

Usage

```
sir(formula1=NULL, formula2=NULL)
```

Arguments

`formula1`	formula
`formula2`	formula

Value

design matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
fac1<-factor(sample(letters[1:3], 5, TRUE), levels=letters[1:3])
fac2<-factor(sample(letters[1:3], 5, TRUE), levels=letters[1:3])
cbind(fac1, fac2)
sir(~fac1, ~fac2)
```

sm2asreml *Converts sparseMatrix to asreml's giv format*

Description

Converts sparseMatrix to asreml's giv format: row-ordered, upper triangle sparse matrix.

Usage

```
sm2asreml(A=NULL, rownames=NULL)
```

Arguments

A	sparseMatrix
rownames	rownames of A

Value

data.frame: if A was formed from a pedigree equivalent to giv format returned by `asreml.Ainverse`

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

inverseA

Examples

```
data(bird.families)
A<-inverseA(bird.families)
Aasreml<-sm2asreml(A$Ainv, A$node.names)
```

spl *Orthogonal Spline Design Matrix*

Description

Orthogonal Spline Design Matrix

Usage

```
spl(x,  k=10, knots=NULL, type="LRTP")
```

Arguments

x	a numeric covariate
k	integer, defines knot points at the 1:k/(k+1) quantiles of x
knots	vector of knot points
type	type of spline - currently only low-rank thin-plate ("LRTP") are implemented

Value

Design matrix post-multiplied by the inverse square root of the penalty matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
## Not run:
x<-rnorm(100)
y<-x^2+cos(x)-x+0.2*x^3+rnorm(100)
plot(y~x)
lines((x^2+cos(x)-x+0.2*x^3)[order(x)]~sort(x))

dat<-data.frame(y=y, x=x)

m1<-MCMCglmm(y~x, random=~idv(spl(x)), data=dat, pr=TRUE, verbose=FALSE) # penalised smoother
m2<-MCMCglmm(y~x+spl(x),data=dat,  verbose=FALSE)                        # non-penalised

pred1<-(cBind(m1$X,m1$Z)%*%colMeans(m1$Sol))@x
pred2<-(cBind(m2$X)%*%colMeans(m2$Sol))@x

lines(pred1[order(x)]~sort(x), col="red")
lines(pred2[order(x)]~sort(x), col="green")

m1$DIC-mean(m1$Deviance)  # effective number of parameters < 13
m2$DIC-mean(m2$Deviance)  # effective number of parameters ~ 13

## End(Not run)
```

SShorns *Horn type and genders of Soay Sheep*

Description

Horn type and genders of Soay Sheep *Ovis aires*

Usage

```
BTdata
```

Format

a data frame with 666 rows and 3 columns, with individual idenitifier (id), horn type (horn) and gender (sex).

References

Clutton-Brock T., Pemberton, J. Eds. 2004 Soay Sheep: Dynamics \& Selection in an Island Population

---

summary.MCMCglmm *Summarising GLMM Fits from MCMCglmm*

Description

summary method for class "MCMCglmm". The returned object is suitable for printing with the print.summary.MCMCglmm method.

Usage

```
## S3 method for class 'MCMCglmm'
summary(object, random=FALSE, ...)
```

Arguments

object	an object of class "MCMCglmm"
random	logical: should the random effects be summarised
...	Further arguments to be passed

Value

DIC	Deviance Information Criterion
fixed.formula	model formula for the fixed terms
random.formula	model formula for the random terms
residual.formula	model formula for the residual terms
solutions	posterior mean, 95% HPD interval, MCMC p-values and effective sample size of fixed (and random) effects
Gcovariances	posterior mean, 95% HPD interval and effective sample size of random effect (co)variance components
Gterms	indexes random effect (co)variances by the component terms defined in the random formula
Rcovariances	posterior mean, 95% HPD interval and effective sample size of residual (co)variance components

Rterms	indexes residuals (co)variances by the component terms defined in the rcov formula
csats	chain length, burn-in and thinning interval
cutpoints	posterior mean, 95% HPD interval and effective sample size of cut-points from an ordinal model

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

See Also

MCMCglmm

Tri2M *Lower/Upper Triangle Elements of a Matrix*

Description

Lower/Upper triangle elements of a matrix or forms a matrix from a vector of lower/upper triangle elements

Usage

```
Tri2M(x, lower.tri = TRUE, reverse = TRUE, diag = TRUE)
```

Arguments

x	Matrix or vector
lower.tri	If x is a matrix then the lower triangle (TRUE) or upper triangle FALSE elements (including diagonal elements) are returned. If x is a vector a matrix is formed under the assumption that x are the lower triangle (TRUE) or upper triangle (FALSE) elements.
reverse	logical: ifTRUE a symmetric matrix is formed, if FALSE the remaining triangle is left as zeros.
diag	logical: ifTRUE diagonal elements are included.

Value

numeric or matrix

Author(s)

Jarrod Hadfield <j.hadfield@ed.ac.uk>

Examples

```
M<-rIW(diag(3), 10)
x<-Tri2M(M)
x
Tri2M(x, reverse=TRUE)
Tri2M(x, reverse=FALSE)
```

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