

# Package ‘MCMCglmm’

March 20, 2012

**Title** MCMC Generalised Linear Mixed Models

**Version** 2.16

**Depends** tensorA, Matrix, coda, ape, corpcor

**Suggests** rgl, combinat, mvtnorm, orthopolynom

**Date** 2012-03-19

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**Description** MCMC Generalised Linear Mixed Models

**License** GPL (>= 2)

**Repository** CRAN

**Date/Publication** 2012-03-20 11:52:01

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MCMCglimm-package

*Multivariate Generalised Linear Mixed Models*


---

## Description

MCMCglimm 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 <jarrod.hadfield@zoo.ox.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 <jarrod.hadfield@zoo.ox.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 <jarrod.hadfield@zoo.ox.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](#)

---

`commutation`*Commutation Matrix*

---

**Description**

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

**Usage**`commutation(m, n)`**Arguments**

`m` integer; number of rows of  $\mathbf{A}$   
`n` integer; number of columns of  $\mathbf{A}$

**Value**

Commutation Matrix

**Author(s)**

Jarrod Hadfield &lt;jarrod.hadfield@zoo.ox.ac.uk&gt;

**References**Magnus, J. R. & Neudecker, H. (1979) *Annals of Statistics* 7 (2) 381-394**Examples**`commutation(2,2)`

---

Ddivergence	<i>d-divergence</i>
-------------	---------------------

---

**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

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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	<i>List of unevaluated expressions for (mixed) partial derivatives of fitness with respect to linear predictors.</i>
--------------	--

---

### 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 predictor 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)

Jarrold Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

### See Also

[Dtensor](#)

---

Dtensor	<i>Tensor of (mixed) partial derivatives</i>
---------	--

---

**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)**

Jarrold Hadfield [j.hadfield@ed.ac.uk](mailto: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	<i>Evaluates a list of (mixed) partial derivatives</i>
-------------	--

---

**Description**

Evaluates a list of (mixed) partial derivatives

**Usage**

```
evalDtensor(x, mu)
```

**Arguments**

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

**Value**

tensor

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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)
```

---

inverseA	<i>Inverse Relatedness Matrix and Phylogenetic Covariance Matrix</i>
----------	--

---

**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)
```

**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)?

**Value**

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

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

**References**

- Henderson, C.R. (1976) *Biometrics* 32 (1) 69:83  
 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 &lt;jarrod.hadfield@zoo.ox.ac.uk&gt;

**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  $m \times m$  Kronecker Product Permutation Matrix**Usage**

KPPM(m, k)

**Arguments**

m	integer
k	integer

**Value**

Matrix

**Author(s)**

Jarrod Hadfield &lt;jarrod.hadfield@zoo.ox.ac.uk&gt;

**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 indicating 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 <jarrod.hadfield@zoo.ox.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)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

**See Also**

[dunif](#)

**Examples**

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

---

`leg`*Evaluates Orthogonal Legendre Polynomials*

---

**Description**

Evaluates orthogonal Legendre polynomials of degree 1 to degree over the specified set of points `x`

**Usage**

```
leg(x, degree, normalized=TRUE)
```

**Arguments**

x                    a numeric vector at which to evaluate the polynomial  
degree              the degree of the polynomial. If negative, degree 0 is not evaluated  
normalized          logical: should the polynomial be normalised

**Details**

Please refer to [legendre.polynomials](#) in the package orthopolynom for more details.

**Value**

Matrix of evaluated polynomials

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

**See Also**

[legendre.polynomials](#)

**Examples**

```
x<-rnorm(30)
model.matrix(~leg(x,2)-1)
```

---

list2bdiag	<i>Forms the direct sum from a list of matrices</i>
------------	---

---

**Description**

Forms a block-diagonal matrix from a list of matrices

**Usage**

```
list2bdiag(x)
```

**Arguments**

x                    list of square matrices

**Value**

matrix

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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", "MCMCglmm")`

**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)
```

**Arguments**

- |        |  |
|--------|--|
| fixed  | <code>formula</code> for the fixed effects, multiple responses are passed as a matrix using <code>cbind</code>   |
| random | <code>formula</code> for the random effects. Multiple random terms can be passed using the <code>+</code> operator, and in the most general case each random term has the form <code>variance.function(formula):random.term</code> . Currently, the only <code>variance.functions</code> available are <code>idv</code> , <code>idh</code> , <code>us</code> and <code>cor</code> . <code>idv</code> fits a constant variance across all components in <code>formula</code> , and <code>cor</code> fixes the variances to 1. Both <code>idh</code> and <code>us</code> fit different variances across each component in <code>formula</code> , but <code>us</code> will also fit the covariances. The <code>formula</code> 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 <code>random.term</code> effects. For simple random effects the <code>variance.function(formula)</code> can be omitted and the model syntax has the simpler form <code>~random1+random2+...</code> . There are two reserved variables: <code>units</code> which index rows of the response variable and <code>trait</code> which index columns of the response variable |
| rcov   | <code>formula</code> 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 <code>~us(trait):units</code>   |
| family | optional character vector of trait distributions. Currently, "gaussian", "poisson", "categorical", "multinomial", "ordinal", "exponential", "geometric", "cengaussian", "cenpoisson", "cenexponential", "zipoisson", "zapoisson",  |

"ztpoisson", "hupoisson" and "zibinomial" 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 $BV=I*1e+10$ , 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 compatability - 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 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 from 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.

### Value

SoI	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 $-2*\log(p(y ...))$
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

### Author(s)

Jarrod Hadfield <jarrod.hadfield@zoo.ox.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(PlodiaP0)
model1<-MCMCgImm(P0~1, random=~FSfamily, data=PlodiaP0, verbose=FALSE)
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 phylogenetic history

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

model2<-MCMCgImm(phenotype~1, random=~taxon, ginverse=list(taxon=Ainv),
data=test.data, prior=prior, verbose=FALSE)

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 several factors that have the same factor levels.

**Value**

design matrix

**Author(s)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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)
```

---

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	<i>Resistance of Indian meal moth caterpillars to the granulosis virus PiGV.</i>
---------	--

---

**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 (FSfamily), 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	<i>Resistance (as a binary trait) of Indian meal moth caterpillars to the granulosis virus PiGV.</i>
----------	--

---

**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 (FSfamily), 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.MCMCg1mm	<i>Plots MCMC chains from MCMCg1mm using plot.mcmc</i>
---------------	--

---

**Description**

plot method for class "MCMCg1mm".

**Usage**

```
## S3 method for class 'MCMCg1mm'
plot(x, random=FALSE, ...)
```

**Arguments**

x	an object of class "MCMCg1mm"
random	logical; should saved random effects be plotted
...	Further arguments to be passed

**Author(s)**

Jarrod Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

**See Also**

plot.mcmc, [MCMCg1mm](#)

---

plotsubspace	<i>Plots covariance matrices</i>
--------------	----------------------------------

---

**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 <jarrod.hadfield@zoo.ox.ac.uk> with code taken from the rgl package

**See Also**

[rgl](#)

**Examples**

```
if(require(rgl)!=FALSE){
  G1<-rIW(diag(4),10)
  G2<-G1*1.2
  plotsubspace(G1, G2, shadeCB=FALSE)
}
```

---

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)**

Jarrold Hadfield <jarrold.hadfield@zoo.ox.ac.uk>

**See Also**

[posterior.evals](#)

**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)**

Jarrold Hadfield <jarrold.hadfield@zoo.ox.ac.uk>

**See Also**

[posterior.cor](#)

**Examples**

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

---

posterior.mode	<i>Estimates the marginal parameter modes using kernel density estimation</i>
----------------	---

---

### 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 <a href="#">density</a> to adjust the bandwidth of the kernel density
...	other arguments to be passed

### Value

modes of the kernel density estimates

### Author(s)

Jarrod Hadfield <jarrod.hadfield@zoo.ox.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, ...)
```

### 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 marginalised
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.
...	Further arguments to be passed

### Value

Expectation and credible interval

### Author(s)

Jarrod Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

### See Also

[MCMCglmm](#)

---

prunePed	<i>Pedigree pruning</i>
----------	-------------------------

---

**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**

subsetting 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)**

Jarrold Hadfield <jarrold.hadfield@zoo.ox.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)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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)**

Jarrold Hadfield <jarrod.hadfield@zoo.ox.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 <sub>22</sub> 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 partitioning  $\mathbf{W}^{-1}$  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  $n \times \text{length}(V)$

**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](http://en.wikipedia.org/wiki/Inverse-Wishart_distribution)) the inverse scale matrix  $\Psi = (V * nu)$ . In earlier versions of MCMCglmm ( $< 1.11$ )  $\Psi = V^{-1}$ . 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:

<code>riwish(nu, nu*V)</code>	from MCMCpack
<code>rwishart(nu, solve(nu*V))\$IW</code>	from bayesm
<code>rIW(nu, solve(nu*V))</code>	from MCMCglmm $< 1.11$
<code>rIW(V, nu)</code>	from MCMCglmm $\geq 1.11$

**Author(s)**

Jarrod Hadfield <jarrod.hadfield@zoo.ox.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)
```

---

 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 <jarrod.hadfield@zoo.ox.ac.uk>

**References**

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

**See Also**

[rtnorm](#)

**Examples**

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

---

sir	<i>Design Matrix for Simultaneous and Recursive Relationships between Responses</i>
-----	---

---

**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 <jarrod.hadfield@zoo.ox.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 <jarrod.hadfield@zoo.ox.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 <jarrod.hadfield@zoo.ox.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<-MCMCg1mm(y~x, random=~idv(spl(x)), data=dat, pr=TRUE, saveX=TRUE, saveZ=TRUE, verbose=FALSE) # penalised smoo
m2<-MCMCg1mm(y~x+spl(x),data=dat, saveX=TRUE, verbose=FALSE) # non-penalised

pred1<-(cBind(m1$X,m1$Z))
pred2<-(cBind(m2$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 identifier (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
Rcovariances	posterior mean, 95% HPD interval and effective sample size of residual (co)variance components
cutpoints	posterior mean, 95% HPD interval and effective sample size of cut-points from an ordinal model
csats	chain length, burn-in and thinning interval
Gterms	indexes random effect (co)variances by the component terms defined in the random formula

**Author(s)**

Jarrod Hadfield <jarrod.hadfield@zoo.ox.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)
```

**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: if TRUE a symmetric matrix is formed, if FALSE the remaining triangle is left as zeros.

**Value**

numeric or matrix

**Author(s)**

Jarrod Hadfield <jarrod.hadfield@zoo.ox.ac.uk>

**Examples**

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

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