

# Package ‘BNSP’

May 8, 2020

**Title** Bayesian Non- And Semi-Parametric Model Fitting

**Version** 2.1.4

**Date** 2020-05-08

**Author** Georgios Papageorgiou

**Maintainer** Georgios Papageorgiou <gpapageo@gmail.com>

**Description** MCMC algorithms & processing functions for: 1. multivariate (and univariate) regression, with nonparametric models for the means, the variances and the correlation matrix, with variable selection, and 2. Dirichlet process mixtures.

**Depends** R (>= 3.1.0)

**Imports** coda, ggplot2, plot3D, threejs, gridExtra, cubature, Formula, plyr, mgcv, corrplot, label.switching

**LinkingTo** cubature

**Suggests** mvtnorm, np

**License** GPL (>= 2)

**URL** <http://www.bbk.ac.uk/ems/faculty/papageorgiou/BNSP>

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2020-05-08 08:40:17 UTC

## R topics documented:

BNSP-package	2
chol	3
clustering	4
continue	5
dpmj	6
histCorr	13
mvrn	14
mvrn2mcmc	19
plot.mvrn	20
plotCorr	21

predict.mvrm . . . . .	22
print.mvrm . . . . .	23
s . . . . .	24
simD . . . . .	25
sm . . . . .	26
summary.mvrm . . . . .	27
te . . . . .	28
ti . . . . .	29

<b>Index</b>	<b>31</b>
--------------	-----------

---

BNSP-package	<i>Bayesian non- and semi-parametric model fitting</i>
--------------	--

---

## Description

Markov chain Monte Carlo algorithms for non- and semi-parametric models: 1. spike-slab variable selection in multivariate mean/variance regression models with function `mvrm`, and 2. Dirichlet process mixture models with function `dpmj`.

## Details

Package: BNSP  
 Type: Package  
 Version: 2.1.4  
 Date: 2020-05-08  
 License: GPL (>=2)

This program is free software; you can redistribute it and/or modify it under the terms of the GNU General Public License as published by the Free Software Foundation; either version 2 of the License, or (at your option) any later version.

This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details.

For details on the GNU General Public License see <http://www.gnu.org/copyleft/gpl.html> or write to the Free Software Foundation, Inc., 51 Franklin Street, Fifth Floor, Boston, MA 02110-1301, USA.

## Acknowledgments

This work was partly supported by the Medical Research Council grant number G09018401.

## Author(s)

Georgios Papageorgiou (2014)

Maintainer: Georgios Papageorgiou <gpapageo@gmail.com>

## References

- Papageorgiou, G. and Marshall, B.C. (2020). Bayesian semiparametric analysis of multivariate continuous responses, with variable selection. *Journal of Computational and Graphical Statistics*, DOI: 10.1080/10618600.2020.1739534
- Papageorgiou, G. (2018). BNSP: an R Package for fitting Bayesian semiparametric regression models and variable selection. *The R Journal*, 10(2):526-548.
- Papageorgiou, G. (2018). Bayesian density regression for discrete outcomes. *Australian and New Zealand Journal of Statistics*, arXiv:1603.09706v3 [stat.ME].
- Papageorgiou, G., Richardson, S. and Best, N. (2015). Bayesian nonparametric models for spatially indexed data of mixed type. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 77:973-999.

---

 chol

*The Cholesky and modified Cholesky decompositions*


---

## Description

Computes the Cholesky factorization and modified Cholesky factorizations of a real symmetric positive-definite square matrix.

## Usage

```
chol(x, mod = TRUE, p = 1, ...)
```

## Arguments

x	A symmetric, positive-definite matrix.
mod	Defaults to TRUE. With this choice, the function returns the modified Cholesky decomposition. When mod = FALSE, the function returns the usual Cholesky decomposition.
p	Relevant only when mod = TRUE. It determines the size of the blocks of the block diagonal matrix.
...	other arguments.

## Details

The function computes the modified Cholesky decomposition of a real symmetric positive-definite square matrix  $\Sigma$ . This is given by

$$L\Sigma L^\top = D,$$

where  $L$  is a lower triangular matrix with ones on its main diagonal and  $D$  is a block diagonal matrix with block size determined by argument  $p$ .

## Value

The function returns matrices  $L$  and  $D$ .

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

The default function from **base**, [chol](#)

**Examples**

```
Sigma <- matrix(c(1.21,0.18,0.13,0.41,0.06,0.23,
                 0.18,0.64,0.10,-0.16,0.23,0.07,
                 0.13,0.10,0.36,-0.10,0.03,0.18,
                 0.41,-0.16,-0.10,1.05,-0.29,-0.08,
                 0.06,0.23,0.03,-0.29,1.71,-0.10,
                 0.23,0.07,0.18,-0.08,-0.10,0.36),6,6)

LD <- chol(Sigma)
L <- LD$L
D <- LD$D
round(L,5)
round(D,5)
solve(L) %*% D %*% solve(t(L))
LD <- chol(Sigma, p = 2)
L <- LD$L
D <- LD$D
round(L, 5)
round(D, 5)
solve(L) %*% D %*% solve(t(L))
```

---

clustering

*Computes the similarity matrix*

---

**Description**

Computes the similarity matrix.

**Usage**

```
clustering(object, ...)
```

**Arguments**

object	an object of class "mvrn", usually a result of a call to <code>mvrn</code> .
...	other arguments.

**Details**

The function computes the similarity matrix for clustering based on correlations or variables.

**Value**

Similarity matrix.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrn](#)

**Examples**

```
#see \code{mvrn} example
```

---

continue

*Continues the sampler from where it stopped*

---

**Description**

Allows the user to continue the sampler from the state it stopped in the previous call to `mvrn`.

**Usage**

```
continue(object, sweeps, discard = FALSE, ...)
```

**Arguments**

<code>object</code>	An object of class "mvrn", usually a result of a call to <code>mvrn</code> .
<code>sweeps</code>	The number of additional sweeps, maintaining the same thinning interval as specified in the original call to <code>mvrn</code> .
<code>discard</code>	If set to true, the previous samples are discarded.
<code>...</code>	other arguments.

**Details**

The function allows the sampler to continue from the state it last stopped.

**Value**

The function returns an object of class `mvrn`.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**[mvrn](#)**Examples**

```
#see \code{mvrn} example
```

---

`dpmj`*Dirichlet process mixtures of joint models*

---

**Description**

Fits Dirichlet process mixtures of joint response-covariate models, where the covariates are of mixed type while the discrete responses are represented utilizing continuous latent variables. See ‘Details’ section for a full model description and Papageorgiou (2018) for all technical details.

**Usage**

```
dpmj(formula, Fcdf, data, offset, sampler = "truncated", Xpred, offsetPred,
      StorageDir, ncomp, sweeps, burn, thin = 1, seed, H, Hdf, d, D,
      Alpha.xi, Beta.xi, Alpha.alpha, Beta.alpha, Trunc.alpha, ...)
```

**Arguments**

<code>formula</code>	a formula defining the response and the covariates e.g. $y \sim x$ .
<code>Fcdf</code>	a description of the kernel of the response variable. Currently five options are supported: 1. "poisson", 2. "negative binomial", 3. "generalized poisson", 4. "binomial" and 5. "beta binomial". The first three kernels are used for count data analysis, where the third kernel allows for both over- and under-dispersion relative to the Poisson distribution. The last two kernels are used for binomial data analysis. See ‘Details’ section for some of the kernel details.
<code>data</code>	an optional data frame, list or environment (or object coercible by ‘as.data.frame’ to a data frame) containing the variables in the model. If not found in ‘data’, the variables are taken from ‘environment(formula)’.
<code>offset</code>	this can be used to specify an a priori known component to be included in the model. This should be ‘NULL’ or a numeric vector of length equal to the sample size. One ‘offset’ term can be included in the formula, and if more are required, their sum should be used.
<code>sampler</code>	the MCMC algorithm to be utilized. The two options are <code>sampler = "slice"</code> which implements a slice sampler (Walker, 2007; Papaspiliopoulos, 2008) and <code>sampler = "truncated"</code> which proceeds by truncating the countable mixture at <code>ncomp</code> components (see argument <code>ncomp</code> ).
<code>Xpred</code>	an optional design matrix the rows of which include the values of the covariates $x$ for which the conditional distribution of $Y x, D$ (where $D$ denotes the data) is calculated. These are treated as ‘new’ covariates i.e. they do not contribute to the likelihood. The matrix shouldn’t include a column of 1’s. NA’s can be included to obtain averaged effects.

offsetPred	the offset term associated with the new covariates Xpred. It is of dimension one i.e. the same offset term is used for all rows of Xpred. If Fcdf is one of "poisson" or "negative binomial" or "generalized poisson", then offsetPred is the Poisson offset term. If Fcdf is one of "binomial" or "beta binomial", then offsetPred is the number of Binomial trials. If offsetPred is missing, it is taken to be the mean of offset, rounded to the nearest integer.
StorageDir	a directory to store files with the posterior samples of models parameters and other quantities of interest. If a directory is not provided, files are created in the current directory and removed when the sampler completes.
ncomp	number of mixture components. It defines where the countable mixture of densities [in (1) below] is truncated. Even if sampler="slice" is chosen, ncomp needs to be specified as it is used in the initialization process.
sweeps	total number of posterior samples, including those discarded in burn-in period (see argument burn) and those discarded by the thinning process (see argument thin).
burn	length of burn-in period.
thin	thinning parameter.
seed	optional seed for the random generator.
H	optional scale matrix of the Wishart-like prior assigned to the restricted covariance matrices $\Sigma_h^*$ . See 'Details' section.
Hdf	optional degrees of freedom of the prior Wishart-like prior assigned to the restricted covariance matrices $\Sigma_h^*$ . See 'Details' section.
d	optional prior mean of the mean vector $\mu_h$ . See 'Details' section.
D	optional prior covariance matrix of the mean vector $\mu_h$ . See 'Details' section.
Alpha.xi	<p>an optional parameter that depends on the specified Fcdf argument.</p> <ol style="list-style-type: none"> <li>1. If Fcdf = "poisson", this argument is parameter <math>\alpha_\xi</math> of the prior of the Poisson rate: <math>\xi \sim \text{Gamma}(\alpha_\xi, \beta_\xi)</math>.</li> <li>2. If Fcdf = "negative binomial", this argument is a two-dimensional vector that includes parameters <math>\alpha_{1\xi}</math> and <math>\alpha_{2\xi}</math> of the priors: <math>\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})</math> and <math>\xi_2 \sim \text{Gamma}(\alpha_{2\xi}, \beta_{2\xi})</math>, where <math>\xi_1</math> and <math>\xi_2</math> are the two parameters of the Negative Binomial pmf.</li> <li>3. If Fcdf = "generalized poisson", this argument is a two-dimensional vector that includes parameters <math>\alpha_{1\xi}</math> and <math>\alpha_{2\xi}</math> of the priors: <math>\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})</math> and <math>\xi_2 \sim \text{N}(\alpha_{2\xi}, \beta_{2\xi})I[\xi_2 \in R_{\xi_2}]</math>, where <math>\xi_1</math> and <math>\xi_2</math> are the two parameters of the Generalized Poisson pmf. Parameter <math>\xi_2</math> is restricted in the range <math>R_{\xi_2} = (0.05, \infty)</math> as it is a dispersion parameter.</li> <li>4. If Fcdf = "binomial", this argument is parameter <math>\alpha_\xi</math> of the prior of the Binomial probability: <math>\xi \sim \text{Beta}(\alpha_\xi, \beta_\xi)</math>.</li> <li>5. If Fcdf = "beta binomial", this argument is a two-dimensional vector that includes parameters <math>\alpha_{1\xi}</math> and <math>\alpha_{2\xi}</math> of the priors: <math>\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})</math> and <math>\xi_2 \sim \text{Gamma}(\alpha_{2\xi}, \beta_{2\xi})</math>, where <math>\xi_1</math> and <math>\xi_2</math> are the two parameters of the Beta Binomial pmf.</li> </ol> <p>See 'Details' section.</p>
Beta.xi	an optional parameter that depends on the specified family.

1. If Fcdf = "poisson", this argument is parameter  $\beta_\xi$  of the prior of the Poisson rate:  $\xi \sim \text{Gamma}(\alpha_\xi, \beta_\xi)$ .
2. If Fcdf = "negative binomial", this argument is a two-dimensional vector that includes parameters  $\beta_{1\xi}$  and  $\beta_{2\xi}$  of the priors:  $\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})$  and  $\xi_2 \sim \text{Gamma}(\alpha_{2\xi}, \beta_{2\xi})$ , where  $\xi_1$  and  $\xi_2$  are the two parameters of the Negative Binomial pmf.
3. If Fcdf = "generalized poisson", this argument is a two-dimensional vector that includes parameters  $\beta_{1\xi}$  and  $\beta_{2\xi}$  of the priors:  $\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})$  and  $\xi_2 \sim \text{Normal}(\alpha_{2\xi}, \beta_{2\xi})I[\xi_2 \in R_{\xi_2}]$ , where  $\xi_1$  and  $\xi_2$  are the two parameters of the Generalized Poisson pmf. Parameter  $\xi_2$  is restricted in the range  $R_{\xi_2} = (0.05, \infty)$  as it is a dispersion parameter. Note that  $\beta_{2\xi}$  is a standard deviation.
4. If Fcdf = "binomial", this argument is parameter  $\beta_\xi$  of the prior of the Binomial probability:  $\xi \sim \text{Beta}(\alpha_\xi, \beta_\xi)$ .
5. If Fcdf = "beta binomial", this argument is a two-dimensional vector that includes parameters  $\beta_{1\xi}$  and  $\beta_{2\xi}$  of the priors:  $\xi_1 \sim \text{Gamma}(\alpha_{1\xi}, \beta_{1\xi})$  and  $\xi_2 \sim \text{Gamma}(\alpha_{2\xi}, \beta_{2\xi})$ , where  $\xi_1$  and  $\xi_2$  are the two parameters of the Beta Binomial pmf.

See 'Details' section.

Alpha.alpha	optional shape parameter $\alpha_\alpha$ of the Gamma prior assigned to the concentration parameter $\alpha$ . See 'Details' section.
Beta.alpha	optional rate parameter $\beta_\alpha$ of the Gamma prior assigned to concentration parameter $\alpha$ . See 'Details' section.
Trunc.alpha	optional truncation point $c_\alpha$ of the Gamma prior assigned to concentration parameter $\alpha$ . See 'Details' section.
...	Other options that will be ignored.

## Details

Function dpmj returns samples from the posterior distributions of the parameters of the model:

$$f(y_i, x_i) = \sum_{h=1}^{\infty} \pi_h f(y_i, x_i | \theta_h), \quad (1)$$

where  $y_i$  is a univariate discrete response,  $x_i$  is a  $p$ -dimensional vector of mixed type covariates, and  $\pi_h, h \geq 1$ , are obtained according to Sethuraman's (1994) stick-breaking construction:  $\pi_1 = v_1$ , and for  $l \geq 2, \pi_l = v_l \prod_{j=1}^{l-1} (1 - v_j)$ , where  $v_k$  are iid samples  $v_k \sim \text{Beta}(1, \alpha), k \geq 1$ .

Let  $Z$  denote a discrete variable (response or covariate). It is represented as discretized version of a continuous latent variable  $Z^*$ . Observed discrete  $Z$  and continuous latent variable  $Z^*$  are connected by:

$$z = q \iff c_{q-1} < z^* < c_q, q = 0, 1, 2, \dots,$$

where the cut-points are obtained as:  $c_{-1} = -\infty$ , while for  $q \geq 0, c_q = c_q(\lambda) = \Phi^{-1}\{F(q; \lambda)\}$ . Here  $\Phi(\cdot)$  is the cumulative distribution function (cdf) of a standard normal variable and  $F(\cdot)$  denotes an appropriate cdf. Further, latent variables are assumed to independently follow a  $N(0, 1)$  distribution, where the mean and variance are restricted to be zero and one as they are non-identifiable by the data. Choices for  $F(\cdot)$  are described next.



For counts, three options are supported. First,  $F(\cdot; \lambda_i)$  can be specified as the cdf of a Poisson( $H_i \xi_h$ ) variable. Here  $\lambda_i = (\xi_h, H_i)^T$ ,  $\xi_h$  denotes the Poisson rate associated with cluster  $h$ , and  $H_i$  the offset term associated with sampling unit  $i$ . Second,  $F(\cdot; \lambda_i)$  can be specified as the negative binomial cdf, where  $\lambda_i = (\xi_{1h}, \xi_{2h}, H_i)^T$ . This option allows for overdispersion within each cluster relative to the Poisson distribution. Third,  $F(\cdot; \lambda_i)$  can be specified as the Generalized Poisson cdf, where, again,  $\lambda_i = (\xi_{1h}, \xi_{2h}, H_i)^T$ . This option allows for both over- and under-dispersion within each cluster.

For Binomial data, two options are supported. First,  $F(\cdot; \lambda_i)$  may be taken to be the cdf of a Binomial( $H_i, \xi_h$ ) variable, where  $\xi_h$  denotes the success probability of cluster  $h$  and  $H_i$  the number of trials associated with sampling unit  $i$ . Second,  $F(\cdot; \lambda_i)$  may be specified to be the beta-binomial cdf, where  $\lambda = (\xi_{1h}, \xi_{2h}, H_i)^T$ .

The special case of Binomial data is treated as

$$Z = 0 \iff z^* < 0, z^* \sim N(\mu_z^*, 1).$$

Details on all kernels are provided in the two tables below. The first table provides the probability mass functions and the mean in the presence of an offset term (which may be taken to be one). The column ‘Sample’ indicates for which parameters the routine provides posterior samples. The second table provides information on the assumed priors along with the default values of the parameters of the prior distributions and it also indicates the function arguments that allow the user to alter these.

Kernel	PMF	Offset	Mean	Sample
Poisson	$\exp(-H\xi)(H\xi)^y/y!$	$H$	$H\xi$	$\xi$
Negative Binomial	$\frac{\Gamma(y+\xi_1)}{\Gamma(\xi_1)\Gamma(y+1)} \left(\frac{\xi_2}{H+\xi_2}\right)^{\xi_1} \left(\frac{H}{H+\xi_2}\right)^y$	$H$	$H\xi_1/\xi_2$	$\xi_1, \xi_2$
Generalized Poisson	$\xi_1 \{\xi_1 + (\xi_2 - 1)y\}^{y-1} \xi_2^{-y} \times \exp\{-[\xi_1 + (\xi_2 - 1)y]/\xi_2\}/y!$	$H$	$H\xi_1$	$\xi_1, \xi_2$
Binomial	$\binom{N}{y} \xi^y (1-\xi)^{N-y}$	$N$	$N\xi$	$\xi$
Beta Binomial	$\binom{N}{y} \frac{\text{Beta}(y+\xi_1, N-y+\xi_2)}{\text{Beta}(\xi_1, \xi_2)}$	$N$	$N\xi_1/(\xi_1 + \xi_2)$	$\xi_1, \xi_2$

Kernel	Priors	Default Values
Poisson	$\xi \sim \text{Gamma}(\alpha_\xi, \beta_\xi)$	Alpha.xi = 1.0, Beta.xi = 0.1
Negative Binomial	$\xi_i \sim \text{Gamma}(\alpha_{\xi_i}, \beta_{\xi_i}), i = 1, 2$	Alpha.xi = c(1.0,1.0), Beta.xi = c(0.1,0.1)
Generalized Poisson	$\xi_1 \sim \text{Gamma}(\alpha_{\xi_1}, \beta_{\xi_1})$ $\xi_2 \sim \text{N}(\alpha_{\xi_2}, \beta_{\xi_2}) I[\xi_2 > 0.05]$ where $\beta_{\xi_2}$ denotes st.dev.	Alpha.xi = c(1.0,1.0), Beta.xi = c(0.1,1.0)
Binomial	$\xi \sim \text{Beta}(\alpha_\xi, \beta_\xi)$	Alpha.xi = 1.0, Beta.xi = 1.0
Beta Binomial	$\xi_i \sim \text{Gamma}(\alpha_{\xi_i}, \beta_{\xi_i}), i = 1, 2$	Alpha.xi = c(1.0,1.0), Beta.xi = c(0.1,0.1)

Let  $z_i = (y_i, x_i^T)^T$  denote the joint vector of observed continuous and discrete variables and  $z_i^*$  the corresponding vector of continuous observed and latent variables. With  $\theta_h$  denoting model parameters associated with the  $h$ th cluster, the joint density  $f(z_i|\theta_h)$  takes the form

$$f(z_i|\theta_h) = \int_{R(y)} \int_{R(x_d)} N_q(z_i^*; \mu_h^*, \Sigma_h^*) dx_d^* dy^*,$$

where

$$\mu_h^* = \begin{pmatrix} 0 \\ \mu_h \end{pmatrix}, \quad \Sigma_h^* = \begin{bmatrix} C_h & \nu_h^T \\ \nu_h & \Sigma_h \end{bmatrix},$$

where  $C_h$  is the covariance matrix of the latent continuous variables and it has diagonal elements equal to one i.e. it is a correlation matrix.

In addition to the priors defined in the table above, we specify the following:

1. The restricted covariance matrix  $\Sigma_h^*$  is assigned a prior distribution that is based on the Wishart distribution with degrees of freedom set by default to dimension of matrix plus two and diagonal scale matrix, with the sub-matrix that corresponds to discrete variables taken to be the identity matrix and with sub-matrix that corresponds to continuous variables having entries equal to 1/8 of the square of the observed data range. Default values can be changed using arguments `H` and `Hdf`.
2. The prior on  $\mu_h$ , the non-zero part of  $\mu_h^*$ , is taken to be multivariate normal  $\mu_h \sim N(d, D)$ . The mean  $d$  is taken to be equal to the center of the dataset. The covariance matrix  $D$  is taken to be diagonal. Its elements that correspond to continuous variables are set equal to 1/8 of the square of the observed data range while the elements that correspond to binary variables are set equal to 5. Arguments `Mu.mu` and `Sigma.mu` allow the user to change the default values.
3. The concentration parameter  $\alpha$  is assigned a  $\text{Gamma}(\alpha_\alpha, \beta_\alpha)$  prior over the range  $(c_\alpha, \infty)$ , that is,  $f(\alpha) \propto \alpha^{\alpha_\alpha - 1} \exp\{-\alpha\beta_\alpha\} I[\alpha > c_\alpha]$ , where  $I[\cdot]$  is the indicator function. The default values are  $\alpha_\alpha = 2.0$ ,  $\beta_\alpha = 5.0$ , and  $c_\alpha = 0.25$ . Users can alter the default using using arguments `Alpha.alpha`, `Beta.alpha` and `Turnc.alpha`.

## Value

Function `dpmj` returns the following:

<code>call</code>	the matched call.
<code>seed</code>	the seed that was used (in case replication of the results is needed).
<code>meanReg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean of the conditional expectation of the response $y$ given each new covariate $x$ .
<code>medianReg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean of the conditional 50% quantile of the response $y$ given each new covariate $x$ .
<code>q1Reg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean of the conditional 25% quantile of the response $y$ given each new covariate $x$ .
<code>q3Reg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean of the conditional 75% quantile of the response $y$ given each new covariate $x$ .
<code>modeReg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean of the conditional mode of the response $y$ given each new covariate $x$ .
<code>denReg</code>	if <code>Xpred</code> is specified, the function returns the posterior mean conditional density of the response $y$ given each new covariate $x$ . Results are presented in a matrix the rows of which correspond to the different $x$ s.
<code>denVar</code>	if <code>Xpred</code> is specified, the function returns the posterior variance of the conditional density of the response $y$ given each new covariate $x$ . Results are presented in a matrix the rows of which correspond to the different $x$ s.

Further, function `dpmj` creates files where the posterior samples are written. These files are (with all file names preceded by ‘BNSP.’):

<code>alpha.txt</code>	this file contains samples from the posterior of the concentration parameters $\alpha$ . The file is arranged in $(\text{sweeps-burn})/\text{thin}$ lines and one column, each line including one posterior sample.
<code>compAlloc.txt</code>	this file contains the allocations to clusters obtained during posterior sampling. It consists of $(\text{sweeps-burn})/\text{thin}$ lines, that represent the posterior samples, and $n$ columns, that represent the sampling units. Clusters are represented by integers ranging from 0 to $\text{ncomp}-1$ .
<code>MeanReg.txt</code>	this file contains the conditional means of the response $y$ given covariates $x$ obtained during posterior sampling. The rows represent the $(\text{sweeps-burn})/\text{thin}$ posterior samples. The columns represent the various covariate values $x$ for which the means are obtained.
<code>MedianReg.txt</code>	this file contains the 50% conditional quantile of the response $y$ given covariates $x$ obtained during posterior sampling. The rows represent the $(\text{sweeps-burn})/\text{thin}$ posterior samples. The columns represent the various covariate values $x$ for which the medians are obtained.
<code>muh.txt</code>	this file contains samples from the posteriors of the $p$ -dimensional mean vectors $\mu_h, h = 1, 2, \dots, \text{ncomp}$ . The file is arranged in $((\text{sweeps-burn})/\text{thin}) * \text{ncomp}$ lines and $p$ columns. In more detail, sweeps create $\text{ncomp}$ lines representing samples $\mu_h^{(sw)}, h = 1, \dots, \text{ncomp}$ , where superscript $sw$ represents a particular sweep. The elements of $\mu_h^{(sw)}$ are written in the columns of the file.
<code>nmembers.txt</code>	this file contains $(\text{sweeps-burn})/\text{thin}$ lines and $\text{ncomp}$ columns, where the lines represent posterior samples while the columns represent the components or clusters. The entries represent the number of sampling units allocated to each component.
<code>Q05Reg.txt</code>	this file contains the 5% conditional quantile of the response $y$ given covariates $x$ obtained during posterior sampling. The rows represent the $(\text{sweeps-burn})/\text{thin}$ posterior samples. The columns represent the various covariate values $x$ for which the quantiles are obtained.
<code>Q10Reg.txt</code>	as above, for the 10% conditional quantile.
<code>Q15Reg.txt</code>	as above, for the 15% conditional quantile.
<code>Q20Reg.txt</code>	as above, for the 20% conditional quantile.
<code>Q25Reg.txt</code>	as above, for the 25% conditional quantile.
<code>Q75Reg.txt</code>	as above, for the 75% conditional quantile.
<code>Q80Reg.txt</code>	as above, for the 80% conditional quantile.
<code>Q85Reg.txt</code>	as above, for the 85% conditional quantile.
<code>Q90Reg.txt</code>	as above, for the 90% conditional quantile.
<code>Q95Reg.txt</code>	as above, for the 95% conditional quantile.
<code>Sigmah.txt</code>	this file contains samples from the posteriors of the $q \times q$ restricted covariance matrices $\Sigma_h^*, h = 1, 2, \dots, \text{ncomp}$ . The file is arranged in $((\text{sweeps-burn})/\text{thin}) * \text{ncomp}$ lines and $q^2$ columns. In more detail, sweeps create $\text{ncomp}$ lines representing samples $\Sigma_h^{(sw)}, h = 1, \dots, \text{ncomp}$ , where superscript $sw$ represents a particular sweep. The elements of $\Sigma_h^{(sw)}$ are written in the columns of the file.

xih.txt            this file contains samples from the posteriors of parameters  $\xi_h$ ,  $h = 1, 2, \dots, ncomp$ . The file is arranged in  $((sweeps-burn)/thin)*ncomp$  lines and one or two columns, depending on the number of parameters in the selected Fcdf. Sweeps write in the file  $ncomp$  lines representing samples  $\xi_h^{(sw)}$ ,  $h = 1, \dots, ncomp$ , where superscript  $sw$  represents a particular sweep.

Updated.txt        this file contains  $(sweeps-burn)/thin$  lines with the number of components updated at each iteration of the sampler (relevant for slice sampling).

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

### References

- Consul, P. C. & Famoye, G. C. (1992). Generalized Poisson regression model. *Communications in Statistics - Theory and Methods*, 1992, 89-109.
- Papageorgiou, G. (2018). Bayesian density regression for discrete outcomes. arXiv:1603.09706v3 [stat.ME].
- Papaspiliopoulos, O. (2008). A note on posterior sampling from Dirichlet mixture models. Technical report, University of Warwick.
- Sethuraman, J. (1994). A constructive definition of Dirichlet priors. *Statistica Sinica*, 4, 639-650.
- Walker, S. G. (2007). Sampling the Dirichlet mixture model with slices. *Communications in Statistics Simulation and Computation*, 36(1), 45-54.

### Examples

```
#Bayesian nonparametric joint model with binomial response Y and one predictor X
data(simD)
pred<-seq(with(simD,min(X))+0.1,with(simD,max(X))-0.1,length.out=30)
npred<-length(pred)
# fit1 and fit2 define the same model but with different numbers of
# components and posterior samples
fit1 <- dpmj(cbind(Y,(E-Y))~X, Fcdf="binomial", data=simD, ncomp=10, sweeps=20,
            burn=10, sampler="truncated", Xpred=pred, offsetPred=30)
fit2 <- dpmj(cbind(Y,(E-Y))~X, Fcdf="binomial", data=simD, ncomp=50, sweeps=5000,
            burn=1000, sampler="truncated", Xpred=pred, offsetPred=30)
plot(with(simD,X),with(simD,Y)/with(simD,E))
lines(pred,fit2$medianReg/30,col=3,lwd=2)
# with discrete covariate
simD<-data.frame(simD,Xd=sample(c(0,1),300,replace=TRUE))
pred<-c(0,1)
fit3 <- dpmj(cbind(Y,(E-Y))~Xd, Fcdf="binomial", data=simD, ncomp=10, sweeps=20,
            burn=10, sampler="truncated", Xpred=pred, offsetPred=30)
```

---

histCorr *Creates plots of correlation matrices*

---

### Description

This function plots the posterior distribution of the elements of correlation matrices.

### Usage

```
histCorr(x, term = "R", plotOptions = list(),...)
```

### Arguments

x	an object of class 'mvrn', as generated by function mvrn.
term	Admits two possible values: "R" to plot samples from the posterior of the correlation matrix $R$ , and "muR" to plot samples from the posterior of the means $\mu_R$ .
plotOptions	ggplot type options.
...	other arguments.

### Details

Use this function to visualize the elements of a correlation matrix.

### Value

Posterior distributions of elements of correlation matrices.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

### See Also

[mvrn](#)

### Examples

```
#see \code{mvrn} example
```

mvrn

*Bayesian semiparametric analysis of multivariate continuous responses, with variable selection*

## Description

Implements an MCMC algorithm for posterior sampling based on a semiparametric model for continuous multivariate responses and additive models for the mean and variance functions. The model utilizes spike-slab priors for variable selection and regularization. See ‘Details’ section for a full description of the model.

## Usage

```
mvrn(formula, data = list(), sweeps, burn = 0, thin = 1, seed, StorageDir,
      c.betaPrior = "IG(0.5, 0.5 * n * p)", pi.muPrior = "Beta(1, 1)",
      c.alphaPrior = "IG(1.1, 1.1)", sigmaPrior = "HN(2)", pi.sigmaPrior = "Beta(1, 1)",
      mu.RPrior = "N(0, 1)", sigma.RPrior = "HN(1)", corr.Model = c("common", nClust = 1),
      DP.concPrior = "Gamma(5, 2)", tuneAlpha, tuneSigma2, tuneCb, tuneCa, tuneR,
      tuneSigma2R, tau, FT = 1, ...)
```

## Arguments

formula	a formula defining the responses and the covariates in the mean and variance models e.g. $y_1   y_2 \sim x   z$ or for smooth effects $y_1   y_2 \sim sm(x)   sm(z)$ . The package uses the extended formula notation, where the responses are defined on the left of $\sim$ and the mean and variance models on the right.
data	a data frame.
sweeps	total number of posterior samples, including those discarded in burn-in period (see argument burn) and those discarded by the thinning process (see argument thin).
burn	length of burn-in period.
thin	thinning parameter.
seed	optional seed for the random generator.
StorageDir	a required directory to store files with the posterior samples of models parameters.
c.betaPrior	The inverse Gamma prior of $c_\beta$ . The default is "IG(0.5,0.5*n*p)", that is, an inverse Gamma with parameters $1/2$ and $np/2$ , where $n$ is the number of sampling units and $p$ is the length of the response vector.
pi.muPrior	The Beta prior of $\pi_\mu$ . The default is "Beta(1,1)". It can be of dimension 1, of dimension $K$ (the number of effects that enter the mean model), or of dimension $pK$
c.alphaPrior	The inverse Gamma prior of $c_\alpha$ . The default is "IG(1.1,1.1)". Half-normal priors for $\sqrt{c_\alpha}$ are also available, declared using "HN(a)", where "a" is a positive number. It can be of dimension 1 or $p$ (the length of the multivariate response).

sigmaPrior	The prior of $\sigma$ . The default is "HN(2)", a half-normal prior for $\sigma$ with variance equal to two, $\sigma \sim N(0, 2)I[\sigma > 0]$ . Inverse Gamma priors for $\sigma^2$ are also available, declared using "IG(a,b)". It can be of dimension 1 or $p$ (the length of the multivariate response).
pi.sigmaPrior	The Beta prior of $\pi_\sigma$ . The default is "Beta(1,1)". It can be of dimension 1, of dimension $Q$ (the number of effects that enter the variance model), or of dimension $pQ$ .
mu.RPrior	The normal prior for $\mu_R$ . The default is the standard normal distribution.
sigma.RPrior	The half normal prior for $\sigma_R$ . The default is the half normal distribution with variance one.
corr.Model	Specifies the model for the correlation matrix $R$ . The three choices supported are "common", that specifies a common correlations model, "groupC", that specifies a grouped correlations model, and "groupV", that specifies a grouped variables model. When the model chosen is either "groupC" or "groupV", the upper limit on the number of clusters can also be specified, using <code>corr.Model = c("groupC", nClust = d)</code> or <code>corr.Model = c("groupV", nClust = p)</code> . If the number of clusters is left unspecified, for the "groupV" model, it is taken to be $p$ , the number of responses. For the "groupC" model, it is taken to be $d = p(p-1)/2$ , the number of free elements in the correlation matrix.
DP.concPrior	The Gamma prior for the Dirichlet process concentration parameter.
tuneAlpha	Starting value of the tuning parameter for sampling regression coefficients of the variance model $\alpha$ . Defaults at 5.
tuneSigma2	Starting value of the tuning parameter for sampling variances $\sigma_j^2$ . Defaults at 1.
tuneCb	Starting value of the tuning parameter for sampling $c_\beta$ . Defaults at 10.
tuneCa	Starting value of the tuning parameter for sampling $c_\alpha$ . Defaults at 1.
tuneR	Starting value of the tuning parameter for sampling correlation matrices. Defaults at $100(p+2)$ .
tuneSigma2R	Starting value of the tuning parameter for sampling $\sigma_R^2$ . Defaults at 1.
tau	The $\tau$ of the shadow prior. Defaults at 0.01.
FT	Binary indicator. If set equal to 1, the Fisher's z transform of the correlations is modelled, otherwise if set equal to 0, the untransformed correlations are modelled.
...	Other options that will be ignored.

## Details

Function `mmvrn` returns samples from the posterior distributions of the parameters of a regression model with normally distributed multivariate responses and mean and variance functions modeled in terms of covariates. For instance, in the presence of two responses  $(y_1, y_2)$  and two covariates in the mean model  $(u_1, u_2)$  and two in the variance model  $(w_1, w_2)$ , we may choose to fit

$$\begin{aligned}\mu_u &= \beta_0 + \beta_1 u_1 + f_\mu(u_2), \\ \log(\sigma_W^2) &= \alpha_0 + \alpha_1 w_1 + f_\sigma(w_2),\end{aligned}$$

parametrically modelling the effects of  $u_1$  and  $w_1$  and non-parametrically modelling the effects of  $u_2$  and  $w_2$ . Smooth functions, such as  $f_\mu$  and  $f_\sigma$ , are represented by basis function expansion,

$$f_\mu(u_2) = \sum_j \beta_j \phi_j(u_2),$$

$$f_\sigma(w_2) = \sum_j \alpha_j \phi_j(w_2),$$

where  $\phi$  are the basis functions and  $\beta$  and  $\alpha$  are regression coefficients.

The variance model can equivalently be expressed as

$$\sigma_W^2 = \exp(\alpha_0) \exp(\alpha_1 w_1 + f_\sigma(w_2)) = \sigma^2 \exp(\alpha_1 w_1 + f_\sigma(w_2)),$$

where  $\sigma^2 = \exp(\alpha_0)$ . This is the parameterization that we adopt in this implementation.

Positive prior probability that the regression coefficients in the mean model are exactly zero is achieved by defining binary variables  $\gamma$  that take value  $\gamma = 1$  if the associated coefficient  $\beta \neq 0$  and  $\gamma = 0$  if  $\beta = 0$ . Indicators  $\delta$  that take value  $\delta = 1$  if the associated coefficient  $\alpha \neq 0$  and  $\delta = 0$  if  $\alpha = 0$  for the variance function are defined analogously. We note that all coefficients in the mean and variance functions are subject to selection except the intercepts,  $\beta_0$  and  $\alpha_0$ .

*Prior specification:*

For the vector of non-zero regression coefficients  $\beta_\gamma$  we specify a g-prior

$$\beta_\gamma | c_\beta, \sigma^2, \gamma, \alpha, \delta \sim N(0, c_\beta \sigma^2 (\tilde{X}_\gamma^\top \tilde{X}_\gamma)^{-1}).$$

where  $\tilde{X}$  is a scaled version of design matrix  $X$  of the mean model.

For the vector of non-zero regression coefficients  $\alpha_\delta$  we specify a normal prior

$$\alpha_\delta | c_\alpha, \delta \sim N(0, c_\alpha I).$$

Independent priors are specified for the indicators variables  $\gamma$  and  $\delta$  as  $P(\gamma = 1 | \pi_\mu) = \pi_\mu$  and  $P(\delta = 1 | \pi_\sigma) = \pi_\sigma$ . Further, Beta priors are specified for  $\pi_\mu$  and  $\pi_\sigma$

$$\pi_\mu \sim \text{Beta}(c_\mu, d_\mu), \pi_\sigma \sim \text{Beta}(c_\sigma, d_\sigma).$$

We note that blocks of regression coefficients associated with distinct covariate effects have their own probability of selection ( $\pi_\mu$  or  $\pi_\sigma$ ) and this probability has its own prior distribution.

Further, we specify inverse Gamma priors for  $c_\beta$  and  $c_\alpha$

$$c_\beta \sim \text{IG}(a_\beta, b_\beta), c_\alpha \sim \text{IG}(a_\alpha, b_\alpha)$$

For  $\sigma^2$  we consider inverse Gamma and half-normal priors

$$\sigma^2 \sim \text{IG}(a_\sigma, b_\sigma), |\sigma| \sim N(0, \phi_\sigma^2).$$

Lastly, for the elements of the correlation matrix, we specify normal distributions with mean  $\mu_R$  and variance  $\sigma_R^2$ , with the priors on these two parameters being normal and half-normal, respectively. This is the common correlations model. Further, the grouped correlations model can be specified. It considers a mixture of normal distributions for the means  $\mu_R$ . The grouped correlations model can also be specified. It clusters the variables instead of the correlations.



**Value**

Function `mmvrn` returns the following:

<code>call</code>	the matched call.
<code>formula</code>	model formula.
<code>seed</code>	the seed that was used (in case replication of the results is needed).
<code>data</code>	the dataset
<code>X</code>	the mean model design matrix.
<code>Z</code>	the variance model design matrix.
<code>LG</code>	the length of the vector of indicators $\gamma$ .
<code>LD</code>	the length of the vector of indicators $\delta$ .
<code>mcp</code>	the MCMC parameters: length of burn in period, total number of samples, thinning period.
<code>nSamples</code>	total number of posterior samples
<code>DIR</code>	the storage directory

Further, function `mvrn` creates files where the posterior samples are written. These files are (with all file names preceded by 'BNSP.')

<code>alpha.txt</code>	contains samples from the posterior of vector $\alpha$ . Rows represent posterior samples and columns represent the regression coefficient, and they are in the same order as the columns of design matrix $Z$ .
<code>beta.txt</code>	contains samples from the posterior of vector $\beta$ . Rows represent posterior samples and columns represent the regression coefficients, and they are in the same order as the columns of design matrix $X$ .
<code>gamma.txt</code>	contains samples from the posterior of the vector of the indicators $\gamma$ . Rows represent posterior samples and columns represent the indicator variables, and they are in the same order as the columns of design matrix $X$ .
<code>delta.txt</code>	contains samples from the posterior of the vector of the indicators $\delta$ . Rows represent posterior samples and columns represent the indicator variables, and they are in the same order as the columns of design matrix $Z$ .
<code>sigma2.txt</code>	contains samples from the posterior of the error variance $\sigma^2$ of each response.
<code>cbeta.txt</code>	contains samples from the posterior of $c_\beta$ .
<code>calpha.txt</code>	contains samples from the posterior of $c_\alpha$ .
<code>R.txt</code>	contains samples from the posterior of the correlation matrix $R$ .
<code>theta.txt</code>	contains samples from the posterior of $\theta$ of the shadow prior (probably not needed).
<code>muR.txt</code>	contains samples from the posterior of $\mu_R$ .
<code>sigma2R.txt</code>	contains samples from the posterior of $\sigma_R^2$ .
<code>deviance.txt</code>	contains the deviance, minus twice the log likelihood evaluated at the sampled values of the parameters.

In addition to the above, for models that cluster the correlations we have

compAlloc.txt The cluster at which the correlations were allocated,  $\lambda_{kl}$ . These are integers from zero to the specified number of clusters minus one.

nmembers.txt The numbers of correlations assigned to each cluster.

DPconc.txt Contains samples from the posterior of the Dirichlet process concentration parameter.

In addition to the above, for models that cluster the variables we have

compAllocV.txt The cluster at which the variables were allocated,  $\lambda_k$ . These are integers from zero to the specified number of clusters minus one.

nmembersV.txt The numbers of variables assigned to each cluster.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

### References

Papageorgiou, G. and Marshall, B.C. (2019). Bayesian semiparametric analysis of multivariate continuous responses, with variable selection. arXiv.

Papageorgiou, G. (2018). BNSP: an R Package for fitting Bayesian semiparametric regression models and variable selection. *The R Journal*, 10(2):526-548.

Chan, D., Kohn, R., Nott, D., & Kirby, C. (2006). Locally adaptive semiparametric estimation of the mean and variance functions in regression models. *Journal of Computational and Graphical Statistics*, 15(4), 915-936.

### Examples

```
# Fit a mean/variance regression model on the cps71 dataset from package np
require(np)
require(ggplot2)
data(cps71)
model <- logwage ~ sm(age,k=30,bs="rd") | sm(age,k=30,bs="rd")
DIR<-getwd()
## Not run: m1 <- mvrm(formula=model,data=cps71,sweeps=10000,burn=5000,thin=2, seed=1,StorageDir=DIR)
#Print information and summarize the model
print(m1)
summary(m1)
#Summarize and plot one parameter of interest
alpha<-mvrm2mcmc(m1,"alpha")
summary(alpha)
plot(alpha)
#Obtain a plot of a term in the mean model
wagePlotOptions<-list(geom_point(data=cps71,aes(x=age,y=logwage)))
plot(x=m1,model="mean",term="sm(age)",plotOptions=wagePlotOptions)
plot(m1)
#Obtain predictions for new values of the predictor "age"
predict(m1,data.frame(age=c(21,65)),interval="credible")

# Fit a bivariate mean/variance model on the marks dataset from package ggm
```

```
# two responses: marks mechanics and vectors, and one covariate: marks on algebra
model2 <- mechanics | vectors ~ sm(algebra,k=5) | sm(algebra,k=3)
m2 <- mvrn(formula=model2, data=marks, sweeps = 100000, burn = 50000,
           thin = 2, seed = 1, StorageDir = DIR)

plot(m2)

## End(Not run)
```

---

mvrn2mcmc	<i>Convert posterior samples from function mvrn into an object of class 'mcmc'</i>
-----------	--

---

### Description

Reads in files where the posterior samples were written and creates an object of class 'mcmc' so that functions like summary and plot from package coda can be used

### Usage

```
mvrn2mcmc(mvrnObj, labels)
```

### Arguments

mvrnObj	An object of class 'mvrn' as created by a call to function mvrn.
labels	The labels of the files to be read in. These can be one or more of: "alpha", "beta", "gamma", "delta", "sigma2", "cbeta", "calpha", "R", "muR", "sigma2R", "nmembers", "nmembersV", "compAlloc", "compAllocV", and "DPconc" and they correspond to the parameters of the model that a call to functions mvrn fits. In addition, "deviance" can be read in. If left unspecified, all files are read in.

### Value

An object of class 'mcmc' that holds the samples from the posterior of the selected parameter.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

### See Also

[mvrn](#)

### Examples

```
#see \code{mvrn} example
```

---

plot.mvrm

*Creates plots of terms in the mean and/or variance models*


---

## Description

This function plots estimated terms that appear in the mean and variance models.

## Usage

```
## S3 method for class 'mvrm'
plot(x, model, term, response, response2, intercept = TRUE, grid = 30,
     centre = mean, quantiles = c(0.1, 0.9), contour = TRUE, static = TRUE,
     centreEffects = FALSE, plotOptions = list(), nrow, ask = FALSE,
     plotEmptyCluster = FALSE, ...)
```

## Arguments

x	an object of class 'mvrm' as generated by function mvrm.
model	one of "mean", "stdev", or "both", specifying which model to be visualized.
term	the term in the selected model to be plotted.
response	integer number denoting the response variable to be plotted (in case there is more than one).
response2	only relevant for multivariate longitudinal data.
intercept	specifies if an intercept should be included in the calculations.
grid	the length of the grid on which the term will be evaluated.
centre	a description of how the centre of the posterior should be measured. Usually mean or median.
quantiles	the quantiles to be used when plotting credible regions. Plots without credible intervals may be obtained by setting this argument to NULL.
contour	relevant for 3D plots only. If contour=TRUE then plot.mvrm creates contour plots. contour=FALSE is allowed only for creating one plot at a time. The plot can be static or dynamic. See argument 'static'.
static	relevant for 3D plots only. If static=TRUE then plot.mvrm calls function ribbon3D from package plot3D to create the plot. If static=FALSE then plot.mvrm calls function scatterplot3js from package threejs to create the plot.
centreEffects	if TRUE then the effects in the mean functions are centred around zero over the range of the predictor while the effects in the variance function are scaled around one.
plotOptions	for plots of univariate smooth terms or for plots of bivariate smooth terms where one of the two covariates is discrete, this is a list of plot elements to give to ggplot. For smooths of bivariate continuous covariates, this is a list of plot elements to give to ribbon3D (if static=FALSE) or to scatterplot3js (if static=TRUE).

nrow	the number of rows in the figure with the plots.
ask	if set to TRUE, plots will be displayed one at a time.
plotEmptyCluster	if set to TRUE, plots of empty clusters will be displayed. Relevant for multivariate longitudinal datasets.
...	other arguments.

**Details**

Use this function to obtain predictions.

**Value**

Predictions along with credible/prediction intervals

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrn](#)

**Examples**

```
#see \code{mvrn} example
```

---

plotCorr *Creates plots of the correlation matrices*

---

**Description**

This function plots the posterior mean and credible intervals of the elements of correlation matrices.

**Usage**

```
plotCorr(x, term = "R", centre = mean, quantiles = c(0.1, 0.9), ...)
```

**Arguments**

x	an object of class ‘mmvrn’ as generated by function mmvrn.
term	R or muR,
centre	a description of how the centre of the posterior should be measured. Usually mean or median.
quantiles	the quantiles to be used when plotting credible regions. Plots without credible intervals may be obtained by setting this argument to NULL.
...	other arguments.

**Details**

Use this function to visualize the elements of a correlation matrix.

**Value**

Posterior means and credible intervals of elements of correlation matrices.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrm](#)

**Examples**

```
#see \code{mvrm} example
```

---

predict.mvrm

*Model predictions*

---

**Description**

Provides predictions and posterior credible/prediction intervals for given feature vectors.

**Usage**

```
## S3 method for class 'mvrm'
predict(object, newdata, interval = c("none", "credible", "prediction"),
        level = 0.95, nSamples = 100, ...)
```

**Arguments**

object	an object of class "mvrm", usually a result of a call to mvrm.
newdata	data frame of feature vectors to obtain predictions for. If newdata is missing, the function will use the feature vectors in the data frame used to fit the mvrm object.
interval	type of interval calculation.
level	tolerance level.
nSamples	number of samples to obtain from the posterior predictive distribution (for each sweep of the MCMC). Only relevant for "prediction intervals".
...	other arguments.

**Details**

The function returns predictions of new responses or the means of the responses for given feature vectors. Predictions for new responses or the means of new responses are the same. However, the two differ in the associated level of uncertainty: response predictions are associated with wider (prediction) intervals than mean response predictions. To obtain prediction intervals (for new responses) the function samples from the normal distributions with means and variances as sampled during the MCMC run.

**Value**

Predictions for given covariate/feature vectors.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrm](#)

**Examples**

```
#see \code{mvrm} example
```

---

print.mvrm	<i>Prints an mvrm fit</i>
------------	---------------------------

---

**Description**

Provides basic information from an mvrm fit.

**Usage**

```
## S3 method for class 'mvrm'
print(x, digits = 5, ...)
```

**Arguments**

x	an object of class "mvrm", usually a result of a call to mvrm.
digits	the number of significant digits to use when printing.
...	other arguments.

**Details**

The function prints information about mvrm fits.

**Value**

The function provides a matched call, the number of posterior samples obtained and marginal inclusion probabilities of the terms in the mean and variance models.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrn](#)

**Examples**

```
#see \code{mvrn} example
```

---

<code>s</code>	<i>mgcv constructor s</i>
----------------	---------------------------

---

**Description**

Provides interface between `mgcv::s` and `BNSP.s(...)` calls `mgcv::smoothCon(mgcv::s(...), ...`

**Usage**

```
s(..., data, knots = NULL, absorb.cons = FALSE, scale.penalty = TRUE,
n = nrow(data), dataX = NULL, null.space.penalty = FALSE, sparse.cons = 0,
diagonal.penalty = FALSE, apply.by = TRUE, modCon = 0, k = -1, fx = FALSE,
bs = "tp", m = NA, by = NA, xt = NULL, id = NULL, sp = NULL, pc = NULL)
```

**Arguments**

<code>...</code>	a list of variables. See <code>mgcv::s</code>
<code>data</code>	see <code>mgcv::smoothCon</code>
<code>knots</code>	see <code>mgcv::knots</code>
<code>absorb.cons</code>	see <code>mgcv::smoothCon</code>
<code>scale.penalty</code>	see <code>mgcv::smoothCon</code>
<code>n</code>	see <code>mgcv::smoothCon</code>
<code>dataX</code>	see <code>mgcv::smoothCon</code>
<code>null.space.penalty</code>	see <code>mgcv::smoothCon</code>
<code>sparse.cons</code>	see <code>mgcv::smoothCon</code>
<code>diagonal.penalty</code>	see <code>mgcv::smoothCon</code>
<code>apply.by</code>	see <code>mgcv::smoothCon</code>



modCon	see mgcv::smoothCon
k	see mgcv::s
fx	see mgcv::s
bs	see mgcv::s
m	see mgcv::s
by	see mgcv::s
xt	see mgcv::s
id	see mgcv::s
sp	see mgcv::s
pc	see mgcv::s

### Details

The most relevant arguments for BNSP users are the list of variables . . . , knots, absorb.cons, bs, and by.

### Value

A design matrix that specifies a smooth term in a model.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

---

simD	<i>Simulated dataset</i>
------	--------------------------

---

### Description

Just a simulated dataset to illustrate the model. The success probability and the covariate have a non-linear relationship.

### Usage

```
data(simD)
```

### Format

A data frame with 300 independent observations. Three numerical vectors contain information on

Y number of successes.

E number of trials.

X explanatory variable.

sm

*Smooth terms in mvrm formulae***Description**

Function used to define smooth effects in the mean and variance formulae of function mvrm. The function is used internally to construct the design matrices.

**Usage**

```
sm(..., k = 10, knots = NULL, bs = "rd")
```

**Arguments**

... one or two covariates that the smooth term is a function of. If two covariates are used, they may be both continuous or one continuous and one discrete. Discrete variables should be defined as factor in the data argument of the calling mvrm function.

k the number of knots to be utilized in the basis function expansion.

knots the knots to be utilized in the basis function expansion.

bs a two letter character indicating the basis functions to be used. Currently, the options are "rd" that specifies radial basis functions and is available for univariate and bivariate smooths, and "p1" that specifies thin plate splines that are available for univariate smooths.

**Details**

Use this function within calls to function mvrm to specify smooth terms in the mean and/or variance function of the regression model.

Univariate radial basis functions with  $q$  basis functions or  $q - 1$  knots are defined by

$$\mathcal{B}_1 = \{ \phi_1(u) = u, \phi_2(u) = \|u - \xi_1\|^2 \log(\|u - \xi_1\|^2), \dots, \phi_q(u) = \|u - \xi_{q-1}\|^2 \log(\|u - \xi_{q-1}\|^2) \},$$

where  $\|u\|$  denotes the Euclidean norm of  $u$  and  $\xi_1, \dots, \xi_{q-1}$  are the knots that are chosen as the quantiles of the observed values of explanatory variable  $u$ , with  $\xi_1 = \min(u_i)$ ,  $\xi_{q-1} = \max(u_i)$  and the remaining knots chosen as equally spaced quantiles between  $\xi_1$  and  $\xi_{q-1}$ .

Thin plate splines are defined by

$$\mathcal{B}_2 = \{ \phi_1(u) = u, \phi_2(u) = (u - \xi_1)_+, \dots, \phi_q(u) = (u - \xi_q)_+ \},$$

where  $(a)_+ = \max(a, 0)$ .

Radial basis functions for bivariate smooths are defined by

$$\mathcal{B}_3 = \{ u_1, u_2, \phi_3(u) = \|u - \xi_1\|^2 \log(\|u - \xi_1\|^2), \dots, \phi_q(u) = \|u - \xi_{q-1}\|^2 \log(\|u - \xi_{q-1}\|^2) \}.$$

**Value**

Specifies the design matrices of an mvrm call

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**

[mvrm](#)

**Examples**

```
#see \code{mvrm} example
```

---

summary.mvrm

*Summary of an mvrm fit*

---

**Description**

Provides basic information from an mvrm fit.

**Usage**

```
## S3 method for class 'mvrm'
summary(object, nModels = 5, digits = 5, printTuning = FALSE, ...)
```

**Arguments**

object	an object of class "mvrm", usually a result of a call to mvrm.
nModels	integer number of models with the highest posterior probability to be displayed.
digits	the number of significant digits to use when printing.
printTuning	if set to TRUE, the starting and finishing values of the tuninf parameters are displayed.
...	other arguments.

**Details**

Use this function to summarize mvrm fits.

**Value**

The functions provides a detailed description of the specified model and priors. In addition, the function provides information about the Markov chain ran (length, burn-in, thinning) and the folder where the files with posterior samples are stored. Lastly, the function provides the mean posterior and null deviance and the mean/variance models visited most often during posterior sampling.

**Author(s)**

Georgios Papageorgiou <gpapageo@gmail.com>

**See Also**[mvrn](#)**Examples**

```
#see \code{mvrn} example
```

---

te	<i>mgcv constructor te</i>
----	----------------------------

---

**Description**

Provides interface between `mgcv::te` and `BNSP`. `te(...)` calls `mgcv::smoothCon(mgcv::te(...), ...`

**Usage**

```
te(..., data, knots = NULL, absorb.cons = FALSE, scale.penalty = TRUE,
n = nrow(data), dataX = NULL, null.space.penalty = FALSE, sparse.cons = 0,
diagonal.penalty = FALSE, apply.by = TRUE, modCon = 0, k = NA, bs = "cr",
m = NA, d = NA, by = NA, fx = FALSE, np = TRUE, xt = NULL, id = NULL,
sp = NULL, pc = NULL)
```

**Arguments**

...	a list of variables. See <code>mgcv::te</code>
<code>data</code>	see <code>mgcv::smoothCon</code>
<code>knots</code>	see <code>mgcv::knots</code>
<code>absorb.cons</code>	see <code>mgcv::smoothCon</code>
<code>scale.penalty</code>	see <code>mgcv::smoothCon</code>
<code>n</code>	see <code>mgcv::smoothCon</code>
<code>dataX</code>	see <code>mgcv::smoothCon</code>
<code>null.space.penalty</code>	see <code>mgcv::smoothCon</code>
<code>sparse.cons</code>	see <code>mgcv::smoothCon</code>
<code>diagonal.penalty</code>	see <code>mgcv::smoothCon</code>
<code>apply.by</code>	see <code>mgcv::smoothCon</code>
<code>modCon</code>	see <code>mgcv::smoothCon</code>
<code>k</code>	see <code>mgcv::te</code>
<code>bs</code>	see <code>mgcv::te</code>
<code>m</code>	see <code>mgcv::te</code>
<code>d</code>	see <code>mgcv::te</code>

by	see mgcv::te
fx	see mgcv::te
np	see mgcv::te
xt	see mgcv::te
id	see mgcv::te
sp	see mgcv::te
pc	see mgcv::te

### Details

The most relevant arguments for BNSP users are the list of variables . . . , knots, absorb.cons, bs, and by.

### Value

A design matrix that specifies a smooth term in a model.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

---

ti	<i>mgcv constructor ti</i>
----	----------------------------

---

### Description

Provides interface between mgcv::ti and BNSP. ti(...) calls mgcv::smoothCon(mgcv::ti(...),...

### Usage

```
ti(..., data, knots = NULL, absorb.cons = FALSE, scale.penalty = TRUE,
n = nrow(data), dataX = NULL, null.space.penalty = FALSE, sparse.cons = 0,
diagonal.penalty = FALSE, apply.by = TRUE, modCon = 0, k = NA, bs = "cr",
m = NA, d = NA, by = NA, fx = FALSE, np = TRUE, xt = NULL, id = NULL,
sp = NULL, mc = NULL, pc = NULL)
```

### Arguments

...	a list of variables. See mgcv::ti
data	see mgcv::smoothCon
knots	see mgcv::knots
absorb.cons	see mgcv::smoothCon
scale.penalty	see mgcv::smoothCon
n	see mgcv::smoothCon

dataX            see mgcv::smoothCon  
null.space.penalty    see mgcv::smoothCon  
sparse.cons       see mgcv::smoothCon  
diagonal.penalty    see mgcv::smoothCon  
apply.by          see mgcv::smoothCon  
modCon            see mgcv::smoothCon  
k                 see mgcv::ti  
bs                see mgcv::ti  
m                 see mgcv::ti  
d                 see mgcv::ti  
by                see mgcv::ti  
fx                see mgcv::ti  
np                see mgcv::ti  
xt                see mgcv::ti  
id                see mgcv::ti  
sp                see mgcv::ti  
mc                see mgcv::ti  
pc                see mgcv::ti

### Details

The most relevant arguments for BNSP users are the list of variables . . . , knots, absorb.cons, bs, and by.

### Value

A design matrix that specifies a smooth term in a model.

### Author(s)

Georgios Papageorgiou <gpapageo@gmail.com>

# Index

- \*Topic **cluster**
  - dpmj, 6
- \*Topic **datasets**
  - simD, 25
- \*Topic **models**
  - sm, 26
- \*Topic **nonparametric**
  - dpmj, 6
  - mvrn, 14
- \*Topic **regression**
  - mvrn, 14
  - sm, 26
- \*Topic **smooth**
  - mvrn, 14
  - sm, 26

BNSP (BNSP-package), 2  
BNSP-package, 2

chol, 3, 4  
clustering, 4  
continue, 5

dpmj, 6

histCorr, 13

mvrn, 5, 6, 13, 14, 19, 21–24, 27, 28  
mvrn2mcmc, 19

plot.mvrn, 20  
plotCorr, 21  
predict.mvrn, 22  
print.mvrn, 23

s, 24  
simD, 25  
sm, 26  
summary.mvrn, 27

te, 28  
ti, 29