Package: BCFM (via r-universe)

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Type Package

Title Bayesian Clustering Factor Models

Version 1.0.0

Description Implements the Bayesian Clustering Factor Models (BCFM) for simultaneous clustering and latent factor analysis of multivariate longitudinal data. The model accounts for within-cluster dependence through shared latent factors while allowing heterogeneity across clusters, enabling flexible covariance modeling in high-dimensional settings. Inference is performed using Markov chain Monte Carlo (MCMC) methods with computationally intensive steps implemented via 'Rcpp'. Model selection and visualization tools are provided. The methodology is described in Shin, Ferreira, and Tegge (2018) <doi:10.1002/sim.70350>.

License GPL (>= 3)

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`BCFM.fit` *Fit BCFM Model*

Description

Fits a single Bayesian Clustering Factor Models (BCFM) using C++ implementation. This function serves as a wrapper for the BCFMcpp function, handling timing and output formatting.

Usage

```
BCFM.fit(
  data,
  model.attributes,
  hyp.parm,
  n.iter = 50000,
  vague.mu = FALSE,
  covariance = TRUE,
  p.exponent = 2,
  every = 10
)
```

Arguments

`data`	An array of dimensions (observations, variables, time points)
`model.attributes`	Model attributes generated by initialize.model.attributes
`hyp.parm`	Hyperparameters generated by initialize.hyp.parm
`n.iter`	Number of MCMC iterations. Default is 50000.
`vague.mu`	Logical indicating whether to use vague priors for mu. Default is FALSE.
`covariance`	Logical indicating whether to model covariance structure. Default is TRUE.
`p.exponent`	The Dirichlet priors exponent for probabilities. Default is 2.
`every`	Integer specifying the frequency of progress updates during MCMC. Default is 10.

Value

A list containing:

Result Output from the BCFMcpp C++ function

model.attributes The model attributes used

hyp.parm The hyperparameters used

start.time POSIXct timestamp when model started

end.time POSIXct timestamp when model completed

run.time Total elapsed time for model execution

See Also

`BCFM.model.selection` for fitting multiple models, `initialize.model.attributes`, `initialize.hyp.parm`

Examples

```
# Prepare data using the included simulated dataset
data(sim.data)
data.pre <- init.data(sim.data, paste0("V", 1:5))
```

```
# Initialize model components
model.attributes <- initialize.model.attributes(S = nrow(sim.data), times = 1,
                                                R = 5, L = 2, G = 2)
cluster.hyperparms <- initialize.cluster.hyperparms(data.pre, model.attributes)
hyp.parm <- initialize.hyp.parm(model.attributes, cluster.hyperparms)

# Fit model
result <- BCFM.fit(data.pre, model.attributes, hyp.parm,
                   n.iter = 100, every = 10)
result$run.time
```

`BCFM.model.selection` *BCFM Model Selection Over Multiple Groups and Factors*

Description

Performs Bayesian Clustering Factor Models analysis across a grid of group numbers and factor numbers. For each combination, the function fits the BCFM model, calculates IC, and saves results. This is the primary function for model selection to determine the optimal number of clusters and latent factors.

Usage

```
BCFM.model.selection(
  data,
  cluster.vars,
  grouplist,
  factorlist,
  n.iter = 50000,
  vague.mu = FALSE,
  covariance = TRUE,
  p.exponent = 2,
  every = 10,
  cluster.size = 0.05,
  burnin = NA,
  output_dir = tempdir(),
  seed = NULL
)
```

Arguments

`data`	A data frame containing the variables to be analyzed
`cluster.vars`	A character vector specifying the column names of variables to be used for clustering
`grouplist`	A numeric vector specifying the numbers of groups to test (e.g., c(2, 3, 4, 5))

factorlist	A numeric vector specifying the numbers of latent factors to test (e.g., c(1, 2, 3))
n.iter	Number of MCMC iterations for each model. Default is 50000.
vague.mu	Logical indicating whether to use vague priors for mu. Default is FALSE.
covariance	Logical indicating whether to model covariance structure. Default is TRUE.
p.exponent	The Dirichlet priors exponent for probabilities. Default is 2.
every	Integer specifying the frequency of progress updates during MCMC. Default is 10.
cluster.size	Minimum proportion required for each cluster. Default is 0.05.
burnin	Number of initial MCMC iterations to discard when calculating IC. If NA, an appropriate burnin is determined automatically.
output_dir	Directory where results will be saved. Defaults to tempdir(). The function will create this directory if it doesn't exist.
seed	Optional integer seed for reproducibility.

Details

The function performs the following steps for each group-factor combination:

1. Preprocesses data using init.data
2. Determines optimal variable ordering using permutation.order
3. Initializes model attributes and hyperparameters
4. Fits BCFM model using BCFM.fit
5. Calculates IC for model comparison
6. Saves individual results and cumulative IC matrix

The IC matrix can be used to identify the optimal model configuration by selecting the combination of groups and factors with the lowest IC value.

Value

Invisibly returns NULL. Results are saved to disk:

results-covarianceF-gX-fY.Rdata Individual model results for each group-factor combination (where X is the number of groups and Y is the number of factors), containing SDresult and variable order

IC.Rdata Contains IC.matrix, timing information, and data. Load this file to compare models and identify the optimal configuration.

Note

This function can be computationally intensive as it fits multiple models. Consider running on high-performance computing resources for large datasets or extensive model grids. The function includes error handling to continue execution even if individual models fail to converge.

See Also

BCFM.fit for fitting a single model, init.data, initialize.model.attributes, initialize.hyp.parm

Examples

```
# Run model selection using the included simulated dataset
data(sim.data)
BCFM.model.selection(
  data = sim.data,
  cluster.vars = paste0("V", 1:5),
  grouplist = 2:3,
  factorlist = 1:2,
  n.iter = 100,
  every = 10,
  burnin = 10
)

# Load and examine IC results
load(file.path(tempdir(), "IC.Rdata"))
print(IC.matrix)
```

BCFMcpp *Gibbs sampler of BCFM*

Description

It runs a Gibbs sampler for common factors X, factor loadings B, group mean mu, group covariate Omega, idiosyncratic variances sigma^2, group assignment Z and group probabilities probs. This function uses Rcpp.

Usage

```
BCFMcpp(data, model.attributes, hyp.parm, n.iter, every = 1, verbose = FALSE)
```

Arguments

`data`	The dataset
`model.attributes`	Model attributes generated by initialize.model.attributes
`hyp.parm`	Hyperparameters generated by initialize.hyp.parm
`n.iter`	Total number of iterations
`every`	Save every `every` iterations
`verbose`	Print the results by every 10th step

Value

List of Gibbs sampler of parameters described in description

getmode *Get the mode of a vector*

Description

The function returns the mode of a vector.

Usage

```
getmode(v)
```

Arguments

v	The vector to find the mode.

Value

The mode of v.

ggplot_B.CI *Build factor loadings plot*

Description

The function builds a column-wise plots of factor loadings. The parameters fixed at 1 are displayed with red dashed vertical lines.

Usage

```
ggplot_B.CI(
  Gibbs,
  true.val = NA,
  burnin = NA,
  permutation = NA,
  main.bool = TRUE,
  var_labels = NULL
)
```

Arguments

Gibbs	Result of Gibbs sampler from BCFM function
true.val	True values of factor loadings. If not available, NA.
burnin	Number of burn-in. If not set, it uses the first tenths as burn-in period.
permutation	Permutation of variables. If not set, no permutation.
main.bool	Add title of the plots. Default is TRUE.
var_labels	Character vector of variable names. If NULL, defaults to Variable 1, Variable 2, etc.

Value

A ggplot object

`ggplot_B.trace` *Trace plot for posterior of factor loadings*

Description

It returns a trace plot of factor loadings, B, showing MCMC convergence

Usage

```
ggplot_B.trace(
  Gibbs,
  burnin = NA,
  permutation = NA,
  true.val = NA,
  factor.num = 1,
  var_labels = NULL
)
```

Arguments

`Gibbs`	MCMC sample simulated from `BCFMR` or `BCFMcpp` function
`burnin`	Number of burn-in period. If not specified, no burn-in is removed.
`permutation`	Permutation order vector, if applicable
`true.val`	True values of factor loadings. If not available, NA.
`factor.num`	The index of variable to plot (which variable's loadings across all factors to display). Use NULL to plot all variables.
`var_labels`	Character vector of variable names. If NULL, uses Variable 1, Variable 2, etc.

Value

A ggplot object showing trace plots

ggplot_IC *Plot IC Matrix from Model Selection*

Description

Creates two plots showing IC values across different numbers of groups and factors to help identify the optimal model configuration.

Usage

```
ggplot_IC(matrix, factor_list = 2:4, group_list = 2:4, combine = TRUE)
```

Arguments

matrix	An IC matrix from BCFM.model.selection, with rows representing groups and columns representing factors.
factor_list	Numeric vector of factor values corresponding to matrix columns. Default is 2:6.
group_list	Numeric vector of group values corresponding to matrix rows. Default is 5:11.
combine	Logical. If TRUE (default), returns a combined plot using ggarrange. If FALSE, returns a list of two separate ggplot objects.

Details

The function creates two complementary visualizations:

- Plot 1: IC vs. number of groups, with lines for each number of factors
- Plot 2: IC vs. number of factors, with lines for each number of groups

Lower IC values indicate better model fit.

Value

If combine = TRUE, a combined ggplot object. If combine = FALSE, a list with two elements:

by_groups ggplot showing IC vs. number of groups

by_factors ggplot showing IC vs. number of factors

Examples

```
# Create a toy IC matrix for demonstration
IC.matrix <- matrix(c(100, 95, 90, 92, 88, 85), nrow = 2, ncol = 3)
rownames(IC.matrix) <- paste0("G", 2:3)
colnames(IC.matrix) <- paste0("F", 1:3)

# Combined plot (default)
ggplot_IC(IC.matrix, factor_list = 1:3, group_list = 2:3)
```

```
# Separate ggplot objects
plots <- ggplot_IC(IC.matrix, factor_list = 1:3, group_list = 2:3,
                   combine = FALSE)
plots$by_groups
plots$by_factors
```

---

ggplot_latent.profiles

Plot Latent Factor Profiles by Cluster

Description

Visualizes the latent factor profile means (mu) for each cluster, similar to Latent Profile Analysis (LPA) plots

Usage

```
ggplot_latent.profiles(
  Gibbs,
  burnin = NA,
  factor_labels = NULL,
  cluster_names = NULL,
  colors = NULL,
  title = "Latent Factor Profiles by Cluster",
  x_label = "Factor",
  y_label = "Posterior Mean"
)
```

Arguments

Gibbs	Gibbs sample derived from BCFM function
burnin	Number of burn-in period. If not specified, it uses the first tenth as burn-in period
factor_labels	Character vector of factor names. If NULL, defaults to Factor 1, Factor 2, etc.
cluster_names	Character vector of cluster names. If NULL, defaults to Cluster 1, Cluster 2, etc.
colors	Named vector of colors for each cluster. If NULL, uses default color palette
title	Plot title. Default is "Latent Factor Profiles by Cluster"
x_label	X-axis label. Default is "Factor"
y_label	Y-axis label. Default is "Posterior Mean"

Value

A ggplot object

Examples

```
# Fit a model first using the included simulated dataset
data(sim.data)
data.pre <- init.data(sim.data, paste0("V", 1:5))
model.attributes <- initialize.model.attributes(S = nrow(sim.data), times = 1,
                                                R = 5, L = 2, G = 2)
cluster.hyperparms <- initialize.cluster.hyperparms(data.pre, model.attributes)
hyp.parm <- initialize.hyp.parm(model.attributes, cluster.hyperparms)
result <- BCFM.fit(data.pre, model.attributes, hyp.parm,
                   n.iter = 100, every = 10)

# Plot latent profiles
ggplot_latent.profiles(Gibbs = result$Result)
```

---

ggplot_mu.density *Density of group means mu using ggplot2*

Description

The function returns multiple density plots of group mean parameter mu.

Usage

```
ggplot_mu.density(
  Gibbs,
  true.val = NA,
  add.legend = FALSE,
  burnin = NA,
  layout.dim = NA,
  main.title = "Posterior Densities of Group Means (mu)",
  x.label = "mu",
  y.label = "Density"
)
```

Arguments

Gibbs	The Gibbs sample from BCFM function
true.val	The true value of mu, if applicable
add.legend	Add legend on extra pane
burnin	Number of burn-in period. If not specified, it uses the first tenths as burn-in.
layout.dim	Dimension of panes. If not specified, the plots are in one column.
main.title	Main title for the entire plot. Default is "Posterior Densities of Group Means (mu)"
x.label	X-axis label. Default is "mu"
y.label	Y-axis label. Default is "Density"

Value

A ggplot object (grob from grid.arrange)

`ggplot_omega.density` *The density plot of the diagonal of group covariance, Omega, with ggplot2*

Description

It returns multiple plots of the diagonal of group covariance, Omega using ggplot2 and gridExtra. It returns the result by each factor, different colors representing different factors

Usage

```
ggplot_omega.density(
  Gibbs,
  group.select = 1,
  true.val = NA,
  burnin = NA,
  main.title = "Posterior Densities of Omega",
  x.label = "Value",
  y.label = "Density",
  factor_labels = NULL,
  show.offdiag = TRUE
)
```

Arguments

`Gibbs`	Gibbs sample from BCFM
`group.select`	Group/cluster to plot. If not specified, the first group will be used.
`true.val`	True values of Omega, if applicable.
`burnin`	Number of burn-in period. If not specified, the first tenths is used as burn-in.
`main.title`	Main title for the plot. Default is "Posterior Densities of Omega"
`x.label`	X-axis label. Default is "Value"
`y.label`	Y-axis label. Default is "Density"
`factor_labels`	Character vector of factor names. If NULL, defaults to Factor 1, Factor 2, etc.
`show.offdiag`	Show off-diagonal elements. Default is TRUE for any k.

Value

A ggplot object showing densities of Omega elements

ggplot_probs.density *Density plot for posterior of probabilities*

Description

The function returns a density plot of the cluster assignment probability, p. Different color represent different Clusters.

Usage

```
ggplot_probs.density(
  Gibbs,
  burnin = NA,
  truep = NA,
  main.title = "Posterior Densities of Cluster Probabilities",
  x.label = "Probability",
  y.label = "Density",
  cluster_names = NULL
)
```

Arguments

Gibbs	MCMC sample simulated from BCFMR or BCFMcpp function
burnin	Number of burn-in period. If not specified, it uses the first tenths as burn-in.
truep	True values of probabilities. If not available, NA.
main.title	Title of the plot. Default is "Posterior Densities of Cluster Probabilities"
x.label	X-axis label. Default is "Probability"
y.label	Y-axis label. Default is "Density"
cluster_names	Character vector of cluster names. If NULL, defaults to Cluster 1, Cluster 2, etc.

Value

A ggplot object (grob from grid.arrange) with plot and legend

ggplot_probs.trace *Trace plot of probabilities parameter*

Description

It returns a trace plot of probabilities parameter after burn-in. Different colors represent different groups.

Usage

```
ggplot_probs.trace(
  Gibbs,
  burnin = NA,
  main.title = "Trace Plot: Cluster Probabilities",
  x.label = "BCFM Iteration (post burn-in)",
  y.label = "Probability",
  cluster_names = NULL
)
```

Arguments

Gibbs	Gibbs sample from BCFM function.
burnin	Number of burn-in period. If not specified, it uses the first tenths sample as burn-in.
main.title	Title of the plot. Default is "Trace Plot: Cluster Probabilities"
x.label	X-axis label. Default is "BCFM Iteration (post burn-in)"
y.label	Y-axis label. Default is "Probability"
cluster_names	Character vector of cluster names. If NULL, defaults to Cluster 1, Cluster 2, etc.

Value

A ggplot object showing trace plots

---

ggplot_sigma2.CI *A credible interval plot of posterior of sigma squared*

Description

It returns a credible interval plot of idiosyncratic variance, sigma squared. The lines are 95% intervals, while the circles are posterior mean.

Usage

```
ggplot_sigma2.CI(
  Gibbs,
  burnin = NA,
  permutation = NA,
  main.bool = TRUE,
  main.title = NULL,
  x.label = "Variables",
  y.label = "Variance",
  var_labels = NULL
)
```

Arguments

Gibbs	Gibbs sample from BCFM function
burnin	Number of burn-in period. If not specified, it uses the first tenths sample as burn-in period.
permutation	Permutation vector, if applicable
main.bool	Return main title. Default is TRUE.
main.title	Main title for the plot. Default is expression for sigma squared.
x.label	X-axis label. Default is "Variables"
y.label	Y-axis label. Default is "Variance"
var_labels	Character vector of variable names. If NULL, defaults to Variable 1, Variable 2, etc.

Value

A ggplot object showing the 95\ posterior means (points) of the idiosyncratic variances sigma squared for each variable.

---

ggplot_tau.CI *A credible interval plot of posterior of factor loadings covariance, tau*

Description

It returns a credible interval plot of factor loadings covariance, tau. The lines are 95% intervals, while the circles are posterior mean.

Usage

```
ggplot_tau.CI(
  Gibbs,
  burnin = NA,
  true.val = NA,
  main.bool = TRUE,
  main.title = NULL,
  x.label = "Factor",
  y.label = "Tau",
  factor_labels = NULL
)
```

Arguments

Gibbs	Gibbs sample from BCFM function
burnin	Number of burn-in period. If not specified, it uses the first tenths sample as burn-in period.
true.val	True values of the taus

main.bool	Return main title. Default is TRUE.
main.title	Main title for the plot. Default is expression for tau.
x.label	X-axis label. Default is "Factor"
y.label	Y-axis label. Default is "Tau"
factor_labels	Character vector of factor names. If NULL, defaults to Factor 1, Factor 2, etc.

Value

A ggplot object

---

ggplot_variability *Variability explained by factors*

Description

Plots the proportion of variability explained by each factor based on eigenvalues of the correlation matrix. Useful for determining the number of factors.

Usage

```
ggplot_variability(
  data,
  nfactors = 5,
  main.title = "Proportion of Variability Explained by Factors",
  x.label = "Number of Factors",
  y.label = "Proportion of Variability"
)
```

Arguments

data	The data matrix
nfactors	Number of factors to display. Default is 5.
main.title	Main title for the plot. Default is "Proportion of Variability Explained by Factors"
x.label	X-axis label. Default is "Number of Factors"
y.label	Y-axis label. Default is "Proportion of Variability"

Value

A ggplot object

ggplot_Zit.heatmap *A heatmap of group assignments, Z using ggplot2*

Description

A heatmap of group assignments, Z using ggplot2. It first sorts by the largest group with the most assigned.

Usage

```
ggplot_Zit.heatmap(
  Gibbs,
  true.val = NA,
  burnin = NA,
  main.title = "Cluster Assignment Heatmap",
  x.label = "Cluster",
  y.label = "Subject-Time"
)
```

Arguments

Gibbs	Gibbs sample from BCFM function
true.val	Table of true group assignments, if applicable
burnin	Number of burn-in period. If not specified, it uses the first tenths sample as burn-in.
main.title	Title of the plot. Default is "Cluster Assignment Heatmap"
x.label	X-axis label. Default is "Cluster"
y.label	Y-axis label. Default is "Subject-Time"

Value

A ggplot object

IC *Information Criterion. Very close to the original BIC method, but this uses the integrated likelihood instead.*

Description

It finds a Laplace-Metropolis marginal density of likelihood using posterior mean. It also uses Woodbury lemma for fast calculation

Usage

```
IC(data.row, Gibbs, model.attributes, cluster.size = 0.05, burnin = NA)
```

Arguments

`data.row`	The dataset
`Gibbs`	Gibbs sample derived form `BCFM` function
`model.attributes`	Model attributes generated by `initialize.model.attributes`
`cluster.size`	Minimum proportion required for each cluster (default 0.05)
`burnin`	Number of burn-in period. If not specified, it uses the first tenths as burn-in period

Value

The value of Laplace-Metropolis marginal density

`init.data` *Initialize Data Array for BCFM Model*

Description

Prepares the input data by converting it into a 3D array format required by the BCFM model. If data is already in the correct 3D array format, it returns the data as-is. Takes selected clustering variables and creates an array with dimensions (observations, variables, time points).

Usage

```
init.data(data, cluster.vars = NULL)
```

Arguments

`data`	A data frame, matrix, or 3D array containing the data to be used for clustering. If a 3D array with appropriate dimensions is provided and cluster.vars is NULL, the function returns the data unchanged.
`cluster.vars`	A character vector specifying the column names of variables to be used for clustering (required for data frames). If NULL and data is already a 3D array, the function returns data as-is. If NULL and data is a matrix, all columns are used.

Value

A 3D array with dimensions (n, p, t) where n is the number of observations, p is the number of clustering variables, and t is the number of time points (defaults to 1 for cross-sectional data).

Examples

```
# Example 1: Data frame with variable selection
data <- data.frame(x1 = rnorm(100), x2 = rnorm(100), x3 = rnorm(100))
cluster.vars <- c("x1", "x2", "x3")
data.pre <- init.data(data, cluster.vars)

# Example 2: Matrix (uses all columns)
data_matrix <- matrix(rnorm(300), nrow = 100, ncol = 3)
data.pre <- init.data(data_matrix)

# Example 3: 3D array (returns as-is)
data_3d <- array(rnorm(1500), dim = c(100, 3, 5))
data.pre <- init.data(data_3d)  # Returns unchanged
```

`initialize.cluster.hyperparms` *Initialize cluster hyperparameters*

Description

The function returns list of hyperparmeters for Omegas and mus.

Usage

```
initialize.cluster.hyperparms(
  data,
  model.attributes,
  covariance = FALSE,
  diag.Psi = FALSE,
  vague.mu = FALSE,
  zero.mu = FALSE,
  seed = NULL
)
```

Arguments

`data`	The dataset.
`model.attributes`	Model attributes generated by initialize.model.attributes
`covariance`	Use of covariance matrix of common factors. If FALSE, it uses the correlation matrix.
`diag.Psi`	Diagonal matrix for cluster covariance. If FALSE, it uses the sample covariance.
`vague.mu`	Use of large cluster covariance prior.
`zero.mu`	Set the cluster mean prior at 0. If FALSE, the cluster mean prior are the sample means of the clusters.
`seed`	Optional integer seed for reproducibility.

Value

A list of mean and variance hyperparameter of mu, and scale hyperparameter of Omega

---

`initialize.hyp.parm` *Initialize hyperparmeters for BCFM model*

Description

The function returns a list of hyperparameters of Omega, sigma^2 and mu. It also calls the results from cluster.hyperparms and information from model.attributes.

Usage

```
initialize.hyp.parm(
  model.attributes,
  cluster.hyperparms,
  n.sigma = 2.2,
  n.s2.sigma = 0.1,
  n.tau = 1,
  n.s2.tau = 1,
  omega.diag.nu = 2,
  p.exponent = NA
)
```

Arguments

`model.attributes`	Model attributes generated by initialize.model.attributes
`cluster.hyperparms`	Cluster related hyperparameters generated by initialize.cluster.hyperparms
`n.sigma`	The shape parameter of sigma^2. If not specified, 6.
`n.s2.sigma`	The rate parameter of sigma^2. If not specified, 4.
`n.tau`	The shape parameter of tau^2. If not specified, 6.
`n.s2.tau`	The rate parameter of tau^2. If not specified, 4.
`omega.diag.nu`	The shape parameter for the first cluster covariance
`p.exponent`	The Dirichlet priors of probabilities.

Value

A list of fixed hyperparmeters of mu, Omega and sigma squared.

initialize.model.attributes *Build model attributes from the dataset*

Description

Basic setting and information of the dataset: number of subjects, timepoints, variables, factors and groups.

Usage

```
initialize.model.attributes(S = 216, times = 5, R = 9, L = 3, G = 4)
```

Arguments

S	Number of subjects
times	Number of timepoints
R	Number of covariates
L	Number of factors
G	Number of groups

Value

A list of model attributes

permutation.order *Order of permutation by the largest absolute value in each eigenvector*

Description

It finds the vector of permutation to permute data by its largest absolute value in each eigenvector. It sets the order by specified number of factors, and the rest is ordered as they were.

Usage

```
permutation.order(data, covariance = FALSE, L = 1, fa = TRUE)
```

Arguments

data	The dataset
covariance	Logic variable indicating whether the analysis uses covariance or correlation matrix
L	Number of latent factors
fa	Use factor analysis to sort the variables

Value

The vector of permutation

`permutation.scale` *Permute the dataset by the largest absolute value in each eigenvector, and scale*

Description

It finds the vector of permutation to permute data by its largest absolute value in each eigenvector. It sets the order by specified number of factors, and the rest is ordered as they were. The data is permuted, and if needed, scaled.

Usage

```
permutation.scale(
  data,
  permutation = NA,
  covariance = FALSE,
  return.array = TRUE,
  num.layers = 1
)
```

Arguments

`data`	The dataset
`permutation`	Vector with the permutation of the data
`covariance`	Logic variable indicating whether the analysis uses covariance or correlation matrix
`return.array`	Return the data as 3-dimensional array
`num.layers`	Number of timepoints

Value

The dataset that is permuted, either in matrix or array

`sim.data` *Simulated data for BCFM model*

Description

A simulated dataset for demonstrating the Bayesian Consensus Factor Model.

Usage

```
sim.data
```

Format

A data frame with 200 rows and 20 variables (V1 through V20): All variables are simulated numeric values.

Source

Simulated data generated for package examples

Examples

```
data(sim.data)
dim(sim.data)
head(sim.data)
```

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