

Package ‘heterocop’

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Type Package
Title Semi-Parametric Estimation with Gaussian Copula
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Description A method for generating random vectors which are linked by a Gaussian copula. It also enables to estimate the correlation matrix of the Gaussian copula in order to identify independencies within the data.
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Author Julie Cartier [aut],
Florence Jaffrezic [aut],
Gildas Mazo [aut],
Ekaterina Tomilina [aut, cre]
Maintainer Ekaterina Tomilina <ekaterina.tomilina@inrae.fr>

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CopulaSim	<i>CopulaSim</i>
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Description

This function enables the user to simulate data from a Gaussian copula and arbitrary marginal quantile functions

Usage

```
CopulaSim(n, R, qdist, random = FALSE)
```

Arguments

- n the number of observations
- R a correlation matrix of size dxd
- qdist a vector containing the names of the marginal quantile functions as well as the number of times they are present in the dataset
- random a boolean defining whether the order of the correlation coefficients should be randomized

Value

a list containing an nxd data frame, the shuffled correlation matrix R, and the permutation leading to the new correlation matrix

Examples

```
M <- diag_block_matrix(c(3,4,5),c(0.7,0.8,0.2))
CopulaSim(20,M,c(rep("qnorm(0,1)",6),rep("qexp(0.5)",4),rep("qbinom(4,0.8)",2)),random=TRUE)
```

cor_network_graph	<i>cor_network_graph</i>
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Description

This function enables the user to plot the graph corresponding to the correlations of the Gaussian copula

Usage

```
cor_network_graph(R, TS, binary = TRUE, legend)
```

Arguments

R	a correlation matrix of size dxd (d is the number of variables)
TS	a threshold for the absolute values of the correlation matrix coefficients
binary	a boolean specifying whether the coefficients should be binarized, TRUE by default (zero if the coefficient is less than the threshold in absolute value, 1 otherwise). If FALSE, the edge width is proportional to the coefficient value.
legend	a vector containing the type of each variable used to color the vertices

Value

a graph representing the correlations between the latent Gaussian variables

Examples

```
R <- diag_block_matrix(c(3,4,5),c(0.7,0.8,0.2))
data <- CopulaSim(20,R,c(rep("qnorm(0,1)",6),rep("qexp(0.5)",4),
rep("qbinom(4,0.8)",2)),random=FALSE)[[1]]
cor_network_graph(R,TS=0.3,binary=TRUE,legend=c(rep("Normal",6),
rep("Exponential",4),rep("Binomial",2)))
```

diag_block_matrix	<i>diag_block_matrix</i>
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Description

This function enables the user to generate a diagonal block-matrix with homogeneous blocks

Usage

```
diag_block_matrix(blocks, coeff)
```

Arguments

blocks	a vector containing the sizes of the blocks
coeff	a vector containing the coefficient corresponding to each block, the coefficients must be between 0 and 1

Value

a diagonal block-matrix containing the specified coefficients

Examples

```
diag_block_matrix(c(3,4,5),c(0.3,0.4,0.8))
```

gauss_gen

gauss_gen

Description

This function enables the user to generate gaussian vectors with correlation matrix R

Usage

```
gauss_gen(R, n)
```

Arguments

R a correlation matrix of size dxd
n the number of observations

Value

a nxd data frame containing n observations of the d variables

Examples

```
M <- diag_block_matrix(c(3,4,5),c(0.7,0.8,0.2))
gauss_gen(M,20)
```

icgc_data

ICGC dataset

Description

Dataset containing RNA counts, protein expression and mutations measured on breast cancer tumors.

Usage

```
icgc_data
```

Format

A dataframe of 15 variables and 250 observations containing the following:

ACACA, AKT1S1, ANLN,ANXA1,AR RNA counts (discrete)

ACACA_P, AKT1S1_P, ANLN_P,ANXA_P,AR_P protein expression measurements (discrete)

MU5219,MU4468,MU7870,MU4842,MU6962 5 mutations (binary)

matrix_cor_ts	<i>matrix_cor_ts</i>
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Description

This function enables the user to threshold matrix coefficients

Usage

```
matrix_cor_ts(R, TS, binary = TRUE)
```

Arguments

R	a correlation matrix
TS	a threshold
binary	a boolean specifying whether the coefficients should be binarized, TRUE by default (zero if the coefficient is less than the threshold in absolute value, 1 otherwise)

Value

the thresholded input matrix

Examples

```
M <- diag_block_matrix(c(3,4,5),c(0.7,0.8,0.2))
matrix_cor_ts(M,0.5)
```

matrix_gen	<i>matrix_gen</i>
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Description

This function enables the user to generate a sparse, nonnegative definite correlation matrix via the Cholesky decomposition

Usage

```
matrix_gen(d, gamma)
```

Arguments

d	the number of variables
gamma	an initial sparsity parameter for the lower triangular matrices in the Cholesky decomposition, must be between 0 and 1

Value

a list containing the generated correlation matrix and its final sparsity parameter (ie the proportion of zeros)

Examples

```
matrix_gen(15,0.81)
```

rho_estim

rho_estim

Description

This function enables the user to estimate the correlation matrix of the Gaussian copula for a given dataset

Usage

```
rho_estim(data, Type, parallel = TRUE)
```

Arguments

data	an nxd data frame containing n observations of d variables
Type	a vector containing the type of the variables, "C" for continuous and "D" for discrete
parallel	a boolean encoding whether the computations should be parallelized

Value

the dxd estimated correlation matrix of the Gaussian copula

Examples

```
M <- diag_block_matrix(c(3,4,5),c(0.7,0.8,0.2))
data <- CopulaSim(20,M,c(rep("qnorm(0,1)",6),rep("qexp(0.5)",4),
rep("qbinom(4,0.8)",2)),random=FALSE)[[1]]
rho_estim(data,c(rep("C",10),rep("D",2)),parallel=FALSE)
```

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