

Package ‘RDM’

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Type Package

Title Quantify Dependence using Rearranged Dependence Measures

Version 0.1.1

Description Estimates the rearranged dependence measure ('RDM') of two continuous random variables for different underlying measures.
Furthermore, it provides a method to estimate the (SI)-rearrangement copula using empirical checkerboard copulas.
It is based on the theoretical results presented in Strothmann et al. (2022) <[arXiv:2201.03329](https://arxiv.org/abs/2201.03329)> and Strothmann (2021) <[doi:10.17877/DE290R-22733](https://doi.org/10.17877/DE290R-22733)>.

URL <https://github.com/ChristopherStrothmann/RDM>

BugReports <https://github.com/ChristopherStrothmann/RDM/issues>

License GPL-2

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checkerboardDensity	<i>Estimate the checkerboard mass density</i>
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Description

Estimate a non-square checkerboard mass density

Usage

```
checkerboardDensity(X, Y, resolution1, resolution2)
```

Arguments

X	First coordinate of the observations.
Y	Second coordinate of the observations.
resolution1	A natural number specifying the resolution of the first component.
resolution2	A natural number specifying the resolution of the second component.

Details

This implementation modifies the code of `build_checkerboard_weights()` published in 'qad', version 1.0.4, available at <https://CRAN.R-project.org/package=qad>, to allow for non-square checkerboard mass densities. For more details on the implementation see [ECBC](#) and for more information on the implemented changes, see the file 'src/code.cpp'.

Value

The estimated checkerboard mass density.

Examples

```
checkerboardDensity(runif(20), runif(20), 3, 3)
```

`checkerboardDensityIndex`*Estimate a single entry of the checkerboard mass density*

Description

Estimate the value A_{kl} of the non-square checkerboard mass density.

Usage

```
checkerboardDensityIndex(X, Y, k, l, resolution1, resolution2)
```

Arguments

X	First coordinate of the observations.
Y	Second coordinate of the observations.
k	Index of the first component.
l	Index of the second component.
resolution1	A natural number specifying the resolution of the first component.
resolution2	A natural number specifying the resolution of the second component.

Details

This implementation modifies the code of `build_checkerboard_weights()` published in 'qad', version 1.0.4, available at <https://CRAN.R-project.org/package=qad>, to allow for the evaluation of a single index of the non-square checkerboard mass densities. For more details on the implementation see [ECBC](#) and for more information on the implemented changes, see the file 'src/code.cpp'.

Value

The estimated checkerboard mass density A_{kl} .

Examples

```
U <- runif(20)
V <- runif(20)
checkerboardDensity(U, V, 3, 3)
checkerboardDensityIndex(U, V, 1, 2, 3, 3)
```

computeBandwidth	<i>Compute bandwidth via cross-validation</i>
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Description

An implementation of the cross-validation principle for the bandwidth selection as presented in Strothmann, Dette and Siburg (2022) <arXiv:2201.03329>.

Usage

```
computeBandwidth(X, sL, sU, method = c("cvsym", "cvasym"), reduce = TRUE)
```

Arguments

X	A bivariate data.frame containing the observations. Each row contains one observation.
sL	Lower bound N^{sL} for the possible bandwidth parameters (where N is the number of observations).
sU	Upper bound N^{sU} for the possible bandwidth parameters (where N is the number of observations).
method	"cvsym" uses either a symmetric cross-validation principle ($N_1 = N_2$) and "cvasym" uses an asymmetric cross-validation principle (i.e. N_1 and N_2 may attain different values).
reduce	In case reduce is set to TRUE, the parameter is chosen from $N, N+2, \dots$ instead of $N, N+1, N+2, \dots$

Details

This function computes the optimal bandwidth given the bivariate observations X of length N . Currently, there are two different algorithms implemented:

- "cvsym" - Computes the optimal bandwidth choice for a square checkerboard mass density according to the cross-validation principle. The bandwidth is a natural number between N^{sL}, \dots, N^{sU}
- "cvasym" - Computes the optimal bandwidth choice (N_1, N_2) for a non-square checkerboard mass density according to the cross-validation principle. The bandwidths N_1, N_2 are natural numbers between N^{sL}, \dots, N^{sU} and may possibly attain different values.

Value

The chosen bandwidth depending on the data.frame X.

Examples

```
n <- 20
X <- cbind(runif(n), runif(n))
computeBandwidth(X, sL = 0.25, sU = 0.5, method="cvsym", reduce=TRUE)
```

computeCBMeasure	<i>Dependence measures for the checkerboard copula</i>
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Description

Computes $\mu(C^\#(A))$ for some underlying measure for the checkerboard copula $C^\#(A)$. This measure depends only on the input matrix A .

Usage

```
computeCBMeasure(A, method = c("spearman", "kendall", "bkr", "dss", "zeta1"))
```

Arguments

A	A (possibly non-square) checkerboard mass density.
method	Determines the underlying dependence measure. Options include "spearman", "kendall", "bkr", "dss", "chatterjee" and "zeta1".

Details

This function computes $\mu(C^\#(A))$ for one of several underlying measures for a given checkerboard copula $C^\#(A)$. Most importantly, the value only depends on the (possibly non-square) matrix A and implicitly assumes the form of $C^\#(A)$ given in Strothmann, Dette and Siburg (2022) <arXiv:2201.03329>. Currently, the following underlying measures are implemented:

- "spearman" Implements the concordance measure Spearman's ρ ,
- "kendall" Implements the concordance measure Kendall's τ ,
- "bkr" Implements the Blum–Kiefer–Rosenblatt R , also known as the L^2 -Schweizer-Wolff-measure <doi:10.1214/aos/1176345528>>,
- "dss" Implements the Dette-Siburg-Stoimenov measure of complete dependence <doi:10.1111/j.1467-9469.2011.00767.x>, also known as Chatterjee's ξ <doi:10.1080/01621459.2020.1758115>>,
- "zeta1" Implements the ζ_1 -measure of complete dependence established by W. Trutschnig <doi:10.1016/j.jmaa.2011.06.013>.

Value

The value of $\mu(C^\#(A))$. For a sorted A , this corresponds to the rearranged dependence measure $R_\mu(C^\#(A))$.

Examples

```
n <- 10
A <- diag(n)/n
computeCBMeasure(A, method="spearman")
```

rdm

*Rearranged dependence measure***Description**

This function estimates the asymmetric dependence between X and Y using the rearranged dependence measure $R_\mu(X, Y)$ for different possible underlying measures μ . A value of 0 characterizes independence of X and Y , while a value of 1 characterizes a functional relationship between X and Y , i.e. $Y = f(X)$.

Usage

```
rdm(
  X,
  method = c("spearman", "kendall", "dss", "zeta1", "bkr", "all"),
  bandwidth_method = c("fixed", "cv", "cvsym"),
  bandwidth_parameter = 0.5,
  permutation = FALSE,
  npermutation = 1000,
  checkInput = FALSE
)
```

Arguments

<code>X</code>	A bivariate data.frame containing the observations. Each row contains one bivariate observation.
<code>method</code>	Options include "spearman", "kendall", "bkr", "dss", "chatterjee" and "zeta1". The option "all" returns the value for all aforementioned methods.
<code>bandwidth_method</code>	A character string indicating the use of either a cross-validation principle (square or non-square) or a fixed bandwidth (oftentimes called resolution).
<code>bandwidth_parameter</code>	A numerical vector which contains the necessary optional parameters for the exponent of the chosen bandwidth method. In case of N observations, the <code>bandwidth_parameter</code> (s_1, s_2) determines a lower bound N^{s_1} and upper bound N^{s_2} for the cross-validation methods or a single number s for the fixed bandwidth method resulting in N^s . The parameters have to lie in $(0, 1/2)$ and fulfil $s_1 < s_2$.
<code>permutation</code>	Whether or not to perform a permutation test
<code>npermutation</code>	Number of repetitions of the permutation test
<code>checkInput</code>	Whether or not to perform validity checks of the input

Details

This function estimates $R_\mu(X, Y)$ using the empirical checkerboard mass density A . To arrive at $R_\mu(X, Y)$, A is appropriately sorted and then evaluated for the underlying measure. The estimated R_μ always takes values between 0 and 1 with

- $R_\mu(X, Y) = 0$ if and only if X and Y are independent.
- $R_\mu(X, Y) = 1$ if and only if $Y = f(X)$ for some measurable function f .

Currently, the following underlying measures are implemented:

- "spearman" Implements the concordance measure Spearman's ρ (which is identical to the L_1 -Schweizer-Wolff-measure),
- "kendall" Implements the concordance measure Kendall's τ ,
- "bkr" Implements the Blum–Kiefer–Rosenblatt R , also known as the L^2 -Schweizer-Wolff-measure <doi:10.1214/aos/1176345528>>,
- "dss" Implements the Dette-Siburg-Stoimenov measure of complete dependence <doi:10.1111/j.1467-9469.2011.00767.x>, also known as Chatterjee's ξ <doi:10.1080/01621459.2020.1758115>>,
- "zeta1" Implements the ζ_1 -measure of complete dependence established by W. Trutschnig <doi:10.1016/j.jmaa.2011.06.013>.

The estimation of the checkerboard mass density A depends on the choice of the bandwidth for the checkerboard copula. For a detailed discussion of "cv" and "cvsym", see [computeBandwidth](#).

Value

The estimated value of the rearranged dependence measure

Examples

```
n <- 50
X <- cbind(runif(n), runif(n))
rdm(X, method="spearman", bandwidth_method="fixed", bandwidth_parameter=.3)
n <- 20
U <- runif(n)
rdm(cbind(U, U), method="spearman", bandwidth_method="cv", bandwidth_parameter=c(0.25, 0.5))
```

sortDSMatrix

Sort a (possibly non-square) doubly stochastic matrix

Description

Sorts an arbitrary doubly stochastic $N_1 \times N_2$ matrix A into the matrix A^\uparrow such that the induced checkerboard copula $C(A^\uparrow)$ is stochastically increasing.

Usage

```
sortDSMatrix(A)
```

Arguments

A A (possibly non-square) doubly stochastic matrix or (possibly non-square) checkerboard mass density.

Details

The algorithm to sort a doubly stochastic matrix A is given in Strothmann, Dette and Siburg (2022) <arXiv:2201.03329>. Since this implementation does not depend on the appropriate scaling of the matrix A , both doubly stochastic matrices and checkerboard mass densities are admissible inputs.

Value

The sorted version A^\uparrow of the matrix A .

Examples

```
n <- 4
A <- diag(n)[n:1, ]
print(A)
sortDSMatrix(A)
```


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