Package 'SKIT'

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Title SKIT

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Description Conduct the Semiparametric Kernel Independence Test between two vectors when there are excess zeros.		
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SKIT-package Semiparametric Kernel Independence Test (SKIT) with excess zeros		
Description		
Conduct the test of independence between two vectors when there are excess zeros.		
Details		
The function SKIT() compute the test statistics and compute their p -values based on bootstra samples.	ıŗ	
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skit

Semiparametric Kernel Independence Test (SKIT) with excess zeros

Description

Performs the test of independence between two vectors when there are excess zeros.

Usage

```
skit(x, y, bandwidth=NULL, nboot=1000, print=0)
```

Arguments

X	Numeric vector possibly containing zeros.
у	Numeric vector possibly containing zeros with same length as x.
bandwidth	Bandwith parameter (see details). The default is NULL so that a default value will be computed from the data.
nboot	Number of bootstrap samples to estimate p-values. If p-values are not desired, then set to 0. The default is 1000.
print	0 or 1 to print information. The default is 0.

Details

Non-numeric values in x or y will be removed from both vectors.

If bandwidth = NULL, then the bandwidth parameter will be computed for the observed data, and re-computed for each bootstrap sample. It is computed as $sigma*n^(-0.2)$, where n = length(x), sigma = max(c(sd(x[x != 0]), sd(y[y != 0]))).

Value

A list containing the observed test statistics, bootstrap-estimated p-values, and the bandwith parameter for the observed data.

The overall test statistic \widehat{T} is computed as $\widehat{T}_1 + \widehat{T}_2 + \widehat{T}_3 + \widehat{T}_4$ and for each component, p-value is estimated via bootstrap.

Examples

```
set.seed(123)

n <- 500
b00 <- 0.09; b10 <- 0.21; b01 <- 0.21; b11 <- 0.49
id <- sample(1:4, n, replace = TRUE, prob = c(b00, b10, b01, b11))
subn <- table(factor(id, levels = 1:4))
n2 <- subn[names(subn) == "2"]
n3 <- subn[names(subn) == "3"]
n4 <- subn[names(subn) == "4"]
Biv <- matrix(0, nrow = n, ncol = 2)
if(n2 != 0) Biv[id == 2,1] <- rnorm(n2, 0.4, 0.1)
if(n3 != 0) Biv[id == 3,2] <- rnorm(n3, 0.4, 0.1)
if(n4 != 0) Biv[id == 4,] <- cbind(rnorm(n4, 0.4, 0.1), rnorm(n4, 0.4, 0.1))
x <- Biv[,1]</pre>
```

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