Package 'smirnov'

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Type Package

Title Provides two taxonomic coefficients from E. S. Smirnov ``Taxonomic analysis'' (1969) book

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Author Alexey Shipunov (with help of Eugenij Altshuler)

Maintainer Alexey Shipunov <dactylorhiza@gmail.com>

Description This tiny package contains one function smirnov() which calculates two scaled taxonomic coefficients, Txy (coefficient of similarity) and Txx (coefficient of originality). These two characteristics may be used for the analysis of similarities between any number of taxonomic groups, and also for assessing uniqueness of giving taxon. It is possible to use smirnov() output as a distance measure: convert it to distance by ``as.dist(1 - smirnov(x))''.

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LazyLoad yes

Repository CRAN

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NeedsCompilation no

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Description

Provides two taxonomic coefficients from E. S. Smirnov "Taxonomic analysis" (1969) book

Usage

```
smirnov(x)
```

Arguments

x	is a binary (absence-presence matrix) where taxa are rows and characters are columns.

Details

Function will remove all non-informative characters (e.g., columns of all zeroes) and transform every value greater than 1 to 1 (in order to avoid non-binary matrices).

Please note that function will calculate scaled coefficients Txx and Txy instead of their unscaled variants (txx and txy): see the chapter 11 of Smirnov's (1969) book.

Value

Rectangular matrix where diagonal is filled with Txx coefficients and other cells with Txy coefficients. To convert this matrix to similarity matrix, diagonal should be filled with ones. To convert output to "normal" dissimilarity matrix, use "as.dist(1-smirnov(x))".

Author(s)

Alexey Shipunov

References

Smirnov, E. S. 1969. Taxonomical analysis. Moscow, Moscow University Publishers. [in Russian].

See Also

dist

Examples

```
# Example (21) from p. 45 of Smirnov's book:
s1 <- c(0,1,0,1,0,1,0,1,0,1,1,0,1,0,0)
s2 <- c(0,1,0,1,0,1,1,0,1,0,0,1,0,1,0)
s3 <- c(1,0,1,0,1,0,0,1,0,1,0,1,0,0,1)
smirnov(rbind(s1, s2, s3))
# s3 is most original; s1 and s2 are more similar than other pairs
```

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