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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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))''.

License GPL (>= 2)

LazyLoad yes

Repository CRAN

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NeedsCompilation no

R topics documented:

smirnov	*smirnov*

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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