

Package ‘ethnobotanyR’

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Type Package

Title Calculate Quantitative Ethnobotany Indices

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Author Cory Whitney

Maintainer Cory Whitney <whitney.cory@gmail.com>

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Description Calculate common quantitative ethnobotany indices to assess the cultural significance of plant species based on informant consensus. The package closely follows the paper by Tardio and Pardo-de-Santayana (2008). Tardio, J., and M. Pardo-de-Santayana, 2008. Cultural Importance Indices: A Comparative Analysis Based on the Useful Wild Plants of Southern Cantabria (Northern Spain) 1. Economic Botany, 62(1), 24-39. <doi:10.1007/s12231-007-9004-5>.

Depends R (>= 2.10)

Imports dplyr, reshape, circlize, magrittr, assertthat, ggplot2

License GPL

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LazyData true

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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CIs	<i>Cultural Importance index (CI)</i>
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Description

This function allows you to calculate the Cultural Importance Index (CI) per species.

Usage

```
CIs(data)
```

Arguments

data is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Tardio, J., and M. Pardo-de-Santayana, 2008. Cultural Importance Indices: A Comparative Analysis Based on the Useful Wild Plants of Southern Cantabria (Northern Spain) 1. *Economic Botany*, 62(1), 24-39. <<https://doi.org/10.1007/s12231-007-9004-5>>

Examples

```
#Use built-in ethnobotany data example
CIs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
CIs(eb_data)
```

ethnobotanydata	<i>Ethnobotany data set.</i>
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Description

An ethnobotany dataset from 20 informants, four species and 10 uses column 1 'informant' lists the names or id's of knowledge holders column 2 'sp_name' lists the names or id's of species The other 10 columns are the identified ethnobotany use categories. The data is populated with counts of uses per person (0 and 1 values).

Usage

```
ethnobotanydata
```

Format

A data frame with 80 rows and 12 variables:

informant anonymized id's of 20 knowledge holders

sp_name id's of four species

Use_1 one of the categorized uses of species, 0 and 1 values

Use_2 one of the categorized uses of species, 0 and 1 values

Use_3 one of the categorized uses of species, 0 and 1 values

Use_4 one of the categorized uses of species, 0 and 1 values

Use_5 one of the categorized uses of species, 0 and 1 values

Use_6 one of the categorized uses of species, 0 and 1 values

Use_7 one of the categorized uses of species, 0 and 1 values

Use_8 one of the categorized uses of species, 0 and 1 values

Use_9 one of the categorized uses of species, 0 and 1 values

Use_10 one of the categorized uses of species, 0 and 1 values ...

ethnoChord	<i>Create a chord diagram of ethnobotany uses and species</i>
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Description

This function allows you to create a chord diagram of species and uses for ethnobotany studies.

Usage

```
ethnoChord(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Whitney, C. W., Bahati, J., and Gebauer, J. (2018), Ethnobotany and agrobiodiversity; valuation of plants in the homegardens of southwestern Uganda. *Ethnobiology Letters*, 9(2), 90-100. <<https://doi.org/10.14237/ebl.9.2.2018.503>>

Examples

```
#Use built-in ethnobotany data example
ethnoChord(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
ethnoChord(eb_data)
```

ethnoChordUser

Create a chord diagram of informants and species uses

Description

This function allows you to create a chord diagram of informants and species uses for ethnobotany studies.

Usage

```
ethnoChordUser(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Whitney, C. W., Bahati, J., and Gebauer, J. (2018), Ethnobotany and agrobiodiversity; valuation of plants in the homegardens of southwestern Uganda. *Ethnobiology Letters*, 9(2), 90-100. <<https://doi.org/10.14237/ebl.9.2.2018.503>>

Examples

```
#Use built-in ethnobotany data example
ethnoChordUser(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
ethnoChordUser(eb_data)
```

FCs

*Frequency of citation (FC)***Description**

Allows users to calculate the frequency of citation (FC) per species.

Usage

```
FCs(data)
```

Arguments

data is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Examples

```
#Use built-in ethnobotany data example
FCs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
FCs(eb_data)
```

FLs	<i>Calculate the fidelity level (FL) of species uses in ethnobotany studies</i>
-----	---

Description

Allows users to calculate the fidelity level (FL) of species in ethnobotany studies.

Usage

```
FLs(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Friedman, J., Yaniv, Z., Dafni, A., Palewitch, D., 1986. A preliminary classification of the healing potential of medicinal plants, based on a rational analysis of an ethnopharmacological field survey among Bedouins in the Negev Desert, Israel. *Journal of Ethnopharmacology* 16, 275-287. <<https://www.ncbi.nlm.nih.gov/pubmed/3747566>>

Examples

```
#Use built-in ethnobotany data example
FLs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
FLs(eb_data)
```

NUs	<i>Number of Uses (NU)</i>
-----	----------------------------

Description

This function allows you to calculate the number of uses (NU) per species.

Usage

```
NUs(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Examples

```
#Use built-in ethnobotany data example
NUs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
NUs(eb_data)
```

Radial_plot

Radial bar plot of use reports (UR) per species

Description

Creates a radial bar plot of use reports (UR) per species based on the 'UR function'.

Usage

```
Radial_plot(data, analysis)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

`analysis` is one of the quantitative ethnobotany functions from ethnobotanyR, i.e. ethnobotanyR::FCs.

Examples

```
#Use built-in ethnobotany data example and Frequency of Citation function FCs()
Radial_plot(ethnobotanydata, analysis = FCs)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
Radial_plot(data = eb_data, analysis = FCs)
```

RFCs

Relative Frequency of Citation (RFC)

Description

Allows users to calculate the relative frequency of citation (RFC) per species published by Pardo-de-Santayana (2003).

Usage

```
RFCs(data)
```

Arguments

data is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Tardio, J., and M. Pardo-de-Santayana, 2008. Cultural Importance Indices: A Comparative Analysis Based on the Useful Wild Plants of Southern Cantabria (Northern Spain) 1. *Economic Botany*, 62(1), 24-39. <<https://doi.org/10.1007/s12231-007-9004-5>>

Examples

```
#Use built-in ethnobotany data example
RFCs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
```



```
RFCs(eb_data)
```

```
RIs
```

#Relative Importance Index (RI)

Description

This function allows you to calculate the relative importance index (RI) per species, published by Pardo-de-Santayana (2003).

Usage

```
RIs(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Tardio, J., and M. Pardo-de-Santayana, 2008. Cultural Importance Indices: A Comparative Analysis Based on the Useful Wild Plants of Southern Cantabria (Northern Spain) 1. *Economic Botany*, 62(1), 24-39. <<https://doi.org/10.1007/s12231-007-9004-5>>

Examples

```
#Use built-in ethnobotany data example
RIs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
RIs(eb_data)
```

URs

Calculate the use reports (UR) per species

Description

Allows users to calculate the use reports (UR) per species, a common metric for ethnobotany studies.

Usage

```
URs(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Examples

```
#Use built-in ethnobotany data example
URs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
URs(eb_data)
```

URsum*Sum of all Use Reports (UR) for all species*

Description

Allows users to calculate the sum of all ethnobotany use reports (UR) for all species, a common metric for ethnobotany studies.

Usage

```
URsum(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Examples

```
#Use built-in ethnobotany data example
URsum(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
URsum(eb_data)
```

UVs

Use Value (UV) index per species

Description

Allows users to calculate the use value (UV) index for each species in the data set (see Albuquerque et al. 2006).

Usage

```
UVs(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of species names respectively. The rest of the columns are the identified ethnobotany use categories. The data should be populated with counts of uses per person (should be 0 or 1 values).

Source

Albuquerque, U. P., R. F. P. Lucena, J. M. Monteiro, A. T. N. Florentino, and C. F. C. B. R. Almeida. 2006. Evaluating Two Quantitative Ethnobotanical Techniques. *Ethnobotany Research and Applications* 4:51–60. <<http://hdl.handle.net/10125/237>>

Examples

```
#Use built-in ethnobotany data example
UVs(ethnobotanydata)

#Generate random dataset of three informants uses for four species
eb_data <- data.frame(replicate(10,sample(0:1,20,rep=TRUE)))
names(eb_data) <- gsub(x = names(eb_data), pattern = "X", replacement = "Use_")
eb_data$informant<-sample(c('User_1', 'User_2', 'User_3'), 20, replace=TRUE)
eb_data$sp_name<-sample(c('sp_1', 'sp_2', 'sp_3', 'sp_4'), 20, replace=TRUE)
UVs(eb_data)
```

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