

Package ‘ethnobotanyR’

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Type Package

Title Calculate Quantitative Ethnobotany Indices

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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) I. Economic Botany, 62(1), 24-39. <doi:10.1007/s12231-007-9004-5>.

Depends R (>= 3.6)

Imports circlize, cowplot, dplyr, ggplot2, reshape, magrittr

License GPL

URL <https://github.com/CWWhitney/ethnobotanyR>

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests broom, knitr, pbapply, rmarkdown, tidyr, stringr

VignetteBuilder knitr

NeedsCompilation no

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

Calculates 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 informant (should be 0 or 1 values).
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Value

Data frame of species and Cultural Importance Index (CI) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Tardio, Javier, and Manuel 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.

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)
```

CVe

Cultural Value of ethnospecies (CVe)

Description

Calculates the Cultural Value (CVe) per ethnospecies.

Usage

```
CVe(data)
```

Arguments

`data` is an ethnobotany data set with column 1 'informant' and 2 'sp_name' as row identifiers of informants and of ethnospecies names respectively.

Value

Data frame of ethnospecies and Cultural Value (CVe) values.

Warning

Identification for informants and ethnospecies must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Reyes-Garcia, V., T. Huanca, V. Vadez, and W. Leonard. 2006. "Cultural, Practical, and Economic Value of Wild Plants: A Quantitative Study in the Bolivian Amazon." *Economic Botany*.

Examples

```
#Use built-in ethnobotany data example
CVe(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)

CVe(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`*Chord diagram of ethnobotany uses and species*

Description

Creates a simple chord diagram of species and uses for ethnobotany studies. For more on the circlize package see Zuguang Gu's 'Circular Visualization in R' <https://jokergoo.github.io/circlize_book/book/>

Usage

```
ethnoChord(data, by = "sp_name")
```

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).

`by` indicates the variable that should be mapped to the bottom of the chord diagram. This automatically defaults to the column referring to the species (`by = "sp_name"`)

Value

Chord diagram figure for each use by 'informant' (top half) related to each 'sp_name' (bottom half) in the data set. To change variable names try using the dplyr rename function.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns represent the identified ethnobotany use categories. These 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/eb1.9.2.2018.503>>

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)
```

FCs

Frequency of Citation (FC)

Description

Calculates 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).

Value

Data frame of species and frequency of citation (FC) values.

Source

Prance, G. T., W. Balee, B. M. Boom, and R. L. Carneiro. 1987. "Quantitative Ethnobotany and the Case for Conservation in Amazonia." *Conservation Biology* 1 (4): 296–310.

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 *Fidelity Level (FL)*

Description

Calculates the fidelity level (FL) of species uses, i.e. the ratio between the number of informants who independently cite the use of a species for the same major purposes (URs) and the total number of informants who mentioned the plant for any use (FCs).

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).

Value

Data frame of species and fidelity level (FL) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Friedman, J., Z. Yaniv, A. Dafni, and D. Palewitch. 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 (2-3): 275–87.

Examples

```
#Use built-in ethnobotany data example
FLs(ethnobotanydata)
#returns the primary use category (Primary.use) and the FLs value

#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

Calculates 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).

Value

Data frame of species and number of uses (NU) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Prance, G. T., W. Balee, B. M. Boom, and R. L. Carneiro. 1987. "Quantitative Ethnobotany and the Case for Conservation in Amazonia." *Conservation Biology* 1 (4): 296–310.

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 ethnobotany indices

Description

Creates a radial bar plot of ethnobotany indices in ethnobotanyR package using the ggplot2 library <<https://ggplot2.tidyverse.org/>>.

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.

Value

Radial bar plot of chosen ethnobotany indices in ethnobotanyR package.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

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 = URs)

```

 RFCs

Relative Frequency of Citation (RFC)

Description

Calculates 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).

Value

Data frame of species and relative frequency of citation (RFC) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Tardio, Javier, and Manuel 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.

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

Calculates 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).

Value

Data frame of species and relative importance index (RI) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Tardio, Javier, and Manuel 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.

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)
```

simple_UVs

Use Value (UV) index per species

Description

Calculates the simplified use value (UV) index for each species in the data set (see Albuquerque et al. 2006).

Usage

```
simple_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).

Value

Data frame of species and simplified use value (UV) index values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Albuquerque, Ulysses P., Reinaldo FP Lucena, Julio M.Monteiro, Alissandra TN Florentino, and Cecilia de Fatima CBR Almeida. 2006. "Evaluating Two Quantitative Ethnobotanical Techniques." *Ethnobotany Research and Applications* 4: 51–60.

Examples

```
#Use built-in ethnobotany data example
simple_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)

simple_UVs(eb_data)
```

URs

*Use Report (UR)***Description**

Calculates 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).

Value

Data frame of species and use reports (UR) values.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Prance, G. T., W. Balee, B. M. Boom, and R. L. Carneiro. 1987. "Quantitative Ethnobotany and the Case for Conservation in Amazonia." *Conservation Biology* 1 (4): 296–310.

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

Calculates 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).

Value

Single value sum of all ethnobotany use reports (UR) for all species in the data.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Prance, G. T., W. Balee, B. M. Boom, and R. L. Carneiro. 1987. "Quantitative Ethnobotany and the Case for Conservation in Amazonia." *Conservation Biology* 1 (4): 296–310.

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

Calculates the use value (UV) index for each species in the data set (see Tardio and Pardo-de-Santayana 2008).

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).

Value

Data frame of species and use value (UV) index results.

Warning

Identification for informants and species must be listed by the names 'informant' and 'sp_name' respectively in the data set. The rest of the columns should all represent separate identified ethnobotany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Source

Tardio, Javier, and Manuel Pardo-de-Santayana. "Cultural Importance Indices: A Comparative Analysis Based on the Useful Wild Plants of Southern Cantabria (Northern Spain)1." *Economic Botany* 62, no. 1 (May 2008): 24–39. <<https://doi.org/10.1007/s12231-007-9004-5>>

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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