Package ‘ethnobotanyR’

January 6, 2021

Type Package

Title Calculate Quantitative Ethnobotany Indices


Version 0.1.8

Date 2021-01-04

Depends R (>= 3.2.0)

Imports circlize, cowplot, dplyr, ggalluvial, ggplot2, ggridges, reshape2, magrittr

License GPL

URL https://CRAN.R-project.org/package=ethnobotanyR

BugReports https://github.com/CWWhitney/ethnobotanyR/issues

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-01-06 04:10:02 UTC
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### Description

Cultural Importance index (CI)

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).

### 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).
References


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).
References


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

Ethnobotany data set.

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
ethnoChord

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 ...

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)

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).

References


Examples

# Use built-in ethnobotany data example
ethnoChord(ethnobotanydata, by = "informant")

# Generate random dataset of three informants uses for four species

```r
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, by = "informant")
```

```
ethno_alluvial          Alluvial plot of ethnobotany uses and species
```

Description

 Creates a simple alluvial plot of species and uses for ethnobotany studies.

Usage

```r
ethno_alluvial(data, alpha = 0)
```

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).

- **alpha**: is a number between 0 and 1 for the level of transparency behind the labels on the strata (default is 0).

Value

Alluvial diagram showing all use reports for each use (center) related to each species (left) and informant (right) in the data set.

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).
ethno_bayes_consensus

References


Examples

#Use built-in ethnobotany data example
esthno_alluvial(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)

# Default plot ####
esthno_alluvial(eb_data)

ethno_bayes_consensus  Gives a measure of the confidence we can have in the answers in the ethnobotany data.

Description

Determine the probability that informant citations for a given use are 'correct' given informant responses to the use category for each plant, an estimate of each person's prior_for_answers with this plant and use, and the number of possible answers about this plant use.

Usage

ethno_bayes_consensus(data, answers = 2, prior_for_answers, prior = -1)

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).

answers The number of answers available for each question. These are set to '2' because the way the package works at the moment users can have either a '1' or a '0' in the table. It is however, possible to have more.
ethno_bayes_consensus

prior_for_answers
A matrix representing the probability of a given use being more likely. If not provided the function assumes a uniform distribution across uses.

prior
a prior distribution of probabilities over all answers as a matrix. If this is not provided the function assumes a uniform distribution (prior = -1).

Value

A matrix, where columns represent plant use categories and rows represent responses per person and plant (matching the data). Each value represents the bayes_consensus that an answer was 'correct' for a particular use, within the cultural consensus framework.

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 ethno-botany use categories. These data should be populated with counts of uses per informant (should be 0 or 1 values).

Application

ethnobotanyR users often have a large number of counts in cells of the data set after categorization (i.e one user cites ten different 'food' uses but this is just one category). Most quantitative ethnobotany tools are not equipped for cases where the theoretical maximum number of use reports in one category, for one species by one informant is >1. This function and the bayes_boot function may be useful to work with these richer datasets for the Bayes consensus analysis.

References


Alastair Jamieson Lane and Benjamin Grant Purzycki (2016), AnthroTools: Some custom tools for anthropology.

Examples

#Use built-in ethnobotany data example
#assign a non-informative prior to prior_for_answers with 'prior_for_answers=0.5'
ethno_bayes_consensus(ethnobotanydata, answers = 2, prior_for_answers = 0.5, prior = -1)

#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)
#assign a non-informative prior to prior_for_answers
eb_prior_for_answers <- rep(0.5, len = nrow(eb_data))

ethno_bayes_consensus(eb_data, answers = 5, prior_for_answers = eb_prior_for_answers)

### ethno_boot

**Bootstrap analyses of ethnobotany indices**

**Description**

Creates a non-parametric bootstrap as a Bayesian Model [http://www.sumsar.net/blog/2015/04/the-non-parametric-bootstrap-as-a-bayesian-model/](http://www.sumsar.net/blog/2015/04/the-non-parametric-bootstrap-as-a-bayesian-model/). This is meant to be applied for ethnobotany data and indices in the ethnobotanyR package. Performs a Bayesian bootstrap and returns a sample of size ‘n1’ representing the posterior distribution of the chosen statistic (i.e. ‘mean’). The function returns a vector if the statistic is one-dimensional (like for mean(...)) or a data.frame if the statistic is multi-dimensional (like for the coefficients ‘coefs.’ of a regression model ‘lm’).

**Usage**

```r
ethno_boot(data, statistic, n1 = 1000, n2 = 1000, ...)
```

**Arguments**

- **data**
  
  Can be either a vector, matrix or a data.frame.

- **statistic**
  
  A function that accepts data as its first argument. Should return a numeric vector.

- **n1**
  
  The size of the bootstrap sample.

- **n2**
  
  The sample size used to calculate the statistic for each bootstrap draw.

- **...**
  
  Further arguments passed on to the statistic function.

**Value**

Bayesian bootstrap of chosen ethnobotany indices in ethnobotanyR package.

**Application**

This function was inspired by Rasmus Bååth’s “The Non-Parametric Bootstrap as a Bayesian Model” Publishable Stuff, 2015. [http://www.sumsar.net/blog/2015/04/the-non-parametric-bootstrap-as-a-bayesian-model/](http://www.sumsar.net/blog/2015/04/the-non-parametric-bootstrap-as-a-bayesian-model/).

In order to understand the various possible applications of this function for ethnobotany analyses it is important to read through that work.

ethnobotanyR users often have a large number of counts in cells of the data set after categorization (i.e one user cites ten different ‘food’ uses but this is just one category). Most quantitative ethnobotany tools are not equipped for cases where the theoretical maximum number of use reports in one category, for one species by one informant is >1. This function and the ethno_bayes_consensus function may be useful to work with these richer datasets for the Bayes consensus analysis.
References


Examples

# Use built-in ethnobotany data example
ethno_boot(data = ethnobotanydata$Use_1,
statistic = mean, n1 = 1000)

# 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_")

name(eb_data$informant) <- sample(c("User_1", "User_2", "User_3"), 20, replace=TRUE)

# Simple bootstrap of the mean ####
boot_dataUR <- URs(eb_data)
ethno_boot(data = boot_dataUR$URs, statistic = mean)

---

**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.
FLs

References

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$informant<-sample(c("Var User_1", "Var User_2", "Var User_3"), 20, replace=TRUE)
eb_data$sp_name<-sample(c("Var sp_1", "Var sp_2", "Var sp_3", "Var sp_4"), 20, replace=TRUE)
FCs(eb_data)

FLs

Fidelity Level (FL)

Description
Calculates the fidelity level (FL) of the various uses of a species, i.e. the ratio between the number of informants who independently cite the use of a species for the same purposes (Ns * 100) 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).
References


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_")

# Generate random dataset of three informants uses for four species

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)

<table>
<thead>
<tr>
<th>NUs</th>
<th>Number of Uses (NU)</th>
</tr>
</thead>
</table>

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.
Radial_plot

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).

References


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).

References


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).

References

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$informant <- sample(c("Var User_1", "Var User_2", "Var User_3"), 20, replace=TRUE)
    eb_data$sp_name <- sample(c("sp_1", "sp_2", "sp_3", "sp_4"), 20, replace=TRUE)
    RFCs(eb_data)

---

RIs

<table>
<thead>
<tr>
<th>Relative Importance index (RI)</th>
</tr>
</thead>
</table>

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).

**References**


**Examples**

```r
#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). This is calculated the same as the CIs function.
simple_UVs

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).

References


Examples

# Use built-in ethnobotany data example
simple_UVs(ethnobotanydata)

# Generate random dataset of three informants uses for four species

```
# 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)
### Description
Calculates the use reports (UR) per species, a common metric for ethnobotany studies.

### Usage
`URs(data)`

### Arguments
data
- `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).

### References

### Examples
```r
# 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)
```
URsum

urban

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URsum

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).

References


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)

UVs(eb_data)

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Description

Calculates the use value (UV) index for each species in the data set (see Tardio and Pardo-de-Santayana 2008). This is calculated the same as the CIs function.

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).

References

Examples

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

# Generate random dataset of three informants uses for four species

```r
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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