Package 'ForestSDC'

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Type Package

Title Forest stand Structure, tree Diversity, and species Composition

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Description The package provides tools for forest inventory analysis, including functions to calculate structural diversity indices, biodiversity metrics, and Nearest Neighbour Summary Statistics. It is designed to support researchers and practitioners in assessing forest dynamics, ecosystem health, and biodiversity.

Imports FNN,
dplyr,
tidyr,
rlang

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

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Contents

A_index   *Species Profile Index A*

Description

This function calculates the Species Profile Index A, which measures species diversity across three height zones:

- Zone 1: Trees with heights >= 80% of the maximum height.
- Zone 2: Trees with heights between 50% and 80% of the maximum height.
- Zone 3: Trees with heights < 50% of the maximum height.

Usage

```
A_index(x, y)
```

Arguments

x	A numeric vector representing tree heights.
y	A character or factor vector representing species corresponding to each tree height.

Details

#' For each zone, the species proportions are used to compute a diversity profile index:

$$PI = \sum_{i=1}^{S} |p_i \cdot \ln(p_i)|$$

Where:

- S is the total number of species in the zone.
- p_i is the proportion of the i-th species in the zone.

The Species Profile Index A is the sum of the profile indices across all three zones:

$$A = PI_1 + PI_2 + PI_3$$

Value

A numeric value representing the Species Profile Index A.

References

Pretzsch, H. (2009). Forest Dynamics, Growth and Yield: From Measurement to Model. Springer-Verlag. https://doi.org/10.1007/978-3-540-88307-4

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
y <- c(
  "P. patula", "P. patula", "P. patula", "A. religiosa", "Q. castanea",
  "P. patula", "P. patula", "P. patula", "P. patula", "P. patula"
)
A_index(x, y)
```

A_max   *Maximum Value for the Species Profile Index A*

Description

This function calculates the maximum possible value of the Species Profile Index A, based on the number of distinct species present. It assumes that each species is equally distributed across the three height zones.

Usage

```
A_max(x)
```

Arguments

x   A character or factor vector representing species.

Value

A numeric value representing the maximum possible Species Profile Index A.

Examples

```
x <- c(
  "P. patula", "P. patula", "P. patula", "A. religiosa", "Q. castanea",
  "P. patula", "P. patula", "P. patula", "P. patula", "P. patula"
)
A_max(x)
```

A_rel   *Relative Value for the Species Profile Index A*

Description

This function calculates the relative value of the Species Profile Index A, which represents the observed species diversity in relation to the maximum possible diversity for a given set of species. The relative value is expressed as a percentage.

Usage

```
A_rel(x, y)
```

Arguments

x   A numeric vector representing tree heights.

y   A character or factor vector representing species.

Value

A numeric value representing the relative Species Profile Index A (as a percentage).

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
y <- c(
  "P. patula", "P. patula", "P. patula", "A. religiosa",
  "Q. castanea", "P. patula", "P. patula", "P. patula",
  "P. patula", "P. patula"
)
A_rel(x, y)
```

---

bal   *Calculate Basal Area Larger Index (BAL)*

Description

This function calculates the Basal Area Larger Index (BAL), which is the sum of the basal area of trees larger than a given subject tree in a specified plot area. It provides an index of competition based on tree size.

Usage

```
bal(x, y)
```

Arguments

x   Numeric vector. Diameters of the subject trees in cm.

y   Numeric. Plot area in square meters.

Details

The formula for each tree is:

$$BAL_i = \frac{\sum(BA_j > BA_i)}{A}$$

where:

- BA_i is the basal area of the subject tree.
- BA_j is the basal area of a competing tree larger than BA_i.
- A is the plot area in square meters.

Value

Numeric vector. The BAL values for each tree in x.

Examples

```
x <- c(30, 20, 20, 35, 65) # Tree diameters in cm
bal_result <- bal(x, 400) # Calculate BAL for a plot area of 400 square meters
bal_result
```

BALMOD   *BALMOD Competition Index*

Description

This function calculates the BALMOD competition index for trees based on their diameters, heights, and the area of the plot. The BALMOD index measures competition among trees by integrating basal area proportion, relative spacing, and dominant height.

Usage

```
BALMOD(x, y, z)
```

Arguments

x	A numeric vector representing the diameters of the trees in cm.
y	A numeric vector representing the heights of the trees in meters.
z	A numeric variable representing the plot area in square meters.

Details

The BALMOD index is computed as:

$$\text{BALMOD} = \frac{1 - \pi}{RS}$$

where:

- π is the proportion of the basal area of the individual tree ($\pi = \frac{\text{BAL}}{G_{\text{ha}}}$),
- RS is the relative spacing ($RS = \frac{\sqrt{10000/N}}{h_{\text{dom}}}$),
- N is the total number of trees in the plot,
- h_{dom} is the dominant height, defined as the mean height of the tallest trees.

Value

A numeric vector containing the BALMOD index for each tree.

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10) # Tree diameters in cm
y <- c(12, 23, 33, 45, 43, 22, 31, 32, 13, 11) # Tree heights in meters
z <- 400 # Plot area in square meters

BALMOD(x, y, z) # Calculate BALMOD index
```

---

ca   *Individual Tree Crown Area*

Description

This function calculates the crown area of an individual tree based on two measurements of its crown diameters. The crown area is computed using the average of the two diameters and is assumed to be circular.

Usage

```
ca(x, y)
```

Arguments

x   A numeric variable representing the first tree crown diameter in meters.

y   A numeric variable representing the second tree crown diameter in meters.

Value

A numeric variable representing the tree crown area in square meters.

Examples

```
# Calculate the crown area for two crown diameters of 10 m and 15 m
crown_area <- ca(10, 15)
crown_area # Output: Area in square meters
```

Caha   *Calculate Crown Area Cover per Hectare*

Description

This function calculates the total crown area cover per hectare based on the tree crown diameters provided. It computes the crown area for each tree as the area of a circle using the formula:

$$A = \pi \times \left(\frac{cw}{2}\right)^2$$

where cw is the crown diameter in m. The total crown area is then scaled to a per-hectare value using the specified plot area.

Usage

```
Caha(x, y)
```

Arguments

x	Numeric vector. Tree crown diameters (in meters).
y	Numeric. Total plot area (in square meters).

Value

Numeric. Crown area cover per hectare (in square meters).

Examples

```
# Example crown diameters and plot area
x <- c(10, 8, 6, 8, 5, 7, 2, 3, 11, 10)
y <- 1000

# Calculate crown area cover per hectare
Caha(x, y)
```

---

cat_d   *Diameter Category Classification*

Description

This function categorizes tree diameters into classes of 5 cm, starting from 2.5 cm. It takes a numeric variable or vector representing tree diameters and returns the corresponding diameter categories.

Usage

```
cat_d(x)
```

Arguments

x	A numeric variable or vector representing tree diameters in centimeters.

Value

A factor variable or vector representing tree diameter classes in increments of 10 cm.

Examples

```
# Create a data frame with tree diameters
d_data <- data.frame(d = c(10.1, 23, 31.5, 40, 52.4, 27, 33, 22, 11, 10))

# Categorize the diameters into classes
d_data$diam_cat <- cat_d(d_data$d)

# Display the categorized data
print(d_data)
```

---

coord_xy   *Convert azimuth and distance to XY coordinates*

Description

This function transforms azimuth and distance values into Cartesian coordinates (x, y). Useful for forestry, surveying, or spatial applications where polar measurements are common.

Usage

```
coord_xy(azi, dis, r = NULL, center = NULL, deg = TRUE)
```

Arguments

azi	Numeric vector of azimuth angles.
dis	Numeric vector of distances, same length as azi.
r	Optional numeric scalar for centering. If provided, coordinates will be shifted by r/2.
center	Optional numeric vector of length 2 (c(x0, y0)) to shift the origin. Overrides r if both are provided.
deg	Logical, whether the angles are in degrees (default = TRUE). If FALSE, assumed in radians.

Value

A data.frame with two columns: x and y.

Examples

```
# Example with degrees
coord_xy(azi = c(0, 90, 180), dis = c(10, 10, 10))

# Example with radians
coord_xy(azi = c(0, pi/2, pi), dis = c(10, 10, 10), deg = FALSE)

# Using center
coord_xy(azi = c(0, 90), dis = c(5, 5), center = c(2, 2))
```

---

dg   *Calculate Quadratic Mean Diameter (QMD)*

Description

This function calculates the quadratic mean diameter (QMD) of a set of tree diameters. The QMD is a commonly used forestry measure to assess the average tree diameter in a stand, weighted by the basal area of the trees. It is useful for understanding stand structure and growth.

Usage

```
dg(x)
```

Arguments

x   Numeric vector. A vector of tree diameters (in centimeters).

Details

The formula used is:

$$QMD = \sqrt{\frac{\sum BA}{k \times n}}$$

where: - $\sum BA$ is the sum of the basal areas of all trees. - k is a constant factor for conversion. - n is the number of trees.

Value

Numeric. The quadratic mean diameter (in centimeters).

Examples

```
# Example tree diameters
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)

# Calculate the quadratic mean diameter
dg(x)
```

---

dista   *Compute the Distance between Two Points*

Description

This function calculates the Euclidean distance between two points in a 2D space. The distance is computed using the formula:

$$d = \sqrt{(x1 - x)^2 + (y1 - y)^2}$$

where (x, y) and $(x1, y1)$ are the coordinates of the two points.

Usage

```
dista(x, y, x1, y1)
```

Arguments

x	Numeric. The x-coordinate of the first point.
y	Numeric. The y-coordinate of the first point.
x1	Numeric. The x-coordinate of the second point.
y1	Numeric. The y-coordinate of the second point.

Value

Numeric. The Euclidean distance between the two points.

Examples

```
# Calculate the distance between points (5, 5) and (4, 4)
dista(5, 5, 4, 4)
```

---

dom_trees   *Identify Dominant Trees in a Plot Area*

Description

This function identifies the dominant trees in a specified plot area by selecting the 100 thickest trees based on their diameters. Dominant trees are classified as those whose diameters fall within the top 100 in the given plot area.

Usage

```
dom_trees(x, y)
```

Arguments

x	Numeric vector. A vector of tree diameters measured in centimeters.
y	Numeric variable. The total plot area in square meters.

Value

Character vector. A vector of the same length as 'x', where each entry is labeled as "dom_tree" for dominant trees and "not_dom" for non-dominant trees.

Examples

```
# Example tree diameters
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)

# Specify the plot area
y <- 1000

# Identify dominant trees
dom_trees(x, y)
```

---

d_dom   *Dominant Tree Diameter*

Description

This function calculates the dominant tree diameter, defined as the mean diameter at breast height (dbh) of the 100 thickest trees within a specified plot area. It considers the tree diameters provided and determines which trees qualify as dominant based on their thickness.

Usage

```
d_dom(d, ps)
```

Arguments

d	Numeric vector. A vector of tree diameters (in centimeters).
ps	Numeric variable. The plot area (in square meters).

Value

Numeric value representing the mean diameter at breast height of the dominant trees (in centimeters).

Examples

```
# Example tree diameters and plot area
d <- c(12, 25, 40, 40, 55, 35, 35, 25, 12, 15)
ps <- 400

# Calculate the dominant tree diameter
d_dom(d, ps)
```

ForestSDC   *ForestSDC: Forest stand Structure, tree Diversity, and species Com-*
                                       position

Description

The `ForestSDC` package is a comprehensive tool set for analyzing data from forest inventories and permanent research plots. It includes functions to estimate structural indices, biodiversity metrics, and the nearest neighbor summary statistics. These tools are essential for assessing forest dynamics, biodiversity, and ecosystem health.

Details

Key features include:

- Structural indices such as Shannon's diversity, Simpson's complement, and species richness.
- Spatial analysis using nearest-neighbor methods.
- Customization tools for biodiversity and forest dynamics evaluation.

The package leverages `dplyr` and `tidyr` for data manipulation and `FNN` for efficient nearest-neighbor calculations.

Author(s)

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---

g   *Basal Area from Tree Diameter*

Description

This function calculates the basal area of a tree based on its diameter at breast height (DBH). The formula used is $g = \frac{\pi}{4} \times \left(\frac{d}{100}\right)^2$, where d is the diameter in centimeters.

Usage

```
g(x)
```

Arguments

x   Numeric variable. Tree diameter in centimeters.

Value

Numeric variable. Basal area in square meters.

Examples

```
x <- 25
g(x) # Calculates the basal area for a tree with a 25 cm diameter.
```

Gha   *Calculate Basal Area per Hectare (G/ha)*

Description

This function calculates the basal area per hectare (G/ha) using the formula:

$$G/ha = \frac{\sum g}{A} \times 10000$$

where:

- $\sum g$ is the sum of the basal area of individual trees.
- A is the plot area in square meters.

Usage

```
Gha(x, y)
```

Arguments

x   Numeric vector. A vector of tree diameters (e.g., in cm).

y   Numeric. The plot area (e.g., in square meters).

Value

Numeric. The basal area per hectare (G/ha).

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
y <- 1000
Gha(x, y)
```

---

h_dom   *Dominant Tree Height (Mean Height of the 100 Thickest Trees in a Hectare)*

Description

This function calculates the dominant tree height, which is the mean height of the 100 thickest trees in a specified plot area, based on their diameters.

Usage

```
h_dom(h, d, ps)
```

Arguments

h	Numeric vector. Tree heights (in centimeters).
d	Numeric vector. Tree diameters (in centimeters).
ps	Numeric variable. Plot area (in square meters).

Value

Numeric value representing the dominant tree height, which is the mean height of the 100 thickest trees.

Examples

```
h <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
d <- c(12, 25, 40, 40, 55, 35, 35, 25, 12, 15)
ps <- 400
h_dom(h, d, ps)
```

---

ivi_index_table   *Calculate IVI Index Table*

Description

Computes a table of Importance Value Index (IVI) for tree species based on abundance (Nha), dominance (Xha), and frequency, using plot-level data. It will compute the species frequency based on the number of plots. So it is recommended to compute the IVI per area and not just for individual plots.

Usage

```
ivi_index_table(sp, x, plot, data = NULL, plot_area)
```

Arguments

sp	A column in 'data' indicating species names.
x	A numeric column used for dominance calculation (e.g., basal area or crown area).
plot	A factor or character column indicating plot identifiers.
data	A data frame containing all the input columns.
plot_area	Numeric value representing the area of the individual plots (e.g., 10000 m²).

Value

A data frame with species-wise IVI metrics: Abundance, Dominance, Frequency, and IVI.

Examples

```
# ivi_index_table(sp, x, plot, data = mydata, plot_area = 400)
```

---

margalef   *Margalef's Species Richness Index*

Description

This function calculates Margalef's species richness index, which is an indicator of the species richness in a given sample. The index is based on the number of species and the total number of individuals. It is calculated using the following formula:

Usage

```
margalef(x)
```

Arguments

x   A numeric or factor variable representing the species or individuals in a sample.

Details

$$D = \frac{S - 1}{\log(N)}$$

where:

- S is the number of unique species in the sample,
- N is the total number of individuals in the sample.

Value

A numeric value representing Margalef's species richness index.

Examples

```
x <- c("P. patula", "A. religiosa", "A. religiosa", "Q. castanea", "P. patula")
margalef(x)
```

---

menhinick   *Menhinick's Species Richness Index*

Description

This function calculates Menhinick's species richness index, which is another measure of species diversity in a given sample. The index is calculated using the following formula:

Usage

```
menhinick(x)
```

Arguments

x   A numeric or factor variable representing the species or individuals in a sample.

Details

$$D = \frac{S}{\sqrt{N}}$$

where:

- S is the number of unique species in the sample,
- N is the total number of individuals in the sample.

Value

A numeric value representing Menhinick's species richness index.

Examples

```
x <- c("P. patula", "A. religiosa", "A. religiosa", "Q. castanea", "P. patula")
menhinick(x)
```

Nha   *Number of Trees per Hectare*

Description

This function calculates the number of trees per hectare based on the total number of trees in a given plot area. The index is calculated using the following formula:

Usage

```
Nha(x, y)
```

Arguments

x   A numeric or character vector representing tree diameter or other tree attribute.

y   A numeric variable representing the plot area in square meters.

Details

$$N = \frac{N_{\text{trees}} \times 10000}{A}$$

where:

- N_{trees} is the total number of trees in the sample,
- A is the plot area in square meters.

Value

A numeric value representing the number of trees per hectare.

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
y <- 1000
Nha(x, y)
```

---

nnss_circle	*Calculate Nearest Neighbor Indices for Circular Plots*

Description

This function calculates nearest neighbor indices for trees within a circular plot. It requires coordinates, tree diameter, height, and species information, and returns several indices related to tree competition and spacing.

Usage

```
nnss_circle(x, y, sp, d, h, r, data = NULL, center_point = NULL)
```

Arguments

x	A numeric vector of x-coordinates for each tree.
y	A numeric vector of y-coordinates for each tree.
sp	A factor or character vector representing tree species.
d	A numeric vector representing tree diameters.
h	A numeric vector representing tree heights.
r	A numeric value representing the radius of the circular plot (must be positive).
data	A data frame containing all the required columns (plot, x, y, sp, d, h).
center_point	a vector including the center coordinates of the plots.

Value

A data frame with calculated nearest neighbor indices for each tree. Columns include:

- Ui: Uniformity index
- Mi: Mixture index
- dDomi: Dominance based on diameter
- hDomi: Dominance based on height
- dDif: Diameter differentiation
- hDif: Height differentiation
- NN1: Nearest-neighbor edge-correction

Examples

```
data(pipse_azimuth)

require(dplyr)

pipse_xy <-
pipse_azimuth %>%
mutate(coord_xy(azi = azimuth,dis = distance, r = 17.84*2))

nnss_circle(x = x, y = y, sp = sp, d = d, h = h, r = 17.84, data = pipse_xy)
```

---

nnss_square   *Calculate Nearest Neighbor Indices for Square Plots*

Description

This function calculates nearest neighbor indices for trees within a square plot. It requires coordinates, tree diameter, height, and species information, along with the plot's maximum x and y dimensions. The function returns several indices related to tree competition and spacing.

Usage

```
nnss_square(x, y, sp, d, h, xr, yr, data = NULL)
```

Arguments

x	A numeric vector of x-coordinates for each tree.
y	A numeric vector of y-coordinates for each tree.
sp	A factor or character vector representing tree species.
d	A numeric vector representing tree diameters.
h	A numeric vector representing tree heights.
xr	A numeric vector including the min and the max values of the x-coordinates for the plot.
yr	A numeric vector including the min and the max values of the x-coordinates for the plot.
data	A data frame containing all the required columns (x, y, sp, d, h).

Value

A data frame with calculated nearest neighbor indices for each tree. Columns include:

- Ui: Uniformity index
- Mi: Mixture index
- dDomi: Dominance based on diameter
- hDomi: Dominance based on height
- dDif: Diameter differentiation
- hDif: Height differentiation
- NN1: Nearest-neighbor edge-correction

Examples

```
set.seed(42)
x <- runif(100, min = 1, max = 50)
y <- runif(100, min = 1, max = 50)
sp <- factor(sample(c("Pinus", "Quercus"), 100, replace = TRUE))
d <- runif(100, min = 7.5, max = 60)
h <- 5.4349 + d * 0.4219
plot <- rep("P01", 100)
dataP01 <- data.frame(plot, x, y, sp, d, h)
nnss_square(x = x, y = y, sp = sp, d = d,
h = h, xr = cbind(0,50), yr = cbind(0,50), data = dataP01)
```

---

pielou	*Calculate Pielou's Equitativity Index*

Description

This function calculates Pielou's equitativity index, which measures the evenness of species distribution in a community. The formula is:

$$J' = \frac{H'}{\log(S)}$$

where:

- H' is the Shannon diversity index.
- S is the number of unique categories or species.

Usage

```
pielou(x)
```

Arguments

x   Numeric or factor variable. A vector representing species or categories.

Value

Numeric. The Pielou equitativity index.

Examples

```
x <- c("n", "m", "n", "n", "m")
pielou(x)
```

---

pipse_azimuth   *Azimuth and distance data for Pinus pseudostrobus*

Description

This dataset includes tree measurements and spatial orientation information for *Pinus pseudostrobus* individuals sampled in multiple plots.

Usage

```
pipse_azimuth
```

Format

A data frame with 100 rows and 6 variables:

plot Plot identifier (character)

sp Species code, here 'PIPSE' for *Pinus pseudostrobus* (character)

d Diameter at breast height in cm (numeric)

h Tree height in m (numeric)

azimuth Azimuth from plot center to tree in degrees (numeric, 0–360)

distance Distance from plot center to tree in meters (numeric)

Details

The data were collected to analyze spatial distribution patterns and size variation of *Pinus pseudostrobus* in sampled forest plots. This dataset can be used for modeling spatial structure or basal area estimations.

Source

Field data collected by Ernesto Rubio.

---

pipse_cplot   *Circular plot data for Pinus pseudostrobus*

Description

This dataset contains measurements collected in circular plots established for the study of *Pinus pseudostrobus* stands.

Usage

```
pipse_cplot
```

Format

A data frame with 1743 rows and 12 variables:

tree Unique identifier for the tree

plot Unique identifier for the sample plot

x x coordinate for the tree

y y coordinate for the tree

sp Species code (character)

cond Condition

d Diameter at breast height in cm (numeric)

h Tree total height in m (numeric)

cbh Crown base height in m (numeric)

ca Crown area

x_center x coordinate for the plot center

y_center y coordinate for the plot center

Details

The data were resampled from the original data in circular plots (1000 square meters) following standard forest inventory methodology. They can be used for spatial structure analysis, stand diversity, and structure estimation, or modeling.

Source

Field data collected by Ernesto Rubio.

---

pipse_square   *Square plot data for Pinus pseudostrobus*

Description

This dataset contains measurements collected in square plots (50x50 m) established for the study of *Pinus pseudostrobus* stands.

Usage

```
pipse_square
```

Format

A data frame with 4260 rows and 9 variables:

x x coordinate for the tree

y y coordinate for the tree

sp Species code (character)

d Diameter at breast height in cm (numeric)

h Tree total height in m (numeric)

ca Crown area

x_c x coordinate for the plot center

y_c y coordinate for the plot center

plot Unique identifier for the sample plot

Details

The data were resampled from the original data in square plots (50x50 meters) following standard forest inventory methodology. They can be used for spatial structure analysis, stand diversity, and structure estimation, or modeling.

Source

Field data collected by Ernesto Rubio.

---

rich   *Calculate Species Richness (S)*

Description

This function calculates species richness (S), which represents the number of unique species or categories in the given data. The formula is:

$$S = \sum I(counts > 0)$$

where:

- $counts$ represents the frequency of each unique species or category.

Usage

```
rich(x)
```

Arguments

x   Numeric or factor variable. A vector representing species or categories.

Value

Numeric. The species richness (S).

Examples

```
x <- c("n", "m", "n", "n", "m")
rich(x)
```

---

sdi   *Calculate Stand Density Index (SDI)*

Description

This function calculates the Stand Density Index (SDI) using the formula:

$$SDI = Nha \times \left(\frac{dg}{25.4} \right)^{1.605}$$

where:

- Nha is the number of trees per hectare.
- dg is the quadratic mean diameter (in cm).

Usage

```
sdi(x, y)
```

Arguments

x   Numeric vector. A vector of tree diameters (e.g., in cm).

y   Numeric. The plot area (e.g., in square meters).

Value

Numeric. The stand density index.

Examples

```
x <- c(10, 20, 30, 40, 50, 25, 30, 22, 11, 10)
y <- 1000
sdi(x, y)
```

---

shannon   *Shannon's Entropy Index*

Description

This function calculates Shannon's entropy index (H') for a given dataset. Shannon's entropy index measures the diversity in the dataset, considering both the richness (number of unique categories) and evenness (distribution of individuals).

Usage

```
shannon(x)
```

Arguments

x   A numeric or factor vector representing categories (e.g., species or groups).

Details

The formula is:

$$H' = -\sum_{i=1}^{S} p_i \log(p_i)$$

Where:

- p_i is the proportion of individuals belonging to the i-th category.
- S is the total number of unique categories in the dataset.

Value

A numeric value representing Shannon's entropy index (H').

Examples

```
x <- c("n", "m", "n", "n", "m")
shannon(x)
```

---

shannon_evenness   *Shannon's Evenness Index*

Description

This function calculates Shannon's evenness index, which measures the evenness of the distribution of species (or any type of data) in a community. The formula used is:

Usage

```
shannon_evenness(x)
```

Arguments

x   A numeric or factor vector representing species or groups in the community.

Details

$$E_H = \frac{H'}{H_{\max}}$$

where:

- H' is the Shannon diversity index:

$$H' = -\sum p_i \log(p_i)$$

with p_i being the proportion of individuals of species i.

- $H_{\max}$ is the maximum Shannon index for a given number of unique species S, and is given by $H_{\max} = \log(S)$.

Value

A numeric value representing Shannon's evenness index, which ranges from 0 (uneven) to 1 (perfectly even).

Examples

```
x <- c("n", "m", "n", "n", "m")
shannon_evenness(x)
```

---

simpson	*Simpson's index.*

Description

Simpson's index.

Usage

```
simpson(x)
```

Arguments

x   Numeric or factor variable

Value

Numeric variable.

Examples

```
x <- c("n", "m", "n", "n", "m")

simpson(x)
```

---

simpson_complement	*Simpson's Index Complement*

Description

This function calculates the complement of Simpson's index (D'), a diversity measure that represents the probability of two randomly selected individuals belonging to different categories.

Usage

```
simpson_complement(x)
```

Arguments

x   A numeric or factor vector representing categories (e.g., species or groups).

Details

The formula is:

$$D' = 1 - \sum_{i=1}^{S} p_i^2$$

Where:

- p_i is the proportion of individuals in the i-th category,
- S is the total number of categories.

Value

A numeric value representing the complement of Simpson's index (D').

Examples

```
x <- c("n", "m", "n", "n", "m")
simpson_complement(x)
```

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