Package ‘diversityArch’

May 8, 2026

Type Package

Title Computes Diversity Indices with Archaeological Data

Version 0.3.0

Description Companion package of Arnaud Barat, Andreu Sansó, Maite Arilla-Osuna, Ruth Blasco, Iñaki Pérez-Fernández, Gabriel Cifuentes-Alcobenda, Rubén Llorente, Daniel Vivar-Ríos, Ella Assaf, Ran Barkai, Avi Gopher, & Jordi Rosell-Ardèvol (2025), ``Quantifying Diversity through Entropy Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave''.

License GPL-2

Imports methods

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

Author Andreu Sansó [aut, cre],
Arnaud Barat [aut],
Jordi Rosell [aut]

Maintainer Andreu Sansó <`andreu.sanso@uib.eu`>

Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2026-05-04 17:00:02 UTC

Contents

`all_indices` *Diversity indices*

Description

Computes and prints all the diversity indices

Usage

```
all_indices(x, groups = NULL, B = 1000, cl = 0.95)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`groups`	Vector of dimension S of factors indicating the groups. If omitted, the decomposition of the indicators is not done.
`B`	Number of bootstrap samples. The default is 1000.
`cl`	Confidence level. A value between 0 and 1. The default is 0.95.

Value

No return value. It prints the value of all indicators

References

"Arnaud Barat, Andreu Sansó, Maite Arilla-Osuna, Ruth Blasco, Iñaki Pérez-Fernández, Gabriel Cifuentes-Alcobenda, Rubén Llorente, Daniel Vivar-Ríos, Ella Assaf, Ran Barkai, Avi Gopher, & Jordi Rosell-Ardèvol (2026): Quantifying Diversity through Entropy Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon, dec_shannon, dominance, equitability, evenness, margalef, menhinick, simpson_D, simpson_E

Examples

```
data(Qesem_s)
all_indices(Qesem_s$HU)
all_indices(Qesem_s$HU, Qesem_s$Group)
```

`bs` *Bootstrap estimates of the diversity indices*

Description

Computes bootstrap standard error and confidence interval of the diversity indices

Usage

```
bs(x, ind = "shannon", B = 1000, cl = 0.95)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`ind`	Index to be computed. The default value is "shannon". Other possible values are: "simpson_E", "simpson_D", "menhinick", "margalef", "evenness", "equitability" and "dominance".
`B`	Number of bootstrap samples. The default is 1000.
`cl`	Confidence level. A value between 0 and 1. The default is 0.95.

Value

- `s`: Boostrap standard error.
- `ci`: Confidence interval.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon, dec_shannon, dominance, equitability, evenness, margalef, menhinick, simpson_D, simpson_E

Examples

```
data(Qesem_s)
bs(Qesem_s$HU)
```

`bs_dec` *Bootstrap estimates of the decomposed Shannon's diversity index*

Description

Computes bootstrap confidence intervals of the Shannon's diversity index

Usage

```
bs_dec(x, groups, B = 1000, cl = 0.95)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`groups`	Vector of dimension S of factors indicating the groups of each species.
`B`	Number of bootstrap samples. The default is 1000.
`cl`	Confidence level. A value between 0 and 1. The default is 0.95.

Value

- `ci_bt`: Confidence interval for "between groups".
- `ci_wt`: Confidence interval for "within groups".

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon, dec_shannon

Examples

```
data(Qesem_s)
bs_dec(Qesem_s$HU, Qesem_s$Group)
```

`bs_frag` *Bootstrap estimates of the decomposed Shannon's diversity index with fragments*

Description

Computes bootstrap confidence intervals of the decomposed Shannon's diversity index using evidence from fragments

Usage

```
bs_frag(x, gx, f, gf, B = 1000, cl = 0.95)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`gx`	Vector of dimension S of factors indicating the group of each species. G groups.
`f`	Vector of dimension G with the number (>0) of fragments in each group
`gf`	Vector of dimension G of factors indicating the groups to which the fragments "f" belong.
`B`	Number of bootstrap samples. The default is 1000.
`cl`	Confidence level. A value between 0 and 1. The default is 0.95.

Value

- `ci_sh`: Confidence interval for Shannon's diversity index with fragments.
- `ci_bt`: Confidence interval for "between groups".
- `ci_wt`: Confidence interval for "within groups".

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon, dec_shannon, shannon_frag

Examples

```
data(Qesem_s)
data(Qesem_f)
bs_frag(Qesem_s$HU, Qesem_s$Group, Qesem_f$HU, Qesem_f$Group)
```

`dec_equit` *Decomposition of the equitability index*

Description

Computes equitability and its decomposition

Usage

```
dec_equit(x, groups)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`groups`	Vector of dimension S of factors indicating the group of each species.

Value

- `equitability`: Equitability index.
- `within`: Within groups equitability.
- `between`: Between groups equitability.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

dec_shannon

Examples

```
data(Qesem_s)
dec_equit(Qesem_s$HU, Qesem_s$Group)
```

`dec_shannon` *Shannon diversity decomposition*

Description

Computes Shannon diversity and its decomposition

Usage

```
dec_shannon(x, groups)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`groups`	Vector of dimension S of factors indicating the group of each species.

Value

- `shannon`: Shannon's total Entropy.
- `within`: Within groups entropy.
- `between`: Between groups entropy.
- `groups`: A data frame with information about each group: relative frequency, internal entropy and number of species.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon

Examples

```
data(Qesem_s)
dec_shannon(Qesem_s$HU, Qesem_s$Group)
```

`dominance` *Dominance index*

Description

Modification of the Simpson's dominance index to be restricted between 0 and 1.

Usage

```
dominance(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Dominance index (Modified Simpson's dominance index).

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

simpson_D

Examples

```
data(Qesem_s)
dominance(Qesem_s$HU)
```

`equitability` *Equitability. J Pielou index*

Description

Computes J Pielou index know as equitability

Usage

```
equitability(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Equitability. J Pielou index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon

Examples

```
data(Qesem_s)
equitability(Qesem_s$HU)
```

`evenness` *Evenness index*

Description

Modification of Simpson's evenness index to be restricted between 0 an 1.

Usage

```
evenness(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Evenness index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

simpson_E

Examples

```
data(Qesem_s)
evenness(Qesem_s$HU)
```

`margalef` *Margalef index*

Description

Computes Margalef's index

Usage

```
margalef(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Margalef index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

Examples

```
data(Qesem_s)
margalef(Qesem_s$HU)
```

`menhinick` *Menhinick index*

Description

Computes Menhinick's index

Usage

```
menhinick(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Menhinick index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

Examples

```
data(Qesem_s)
menhinick(Qesem_s$HU)
```

`Qesem_f` *Data used in the examples*

Description

Data frame with number of fragments of bones of unidentified species but identified group for several levels in Qesem (Israel). Data source: Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., (2024)

Usage

```
data(Qesem_f)
```

Value

Data frame with 4 observations (groups) and 7 levels.

Author(s)

Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A.

Source

Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., 2024. Exploring the lack of articular ends at the Middle Pleistocene site of Qesem Cave, Israel. Journal of Human Evolution 189, 103509. doi:10.1016/j.jhevol.2024.103509

References

Barat, A. Sansó, A. Arilla-Osuna, M. Blasco, R., Pérez-Fernández, I., Cifuentes-Alcobenda, G. Llorente, R., Vivar-Ríos, D., Assaf, E. Barkai, R., Gopher, A. & Rosell-Ardèvol, J., 2025. Quantifying Diversity through Entropy Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave. Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., 2024. Exploring the lack of articular ends at the Middle Pleistocene site of Qesem Cave, Israel. Journal of Human Evolution 189, 103509. doi:10.1016/j.jhevol.2024.103509

Examples

```
data(Qesem_f)
names(data)
# The following example replicates some of the results in
# Barat, A. Sansó, A. Arilla-Osuna, M. Blasco, R., Pérez-Fernández, I.,
# Cifuentes-Alcobenda, G. Llorente, R., Vivar-Ríos, D., Assaf, E. Barkai, R.,
# Gopher, A. & Rosell-Ardèvol, J., 2025. "Quantifying Diversity through Entropy
# Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave".
shannon_frag(Qesem_s$HU, Qesem_s$Group, Qesem_f$HU, Qesem_f$Group)
```

`Qesem_s` *Data used in the examples*

Description

Data frame with number of bones of different species and diferent levels in Qesem (Israel), and a factor related to the size of the animal. Data source: Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., (2024)

Usage

```
data(Qesem_s)
```

Value

Data frame with 15 observations and 7 levels.

Author(s)

Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A.

Source

Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., 2024. Exploring the lack of articular ends at the Middle Pleistocene site of Qesem Cave, Israel. Journal of Human Evolution 189, 103509. doi:10.1016/j.jhevol.2024.103509

References

Barat, A. Sansó, A. Arilla-Osuna, M. Blasco, R., Pérez-Fernández, I., Cifuentes-Alcobenda, G. Llorente, R., Vivar-Ríos, D., Assaf, E. Barkai, R., Gopher, A. & Rosell-Ardèvol, J., 2025. Quantifying Diversity through Entropy Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave. Blasco, R., Rosell, J., Assaf, E., Barkai, R., Gopher, A., 2024. Exploring the lack of articular ends at the Middle Pleistocene site of Qesem Cave, Israel. Journal of Human Evolution 189, 103509. doi:10.1016/j.jhevol.2024.103509

Examples

```
data(Qesem_s)
names(Qesem_s)
# The following example replicates some of the results in
# Barat, A. Sansó, A. Arilla-Osuna, M. Blasco, R., Pérez-Fernández, I.,
# Cifuentes-Alcobenda, G. Llorente, R., Vivar-Ríos, D., Assaf, E. Barkai, R.,
# Gopher, A. & Rosell-Ardèvol, J., 2025. "Quantifying Diversity through Entropy
# Decomposition. Insights into Hominin Occupation and Carcass Processing at Qesem cave".
all_indices(Qesem_s$HU)
```

`shannon` *Shannon diversity index*

Description

Computes Shannon's diversity index

Usage

```
shannon(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Shannon's diversity index (Entropy).

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

dec_shannon, equitability

Examples

```
data(Qesem_s)
shannon(Qesem_s$HU)
```

`shannon_frag` *Shannon diversity decomposition*

Description

Computes Shannon diversity and its decomposition

Usage

```
shannon_frag(x, gx, f, gf)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.
`gx`	Vector of dimension S of factors indicating the group of each species. G groups.
`f`	Vector of dimension G with the number (>0) of fragments in each group
`gf`	Vector of dimension G of factors indicating the groups to which the fragments "f" belong.

Value

- `shannon`: Shannon's total Entropy.
- `within`: Within groups entropy.
- `between`: Between groups entropy.
- `groups`: A data frame with information about each group: relative frequency, internal entropy and number of species.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

shannon

Examples

```
data(Qesem_s)
data(Qesem_f)
shannon_frag(Qesem_s$HU, Qesem_s$Group, Qesem_f$HU, Qesem_f$Group)
```

`simpson_D` *Simpson's dominance index*

Description

Computes Simpson's dominance index.

Usage

```
simpson_D(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Simpson's dominance index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

dominance, simpson_E

Examples

```
data(Qesem_s)
simpson_D(Qesem_s$HU)
```

`simpson_E` *Simpson's evenness index*

Description

Computes Simpson's evenness index.

Usage

```
simpson_E(x)
```

Arguments

`x`	Vector of dimension S (number of species) with the number of individuals observed in each species. NA values are allowed. 0 values are converted to NA.

Value

Simpson's evenness index.

References

"Quantifying Diversity through Entropy Decomposition: Insights into Hominin Occupation and Carcass Processing at Qesem cave"

See Also

evenness, simpson_D

Examples

```
data(Qesem_s)
simpson_E(Qesem_s$HU)
```

Index