

Package: diversityArch (via r-universe)

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Type Package

Title Computes Diversity Indices with Archaeological Data

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all_indices	<i>Diversity indices</i>
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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: Bootstrap 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	<i>Bootstrap estimates of the decomposed Shannon's diversity index with fragments</i>
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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	<i>Decomposition of the equitability index</i>
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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	<i>Evenness index</i>
----------	-----------------------

Description

Modification of Simpson's evenness index to be restricted between 0 and 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	<i>Menhinick index</i>
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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	<i>Data used in the examples</i>
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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 different 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)
```

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