Package 'biomonitoR'

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Type Package

Title calculates indices for biomonitoring of running waters.

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Description A package to calculate indices for biomonitoring of running water with a focus on macroinvertebrate community.

Depends hunspell

License GPL-2

LazyLoad Yes

Encoding UTF-8

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GithubRef master

GithubSHA1 b41643a1f4b7188d459618663ab671e942336692

R topics documented:

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aggregatoR   *aggregatoR*

Description

This function prepares data for further calculations.

Usage

```
aggregatoR(z)
```

Arguments

x   results of function asBiomonitoR

See Also

[asBiomonitor](#)

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
```

---

asBiomonitor   *asBiomonitor*

Description

This function merge the user dataframe with the reference database. Options to improve or replace the reference database are provided.

Usage

```
asBiomonitor(x, dfref = NULL, overwrite = F)
```

Arguments

x	a data.frame as specified in details
overwrite	if set to T replace the reference database with the one provided by the user
dref	allow the user to improve (if overwrite = F) or to replace (if overwrite = T) the reference database

Details

data.frame must have a column called "Taxa" where put species, genus or family names. See data(macro_ex) for an example dataset.

asBiomonitor check the correctness of taxa names in the data.frame provided by the user. If names are correct the function will process the data.frame to a biomonitor object, otherwise it provide suggestion for correct names. If dfref = T a custom dictionary will be save in the working directory.

See Also

[rename](#)

Examples

```
data(macro_ex)
asBiomonitor(macro_ex)
```

---

aspt	*aspt*

Description

This function calculates the Average Score Per Taxon following Armitage et al. (1983), Davy-Bowker et al. (2007) and Alba-Tercedor & Sanchez-Ortega (1988) formulations.

Usage

```
aspt(d, method = "a")
```

Arguments

method	the formulation of BMWP needed to calculate ASPT. Possible choises are "a" (Armitage et al. 1983), "b" (Davy-Bowker et al. 2007) and i (Alba-Tercedor & Sanchez Ortega, 1988)
x	results of function aggregatoR

References

ALBA-TERCEDOR, J. & A. SÁNCHEZ-ORTEGA. 1988. Un método rápido y simple para evaluar la calidad biológica de las aguas corrientes basado en el de Hellawell (1978). Limnetica, 4: 51-56.

Armitage, P. D., Moss, D., Wright, J. F., & Furse, M. T. (1983). The performance of a new biological water quality score system based on macroinvertebrates over a wide range of unpolluted running-water sites. Water research, 17(3), 333-347.

Davy-Bowker J., Clarke R., Corbin T., Vincent H, Pretty J., Hawczak A., Blackburn J., Murphy J., Jones I., 2008. River Invertebrate Classification Tool. Final report. WFD72C. SNIFFER. 276 pp

See Also

aggregatoR

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
aspt(data.agR)
```

---

bmwp	*bmwp*

Description

Functions for calculating BMWP and ASPT

Usage

```
bmwp(d, method = "a")
```

Arguments

method	a,b or i. See details.
x	results of function aggregatoR

See Also

aggregatoR

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
bmwp(data.agR)
```

---

ept	*ept*

Description

This function calculates the number of Ephemeroptera, Plecotera and Trichoptera (ept) taxa.

Usage

```
ept(x, taxLev = "Family")
```

Arguments

x	results of function aggregatoR
taxLev	the taxonomic level for calculating EPT richness.

Details

The parameter taxLev can be "Species", "Genus", "Family" or "Order".

See Also

aggregatoR

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
ept(data.agR)
```

---

eptd	*eptd*

Description

This function calculates the log10(Sel_EPTD + 1) metric.

Usage

```
eptd(x)
```

Arguments

x	results of function aggregatoR

Details

log10(Sel_EPTD + 1) the base-10 logarithm of the abundance of the selected EPTD families plus 1.

See Also

[aggregatoR](#)

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
eptd(data.agR)
```

---

gold   *gold*

Description

This function calculates the 1 - GOLD metric.

Usage

```
gold(x)
```

Arguments

x   results of function aggregatoR

See Also

[aggregatoR](#)

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
gold(data.agR)
```

---

macro_ex *Ephemeroptera toy example*

Description

A toy axample to illustrate the biomonitoR package use diamonds.

Usage

```
macro_ex
```

Format

A data frame with 4 rows and 3 variables:

Taxa name of ephemeroptera taxa

ST1 abundance in site 1

ST2 abundance in site 2

---

quickRename *quickRename*

Description

This function allow the user to change the wron taxa names.

Usage

```
quickRename(x, write.table = F)
```

Arguments

x   a data.frame as specified in details

Details

data.frame must have a column called "Taxa" where put species, genus or family names. See data(macro_ex) for an example dataset.
The function rename will suggest correct name and allow the user to insert a name (Enter taxon name).

See Also

asBiomonitor

Examples

```
data(macro_ex)
macro_ex.mod <- quickRename(macro_ex)
```

---

shannon   *shannon*

Description

Functions for calculating shannon, simpson, margalef and menhinick indexes.

Usage

```
shannon(x, base = 2, taxLev = "Family")
```

Arguments

x	results of function aggregatoR
base	the base of the logarithm
taxaLev	taxonimc level on which the calculation has to be made.

See Also

[aggregatoR](#)

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
shannon(data.agR)
```

---

speNumb   *speNumb*

Description

Functions for calculating species, genus, family and order Richness and abundance

Usage

```
speNumb(x)
```

Arguments

x	results of function aggregatoR

Details

By now only species, genus and family richness calculation are reliable. This is because order assignment for order in the reference database is not completely covered. Unassigned taxon are exluded from the calculations.

See Also

aggregatoR

Examples

```
data(macro_ex)
data.bio <- asBiomonitor(macro_ex)
data.agR <- aggregatoR(data.bio)
genNumb(data.agR)
```

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