Package 'metrix'

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Type Package

Title Water Quality Metrics Calculator

Version 1.0.0

Description Calculate different metrics
based on aquatic macroinvertebrate density data (individuals per
square meter) to assess water quality (Prat N et al. (2009) <`http:`
`//www.ub.edu/riosandes/docs/MacroIndLatinAmcompag0908.pdf`>).

License GPL (>= 3)

Depends R (>= 3.5.0)

Imports Matrix, stringr, utils, vegan

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LazyData true

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Suggests spelling, testthat (>= 3.0.0)

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Author Juan Manuel Cabrera [aut, cre],
Julieta Capeleti [aut]

Maintainer Juan Manuel Cabrera <juanmanuelcabrera1@gmail.com>

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biotic_ind	*Biotic indexes*

Description

Calculates BMWP, BMWP', BMWP", IMRP and ICBrio indexes

Usage

```
biotic_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

The biotic indicators consist of the combination of two or three properties of the association: taxa richness and tolerance/intolerance to contamination for qualitative indices, and these together with abundance (absolute or relative) for quantitative indices. They are usually expressed in the form of a single numerical value that synthesizes the characteristics of all the species present.

Value

This function returns a list with the following components:

Bioind_n	The numerical values of the biotic indexes.
Bioind_c	The water quality class assign to each sample site according to the numerical value of the biotic indexes

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Armitage PD, Moss D, Wright JF & Furse MT (1983) doi: 10.1016/00431354(83)901884>
- Alba-Tercedor J & Sánchez-Ortega A (1988) <https://www.limnetica.com/documentos/limnetica/limnetica-4-1-p-51.pdf>
- Loyola RGN (2000) <https://www.iat.pr.gov.br/sites/agua-terra/arquivos_restritos/files/documento/2021-03/bioindicadores_qualidade_aguas_2001_2002.pdf>
- Rodrigues Capítulo A (1999) < https://www.biotaxa.org/RSEA/article/view/32771>
- Kuhlmann M, Imbimbo HV, Ogura LL (2012) <https://cetesb.sp.gov.br/aguas-interiores/wp-content/uploads/sites/12/2013/11/protocolo-biomonitoramento-2012.pdf>

See Also

read_data, bmwp_ind, bmwp_p_ind, bmwp_p_p_ind, imrp_ind, icbrio_ind

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run biotic_ind with that example_data
biotic<-biotic_ind(example_data)

#Check results
biotic$Bioind_n
biotic$Bioind_c
```

---

bmwp_ind *BMWP and ASPT index*

Description

Calculate Biological Monitoring Working Party (BMWP) and Average Score Per Taxon (ASPT) indexes.

Usage

```
bmwp_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

The Biological Monitoring Working Party (BMWP) was set up in 1976. Its terms of reference were to recommend a system which could be used to assess the biological status of a river, and which would be suitable for presenting a broad picture of one aspect of the biological condition of rivers in the UK. Identification to family is sufficient to calculate the BMWP score. The average score per taxon (ASPT) is calculated by dividing the score by the total number of scoring taxa (Armitage et al. 1983).

Value

This function returns a list with the following components:

Ibmwp_n	The numerical BMWP and ASPT index (Armitage et al. 1983).
Ibmwp_c	The BMWP and ASPT water quality class (Armitage et al. 1983).

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Armitage PD, Moss D, Wright JF & Furse MT (1983) doi: 10.1016/00431354(83)901884>

See Also

read_data, bmwp_p_ind, bmwp_p_p_ind, biotic_ind

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run bmwp_ind with that example_data
bmwp<-bmwp_ind(example_data)

#Check results
bmwp$Ibmwp_n
bmwp$Ibmwp_c
```

---

bmwp_p_ind	*BMWP prime index*

Description

Calculate Biological Monitoring Working Party (BMWP) prime index.

Usage

```
bmwp_p_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

The BMWP' is an adaptation of the BMWP (Armitage et al. 1983) created to evaluate the biological quality of the Iberian Peninsula. Most of the macroinvertebrate families living in the Iberian Peninsula have been added to the original index and some of the scores have been changed (Alba Tercedor & Sánchez Ortega 1988).

Value

This function returns a list with the following components:

Ibmwp_p_n	The numerical BMWP' index (Alba Tercedor and Sánchez Ortega 1988).
Ibmwp_p_c	The BMWP' index water quality classes (Alba Tercedor and Sánchez Ortega 1988).

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Armitage PD, Moss D, Wright JF & Furse MT (1983) doi: 10.1016/00431354(83)901884>
- Alba-Tercedor J & Sánchez-Ortega A (1988) <https://www.limnetica.com/documentos/limnetica/limnetica-4-1-p-51.pdf>

See Also

read_data, bmwp_ind, bmwp_p_p_ind, biotic_ind

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run bmwp_p_ind with that example_data
bmwpp<-bmwp_p_ind(example_data)

#Check results
```

```
bmwpp$Ibmwp_p_n
bmwpp$Ibmwp_p_c
```

---

bmwp_p_p_ind   *BMWP prime prime index*

Description

Calculate Biological Monitoring Working Party (BMWP) prime prime index (Loyola, 2000)

Usage

```
bmwp_p_p_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from read_data.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

The new BMWP" is an adaptation of the BMWP (Armitage et al. 1983) for the lotic environments of the Paraná River. This adaptation was based on the observation of the occurrence of the important families in the rivers in the region. Some families were added by ecological equivalence and others by similarity in the level of tolerance to contamination. The scores assigned to the different families were not changed (Loyola, 2000).

Value

This function returns a list with the following components:

Ibmwp_p_p_n	The numerical BMWP" index (Loyola, 2000).
Ibmwp_p_p_c	The BMWP" water quality classes (Loyola, 2000).

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Armitage PD, Moss D, Wright JF & Furse MT (1983) doi: 10.1016/00431354(83)901884>
- Loyola RGN (2000) <https://www.iat.pr.gov.br/sites/agua-terra/arquivos_restritos/files/documento/2021-03/bioindicadores_qualidade_aguas_2001_2002.pdf>

See Also

[read_data](#), [bmwp_ind](#), [bmwp_p_ind](#), [biotic_ind](#)

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run bmwp_p_p_ind with that example_data
bmwpp<-bmwp_p_p_ind(example_data)

#Check results
bmwpp$Ibmwp_p_p_n
bmwpp$Ibmwp_p_p_c
```

---

comp_metrix   *Complete metrix analysis*

Description

This function performs all the calculations availables in metrix package.

Usage

```
comp_metrix(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from read_data.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Value

This function returns a list with the following components:

Bioind_n	The numerical values of the biotic indexes.
Bioind_c	The water quality class assign to each sample site according to the numerical value of the biotic index.
d_diver	A data.frame with all the calculated density measures.
Icbrio_n	The numerical ICBrio index.
Icbrio_c	The ICBrio water quality class.
Indrel	A data.frame with all the calculated tolerance measures.
Perdiver	A data.frame with all the calculated composition measures.
Pred	A data.frame with all the calculated trophic measures.
Richdiver	A data.frame with all the calculated richness measures.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

See Also

read_data, biotic_ind, densi_diver, icbrio_ind, indrel_diver, per_diver, pred_ind, rich_diver

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run comp_metrix with that example_data
complete<-comp_metrix(example_data)

#Check results
complete$Bioind_n
complete$Bioind_c
complete$d_diver
complete$Icb_n
complete$Icb_c
complete$Indrel
complete$Perdiver
complete$Pred
complete$Richdiver
```

---

densi_diver   *Density measures*

Description

Calculates density measures

Usage

```
densi_diver(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

Density is a universal measure used in all types of biological studies. Density is best classified with trophic measurements because it is an element of production; however, it is difficult to interpret because it requires careful quantification and is not monotonous in response (i.e., density can decrease or increase in response to contamination) (Barbour et al., 1996).

Value

This function returns a data.frame with all the calculated density measures:

den_chir_dip	Diptera Chironomidae density.
den_non_chir_dip	
	Diptera no Chironomidae density.
den_ephe	Ephemeroptera density.
den_molus	Mollusca density.
den_gastr	Gastropoda densityv.
den_biv	Bivalvia density.
den_crus	Crustacea density.
den_nais	Naididae density.
den_lhoff	*Limnodrilus* hoffmeisteri density.
den_bothr	*Bothrioneurum* density.
den_tubi	*Tubifex* density.
den_dero	*Dero* density.
den_prist	*Pristina* density.
den_chiro	*Chironomus* density.
den_nais	*Nais* density.
den_hele	*Heleobia* density.
den_subchiro	*Chironominae* density.
den_suborth	Orthocladiinae density.
den_subtany	Tanypodinae density.
den_t	Total density.
den_t_bothr	*Bothrioneurum*/Total density.
den_t_lhoff	*Limnodrilus hoffmeisteri*/Total density.
den_t_tubi	*Tubifex*/Total density.
den_t_dero	*Dero*/Total density.
den_t_prist	*Pristina*/Total density.
den_t_chiro	*Chironomus*/Total density.
den_oli	Oligochaeta density.
den_tricho	Trichoptera density.
den_ostr	Ostracoda density.

den_amph	Amphipoda density.
den_polym	Polymitarcidae density.
den_hyal	Hyalella density.
den_coch	Cochliopidae density.
den_chironomidae	
	Chironomidae density.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Barbour MT, Gerritsen J, Griffith GE, Frydenborg R, McCarron E, White JS & Bastian ML (1996) doi: [10.2307/1467948>](10.2307/1467948>)

See Also

read_data

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run densi_diver with that example_data
dendiver<-densi_diver(example_data)

#Check results
dendiver
```

---

example_data	*Example data for metrix package.*

Description

A dataset containing entries from to sites.

Usage

```
example_data
```

Format

The data is properly formated for being used with metrix functions

---

icbrio_ind *ICBrio index*

Description

Calculate ICBrio index

Usage

```
icbrio_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from read_data.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

ICBrio was created to monitor the quality of inland waters in the state of São Paulo. It is a multimetric index that includes different metrics: richness, Shannon-Wiener diversity index (H'), Sequential Comparison index (ICS), Tanytarsini/Chironomidae ratio, richness of sensitive taxa and dominance of tolerant groups. Only one of the diversity indices (H' or ICS) is considered to calculate it (in this case, the function H' from 'vegan' package). The final value, which generates the diagnosis or classification of habitat quality, combines the arithmetic mean of the value obtained with the sum of the points of each metric.

Value

This function returns a list with the following components:

Icbrio_n	The numerical ICBrio index (Kuhlmann et al. 2012).
Icbrio_c	The ICBrio water quality class (Kuhlmann et al. 2012).

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Kuhlmann M, Imbimbo HV, Ogura LL (2012) <https://cetesb.sp.gov.br/aguas-interiores/wp-content/uploads/sites/12/2013/11/protocolo-biomonitoramento-2012.pdf>

See Also

read_data, biotic_ind

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run icbrio_ind with that example_data
icb<-icbrio_ind(example_data)

#Check results
icb$Icbrio_n
icb$Icbrio_c
```

---

imrp_ind   *IMRP index*

Description

Calculates the Indice de Macroinvertebrados en Rios Pampeanos Index

Usage

```
imrp_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from read_data.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

IMRP was created for the rivers of the Pampean plain (Rodrigues Capítulo 1999). This index is based on the sum of ecological values for each taxon. This value is inversely proportional to the degree of tolerance to contamination, varying from 0.1 for highly tolerant taxa to 2.0 for the most sensitive. Identification to family is sufficient to calculate the IMRP score.

Value

This function returns a list with the following components:

Imrp_n	The numerical IMRP index (Rodrigues Capítulo 1999).
Imrp_c	The IMRP index water quality class (Rodrigues Capítulo 1999).

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Rodrigues Capítulo A (1999) < https://www.biotaxa.org/RSEA/article/view/32771>

See Also

[read_data](), [biotic_ind]()

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run imrp_ind with that example_data
imrp<-imrp_ind(example_data)

#Check results
imrp$Imrp_n
imrp$Imrp_c
```

---

indrel_diver	*Tolerance measures*

Description

Indicate sensitivity of the assemblage and component species to various types of perturbation.

Usage

```
indrel_diver(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

Most of the metrics applied in the study of macroinvertebrates use as a key factor the tolerance or intolerance of the different taxa to a certain disturbance, normally organic contamination. The relationship between the number of organisms that are tolerant and intolerant to contamination is a common resource in the metrics used. Further metrics (multimetric indexes) can be derived from a combination of these primary metrics (Prat et al., 2009). The Limnodrilus hoffmeisteri/total density ratio, which was developed by Marchese & Ezcurra de Drago (1999), increases in environments with organic contamination.

Value

This function returns a data.frame with all the calculated tolerance measures.:

r_oligochir	Oligochaeta/Chironomidae.
r_oligoset	Oligochaeta with setaform chaetae/Oligochaeta without setaform chaetae.
r_tanychir	Tanytarsini/Chironomidae.
den_t_lhoff	*Limnodrilus hoffmeisteri*/Total density.
den_t_bothr	*Bothrioneurum*/Total density.
den_t_tubi	*Tubifex*/Total density.
den_t_dero	*Dero*/Total density.
den_t_prist	*Pristina*/Total density.
den_t_chiro	*Chironomus*/Total density.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Marchese M & Ezcurra de Drago I (1999) <https://agro.icm.edu.pl/agro/element/bwmeta1.element.agro-article-e981d07b-e469-4460-a7fe-3239650cd089>

- Prat N, Ríos B, Acosta R & Rieradevall M (2009) <http://www.ub.edu/riosandes/docs/MacroIndLatinAmcompag0908.p

See Also

[read_data](#)

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run indrel_diver with that example_data
indreld<-indrel_diver(example_data)

#Check results
indreld
```

---

metrix_table_template *Metrix data template*

Description

Metrix compatible table format template creation

Usage

```
metrix_table_template(store = FALSE)
```

Arguments

store   A logical value indicating if the user want to store the results in a file.#'

Details

This function creates a properly formatted table for being used with metrix functions.
The format of the input table must contain 8 columns that refer to the scientific and functional classification of the taxa. The first 7 columns refer to Class, Order, Family, Subfamily, Tribe, Genus and Species. Special care must be taken when entering the taxa nomenclature, because if it is misspelled, the package will not take this classification into account. It is not necessary to put genera and species in italics. Column 8 refers to the functional group of the taxa, which can be filtering collectors (FC), gathering collectors (GC), predators (P), scrapers (SCR) and shredders (SHR). After these columns, the places where you want to calculate the packet metrics are entered. It is essential that the site data are located after these taxonomic and functional classification columns. The user will be able to load the table with the amount of taxa and sites, as desired.
If store = TRUE the function will create a .csv file with properly named columns and saves it as template.csv on the current working directory.

Value

The function returns:

template_table A table that can be used as input for other metrix functions.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

---

per_diver   *Composition measures*

Description

Calculates the relative abundance of particular taxa in the assemblage in percentage terms.

Usage

```
per_diver(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

Provides information on the makeup of the assemblage and the relative contribution of the populations to the total fauna (Barbour et al., 1996).

Value

This function returns a data.frame with all the calculated composition measures:

per_ephe	% Ephemeroptera.
per_molus	% Mollusca.
per_gastr	%Gastropoda.
per_biv	%Bivalvia.
per_crus	%Crustacea.
per_oli	% Oligochaeta.
per_amph	% Amphipoda.
per_ostr	% Ostracoda.
per_ephetricho	% Ephemeroptera + Trichoptera.
per_naid	% Naididae.
per_chir_dip	% Diptera Chironomidae.
per_non_chir_dip	
	%Diptera no Chironomidae.
per_polym	%Polymitarcidae.
per_hyal	%Hyalella.
per_coch	%Cochliopidae.

per_tricho	%Trichoptera.
per_subchiro	%Chironominae.
per_suborth	%Orthocladiinae.
per_subtany	%Tanypodinae.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Barbour MT, Gerritsen J, Griffith GE, Frydenborg R, McCarron E, White JS & Bastian ML (1996) doi: 10.2307/1467948>

See Also

read_data

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run per_diver with that example_data
perdiver<-per_diver(example_data)

#Check results
perdiver
```

---

pred_ind	*Trophic measures*

Description

Calculates trophic measures

Usage

```
pred_ind(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from read_data.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

Trophic metrics are surrogates of complex processes such as trophic interaction, production and food source availability. Specialized feeders, such as scrapers, piercers, and shredders, are the more sensitive, and are thought to be well represented in healthy streams. Generalists, such as collectors and filterers, have a broader range of acceptable food materials than specialists, and are thus more tolerant to pollution that might alter availability of certain food (Barbour et al., 1996).

Value

This function returns a data.frame with all the calculated trophic measures:

per_pred	% Predator.
per_filt	% Filtering collector.
per_shred	% Shredders.
per_scrap	% Scrapers.
per_gath	% Gathering collector.
n_pred	N° of Predator.
n_filt	N° of Filtering collector.
n_shred	N° of Shredders.
n_scrap	N° of Scrapers.
n_gath	N° of Gathering collector.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Barbour MT, Gerritsen J, Griffith GE, Frydenborg R, McCarron E, White JS & Bastian ML (1996) doi: 10.2307/1467948>

See Also

read_data

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run pred_ind with that example_data
pred<-pred_ind(example_data)

#Check results
pred
```

---

read_data   *Read taxon data*

Description

Load data from a formatted taxon table

Usage

```
read_data(file_name, correct = TRUE, verbose = FALSE)
```

Arguments

file_name	Name of formatted taxon table file. Use metrix_table_template to create a new formatted table file.
correct	A logical value indicating if the auto correct system should be used (default correct = TRUE).
verbose	A logical value indicating indicating if progress messages should be given.

Details

This function reads a formatted taxon .csv file and checks whether it is properly formatted. This function will determine which character to use as separator for data and decimals.

The format of the input table must contain 8 columns that refer to the scientific and functional classification of the taxa. The first 7 columns refer to Class, Order, Family, Subfamily, Tribe, Genus and Species. Special care must be taken when entering the taxa nomenclature, because if it is misspelled, the package will not take this classification into account. It is not necessary to put genera and species in italics. Column 8 refers to the functional group of the taxa, which can be filtering collectors (FC), gathering collectors (GC), predators (P), scrapers (SCR) and shredders (SHR). After these columns, the places where you want to calculate the packet metrics are entered. It is essential that the site data are located after these taxonomic and functional classification columns. The user will be able to load the table with the amount of taxa and sites, as desired.

This function also has an autocorrect system that compares the words used to describe a taxon with a list of properly written words in order to find possible input errors. If correct = TRUE the autocorrect system will check all the names and perform corrections when possible (the file will not be modified). The autocorrect system will inform the user if it finds an issue that needs a manual check.

Value

The function returns:

dataset	A table that can be used as input for other metrix functions.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

---

rich_diver   *Richness measures*

Description

Calculates trophic measures

Usage

```
rich_diver(dataset, store = FALSE, dec_c = ".", verbose = FALSE)
```

Arguments

dataset	A data.frame obtained from `read_data`.
store	A logical value indicating if the user want to store the results in a file.
dec_c	A character used for decimal separator on results file.
verbose	A logical value indicating indicating if progress messages should be given.

Details

The richness measures reflect the diversity of the aquatic complex (Resh et al. 1995). Increased diversity correlates with increased assemblage health and suggests that niche space, habitat, and food source are adequate to support the survival and spread of many taxa. The number of taxa measures the general variety of the macroinvertebrate assemblage. Identities of major taxonomic groups are not derived from the total taxa metric, but the removal of taxa from naturally diverse systems can be detected easily (Barbour et al., 1996).

Value

This function returns a data.frame with all the calculated richness measures:

n_taxa	N° total taxa.
n_fam	N° of families.
n_gen	N° of genus.
n_insec_fam	N° of insects families.
n_non_insec_order	
	N° of orders of invertebrates no insects.
n_dip_fam	N° of Diptera families.
n_dip_gen	N° of Diptera genus.
n_dip_chir_gen	N° of Diptera Chironomidae genus.
n_chir_tax	N° of Diptera Chironomidae taxa.
n_tany_tax	N° of Tanytarisni taxa.
n_stemp_tax	N° of Stempellina taxa.

`n_non_chir_dip_tax`	
	N° of Diptera no Chironomidae taxa.
`n_mol_tax`	N° of Mollusca taxa.
`n_gastr_tax`	N° of Gastropoda taxa.
`n_biv_tax`	N° of Bivalvia taxa.
`n_crus_tax`	N° of Crustacea taxa.
`n_crusmol`	N° of Crustacea + Mollusca taxa.
`n_oligo_tax`	N° of Oligochaeta taxa.
`n_ephetrich`	N° of Ephemeroptera + Trichoptera taxa.

Author(s)

Juan Manuel Cabrera and Julieta Capeleti.

References

- Resh VH, Norris RH & Barbour MT (1995) doi: [10.1111/j.14429993.1995.tb00525.x>](10.1111/j.14429993.1995.tb00525.x)
- Barbour MT, Gerritsen J, Griffith GE, Frydenborg R, McCarron E, White JS & Bastian ML (1996) doi: [10.2307/1467948>](10.2307/1467948)

See Also

read_data

Examples

```
#Example data is a properly formatted table with richness measures of two sites
example_data

#Run rich_diver with that example_data
richd<-rich_diver(example_data)

#Check results
richd
```

Index