

Package ‘rspear’

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Type Package

Title Calculate SPEARpesticide in R (<http://www.systemecology.eu/SPEAR/index.php>)

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Description Calculate SPEARpesticide in R (<http://www.systemecology.eu/SPEAR/index.php>)

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Collate 'match_traits.R' 'get_traits.R' 'spear.R' 'rspear-package.R'

Imports plyr (>= 1.0)

Suggests testthat, reshape2

NeedsCompilation no

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rspear-package

Calculate SPEAR in R

Description

Calculate SPEAR in R

Author(s)

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get_traits

Get Trait-data for SPEAR

Description

Download trait-data from SPEAR (<http://www.systemecology.eu/spear/spear-calculator/>).

Usage

```
get_traits(check = TRUE)
```

Arguments

check logical; should the database be checked if up-to-date?

Details

In order to minimize traffic on server trait-data is saved locally. `get_traits()` downloads the trait-data from server to a file 'traits.csv' in the working directory.

If the file already exists in the working directory a check is performed if the file is up-to-date with the database.

Value

a data.frame with the trait-database.

Note

Normally, `get_traits()` is not called separately and is the default in `spear()`. Therefore the trait-table is downloaded once into the workspace and checked if up-to-date with the web-server when `spear()` is used.

'check' should be set to FALSE if working offline (since the check require an internet connection)

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See Also

[spear](#)

match_traits	<i>Match data with Trait-Database</i>
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Description

Match data with Trait-Database

Usage

```
match_traits(x, y, takex, takey)
```

Arguments

x	abundance-data
y	trait-table
takex	character string: taxa column-name
takey	character string: trait-table taxa column-name

Value

a lookuptable, with original and matched data, as well as a match-value

spear	<i>Calculate SPEAR values</i>
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Description

Calculate SPEAR values

Usage

```
spear(x, taxa = NULL, abundance = NULL, group = NULL,
      region = "Eurasia", traits = NULL, sensitivity = -0.36,
      generationTime = 0.5, exposed = 1, migration = 0, ...)
```

Arguments

x	data.frame; data.frame with abundances in the long format.
taxa	character; name of column in x, which holds the taxon-names.
abundance	character string: columnname of abundances
group	character-vector; names of columns for groupings.
region	character; default is set to 'Eurasia', which covers trait-data for Finland, United Kingdom, West Siberia and Central Europe. 'Finland', 'United Kingdom', 'West Siberia' are also allowed and traits may vary between different regions.
traits	NULL or data.frame; If 'NULL' (default) then it is checked if there is a file 'traits.csv' in the working directory and if this file is up-to-date with the database, see get_traits . If there is no such file, it is downloaded from the web-server. If it is a data.frame, this is used as trait-data (after checking if appropriate).
sensitivity	numeric; sensitivity-threshold, default '-0.36'
generationTime	numeric; Generation Time threshold, default '0.5'
exposed	logical; either '1' (exposed) or '0' (not exposed), default '1'
migration	logical; either '1' (migration) '0' (no migration), default '0'
...	additional arguments passed to get_traits . Currently only 'check' is available. By default the file is checked if up-to-date. See get_traits .

Details

The SPEAR index is based on binary classification of species (or other taxonomic categories) into 'species at risk' and 'species not at risk' according to the following biological traits:

- physiological sensitivity to organic toxicant
- generation time
- presence of aquatic stages in water during the maximum pesticide usage period
- migration abilities.

A taxon is classified as a 'SPEcies At Risk' only if it has: (i) Sorganic value > -0.36 , (ii) generation time ≥ 0.5 year, aquatic stages (eggs, larvae, pupae) during the periods of intensive pesticide usage, and (iv) low migration abilities.

The SPEARpesticides index is computed as relative abundance of these taxa for each site and date as follows:

$$SPEAR = \sum \log_{10}(x[i] + 1) * y / \sum \log_{10}(x[i] + 1)$$

where x[i] is the abundance of the taxon i and y is 1 if taxon i is classified as 'at risk', otherwise 0.

For further details about SPEARpesticides see References.

Value

A list of two data.frames:

spear	data.frame; SPEAR-values for every combination of the grouping variables.
traits	a data.frame with the following columns: region, exposed, generationTime, sensitivity, migration species traits used to classify species into SPEAR.
SPEAR	Classification of species into SPEAR.
taxa_data	taxon names as in x.
taxa_matched	matched taxon-names in traits-database.
match_val	goodnes of match. '-1' indicates a direct match, 'NA' indicates a failed match. Values between 0 and 0.5 indicate an approximate match (smaller values - better match).

Note

Threshold-values for classification into SPEAR should only be changed if there is strong indication that they are different than these defaults!

Author(s)

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References

Liess M, Von der Ohe P, 2005. Analyzing effects of pesticides on invertebrate communities in streams. *Environmental Toxicology and Chemistry*, 24, 954-965.

Liess M, Schaefer R, Schriever C, 2008. The footprint of pesticide stress in communities - species traits reveal community effects of toxicants. *Science of the Total Environment*, 406, 484-490.

See Also

[get_traits](#)

Examples

```
require(rspear)
data(spear_example)
head(spear_example)
sp <- spear(spear_example ,
  taxa = "Taxon",
  abundance = "Abundance",
  group = c("Year", "Site"),
  check = FALSE)
sp$traits
sp$spear
```

spear_example

Fictitious Example data for rspear

Description

Abundance data in the long format

Details

Example data

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