

# rspear: Calculate SPEAR in R

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## 1 Theoretical background

For theoretical background please refer to:

- Liess M, von der Ohe PC 2005. Analyzing effects of pesticides on invertebrate communities in streams. Environmental Toxicology and Chemistry. 24, (4):954-965.

For more information please visit:

- <http://www.systemecology.eu/spear/spear-system/>

## 2 Install rspear

rspear can be installed from CRAN:

```
install.packages("rspear")
```

rspear is developed at github. If you want to install the latest development version from github use:

```
install.packages("devtools")
require(devtools)
install_github("rspear", "EDiLD")
require(rspear)
```

```
## Loading required package: rspear
```

## 3 Functions in rspear

### 3.1 spear()

#### 3.1.1 Description

The main function in the rspear-package is spear():

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

It takes the following 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; name of column in x, which holds the 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. If there is no such file, it is downloaded from the web-server. Or a trait-table as returned by spear().

**sensitivity, generationTime, exposed, migration** Threshold values for classification into SPEAR. These values should only be changed if there is strong indication that they are different than these defaults! A species is classified to SPEAR if all criteria are met:

- sensitivity  $\geq -0.36$
- generationTime  $\geq 0.5$
- exposed == 1
- migration == 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()`.

Generally the defaults are appropriate and one must only specify **x, taxa, abundance and group**.

### 3.1.2 `get_traits()`, Trait-database

In order to minimize traffic on server trait-data is saved locally in the **working directory** (ensure that it has been set correctly).

This is done in `spear()`, via the internal function `get_traits()`:

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

`spear()` checks if there is file 'traits.csv' in the working directory and otherwise downloads the trait-data from the web-server <http://www.systemecology.eu/spear/spear-calculator/> to a file 'traits.csv' into the working directory.

If this file already exists, it is checked if this file is up-to-date with the web-server.

`get_traits()` takes one argument 'check' which disables checking when 'FALSE'. Check must be disabled when working offline. Check can be passed directly in `spear()`, as in most of the examples here.

### 3.1.3 Matching taxon names with trait-database

`spear()` matches the taxon-names with the trait table using direct and approximate string matching. It is very likely that the matches are not always 100% (direct) (for example spelling errors, see example in section 'Usage of rspear'). `spear()` then tries to find the species with nearest match (approximate match). However this approximate match must not always be appropriate! When there are non-direct matches a warning is printed and the user is called to check the match:

```
Warning message:
Non-direct taxon matches!
Check trait table if match is appropriate!!

If spear cannot find an appropriate match in the trait table, the SPEAR-value
for this species is set to '0' and a warning printed:

Warning message:
There were unmatched species:
xxxxxxxxxx
Set SPEAR to 0
```

### 3.1.4 Output

`spear()` returns a list of two elements ('spear' and 'traits'):

**spear** a data.frame with the 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** goodness 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)

## 4 Usage of rspear

The usage of the rspear-package is explained on fictitious example data. The example data is shipped with the package:

```
data(spear_example)
head(spear_example)

##           Taxon Abundance Year           Site
## 1          Baetis           1 2007 Sample Point A
## 2 Baetis rhodani           1 2007 Sample Point A
## 3 Baetis rodani           1 2007 Sample Point A
## 4          xxxxxxxxx           1 2007 Sample Point A
## 5          Baetis sp.           1 2007 Sample Point A
## 6    Athericidae           2 2007 Sample Point A
```

Description of the data-set:

**Taxon** The taxon names. There are spelling errors in the taxon names (*'Baetis rodani'*), Baetis is listed as *'Baetis sp.'* and *'Baetis'* and there is weird species named *'xxxxxxx'*.

**Abundance** Abundances

**Year** There is data from different year, so this is a grouping variable (we want SPEAR-values per year)

**Site** Data has been sampled at four sites, so this is also a group-variable

## 4.1 Data requirements

Like the web application rspear requires data in the long format (see `spear_example` from above). Ecologists often organized their data in wide format (eg. species x samples matrix). This data must be transformed into the long-format, eg using the `melt()` function from the `reshape2` package.

For example if we have a columns for every species (wide-format):

```
## Loading required package: reshape2
```

```
df_wide
```

		Site	Year	Athericidae	Baetis	Baetis fuscatus	Baetis rhodani
##	1	Sample Point A	2007	2	1	15	1
##	2	Sample Point A	2008	15	0	0	0
##	3	Sample Point B	2007	0	0	0	0
##	4	Sample Point B	2008	0	0	0	0
##	5	Sample Point C	2007	4	0	3	0
##	6	Sample Point C	2008	0	0	0	0
##	7	Sample Point D	2007	0	0	0	0
##	8	Sample Point D	2008	5	0	0	0

We can transform it to the long format using `melt` from the `reshape2`-package:

```
require(reshape2)
df_long <- melt(df_wide, id = c("Site", "Year"))
head(df_long)
```

		Site	Year	variable	value
##	1	Sample Point A	2007	Athericidae	2
##	2	Sample Point A	2008	Athericidae	15
##	3	Sample Point B	2007	Athericidae	0
##	4	Sample Point B	2008	Athericidae	0
##	5	Sample Point C	2007	Athericidae	4
##	6	Sample Point C	2008	Athericidae	0

## 4.2 Calculation of SPEAR

When we have the data in the long-format we can use `spear()` to calculate the spear values. First argument is our data in the long format (`spear_example`), then we must specify the columns coding for taxon-names, abundances and grouping variables:

```
sp <- spear(spear_example, taxa = "Taxon", abundance = "Abundance", group = c("Year",
  "Site"))
```

Column names can be entered as characters or (less error-prone) using `names()`:

```
names(spear_example)

## [1] "Taxon"      "Abundance" "Year"      "Site"

sp <- spear(spear_example, taxa = names(spear_example)[1], abundance = names(spear_example)
  group = names(spear_example)[3:4], check = FALSE)

## Error: no lines available in input
```

Here we can take advantage of the defaults:

**region = "Eurasia"** subsummarises Finland, UK , West Siberia and Central Europe

**traits = NULL** Will check if we have a local file of the trait-data and otherwise download it.

However we are warned, that there have been approximate matches and even no matches with the trait-table:

Warning messages:

```
1: In spear(spear_example, taxa = names(spear_example)[1],
:
  There were unmatched species:
xxxxxxx
Set SPEAR to 0.
2: In spear(spear_example, taxa = names(spear_example)[1],
:
  Non-direct taxon matches!
Check trait table if match is appropriate!!
```

We can check the matches looking at the trait-table returned by `spear()`:

```
head(sp$traits)

## Error: object 'sp' not found
```

Looking at `match_val` we see that there has been no match (`match_val == NA`) for taxon 'xxxxxxx' and 'Baetis rodani' has been matched approximately (`match_val = 0.1`) with 'Baetis rhodani'. All other taxa have been matched directly (`match_val = -1`). The SPEAR-value for 'xxxxxxx' has been set to '0'. We could check and clean our input data, but the matches are appropriate in this case.

Now let's take a look at the SPEAR-values:

```
sp$spear
## Error: object 'sp' not found
```

`spear()` return the result in a data.frame which can be directly used for further analysis (plotting, hypothesis testing, etc):

```
spear_df <- sp$spear
## Error: object 'sp' not found
plot(SPEAR ~ factor(Year), data = spear_df)
## Error: object 'spear_df' not found
```

### 4.3 Modifying trait-values

To modify trait-values we can use the trait-table returned by `spear()`:

First we make a copy of the returned trait-table and then we can modify this table.

For example we set that *Baetis rhodani* is exposed to pesticides:

```
traits_modi <- sp$traits
## Error: object 'sp' not found
traits_modi[traits_modi$taxa_matched %in% "Baetis rhodani", "exposed"] <- c(1,
  1)
## Error: object 'traits_modi' not found
head(traits_modi)
## Error: object 'traits_modi' not found
```

Note that when selecting *Baetis rhodani* from the trait-table, we have to change two values, because of the spelling error in the data.

This modified trait-table can then be supplied to the 'traits'-Argument of `spear()`:

```
sp_modi <- spear(spear_example, taxa = names(spear_example)[1], abundance = names(spear_example)[2],
  group = names(spear_example)[3:4], traits = traits_modi, check = FALSE)

## Error: object 'traits_modi' not found

head(sp_modi$spear)

## Error: object 'sp_modi' not found

head(sp_modi$traits)

## Error: object 'sp_modi' not found
```

Note that the SPEAR-values have changed, since *Baetis rhodani* is now classified as Species At Risk.

## 4.4 Modifying SPEAR-values

*This is currently not supported.*

However it can be done indirectly by modifying the trait-values (see previous section, most easily migration)

# 5 Miscellaneous

## 5.1 Citation

```
citation("rspear")

##
## To cite rspear in publications, please use:
##
## Liess M, Von der Ohe P, 2005. Analyzing effects of pesticides on
## invertebrate communities in streams. Environmental Toxicology
## and Chemistry, 24, 954-965.
##
## A BibTeX entry for LaTeX users is
##
## @Article{,
##   author = {{Liess} and {Matthias} and Von der Ohe and {Peter}},
##   title = { Analyzing effects of pesticides on invertebrate communities in streams},
##   journal = {Environmental Toxicology and Chemistry},
##   year = {2005},
```



```
##      number = {24},  
##      pages = {954--965},  
##    }
```

## 5.2 Problems

rspear is developed in github.

Any problems/bugs/feature-request may be reported at github or to the author (Eduard Szöcs, szoe8822@uni-landau.de) directly.