rspear: Calculate SPEAR in R

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Contents

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 is currently under development and not available on CRAN yet. To use rspear you have to install it from github:

```
> install.packages("devtools")
> require(devtools)
> install_github("rspear", "EDiLD")
> require(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 > -0.36
- generationTime >= 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 be 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 the right one! 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:
xxxxxxxxx
 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 *'xxxxxxxxx'*.

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):

```
> 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)[2],
+             group = names(spear_example)[3:4],
+             check = FALSE)
```

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:
xxxxxxxxx
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)
```

```
        taxa_data   taxa_matched match_val   region exposed generationTime
18      xxxxxxxxx           <NA>        NA     <NA>      NA             NA
17  Baetis rodani Baetis rhodani       0.1  Eurasia       0        0.50000
1          Baetis         Baetis      -1.0  Eurasia       1        0.64564
2  Baetis rhodani Baetis rhodani      -1.0  Eurasia       0        0.50000
3      Baetis sp.     Baetis sp.      -1.0  Eurasia       1        0.50000
4     Athericidae    Athericidae      -1.0  Eurasia       1        0.68750
   sensitivity migration SPEAR
18          NA        NA     0
17     0.02159         0     0
1      0.02159         0     1
2      0.02159         0     0
3      0.02159         0     1
4     -0.35000         0     1
```

Looking at match_val we see that there has been no match (match_val == NA) for taxon 'xxxxxxxxx' 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 'xxxxxxxx' has been set to '0'. We could check and clean our input data, but the matches are appropriate in this case.

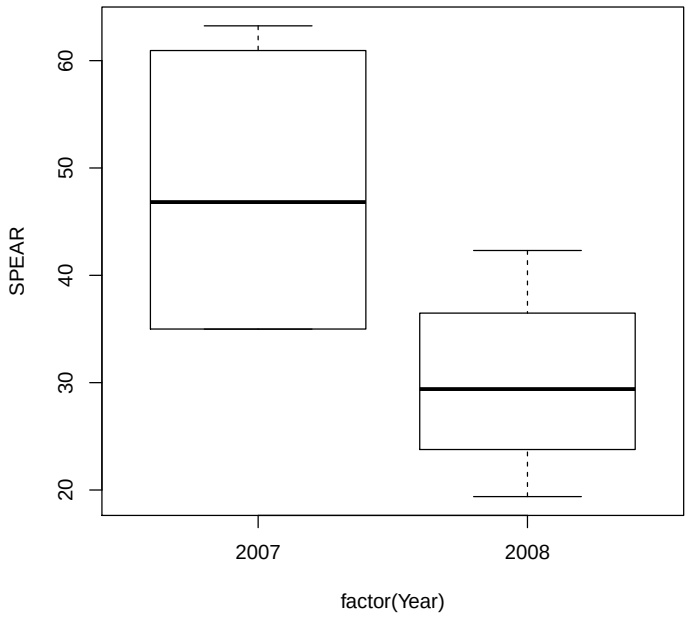
Now let's take a look at the SPEAR-values:

```
> sp$spear
```

```
  Year           Site    SPEAR
1 2007 Sample Point A 35.00612
2 2007 Sample Point B 63.24266
3 2007 Sample Point C 34.98550
4 2007 Sample Point D 58.64163
5 2008 Sample Point A 42.31371
6 2008 Sample Point B 19.38471
7 2008 Sample Point C 28.15862
8 2008 Sample Point D 30.64599
```

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

```
> spear_df <- sp$spear
> plot(SPEAR ~ factor(Year), data = spear_df)
```



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$traits
> traits_modi[traits_modi$taxa_matched %in% "Baetis rhodani", "exposed"] <- c(1,1)
> head(traits_modi)
```

```
        taxa_data   taxa_matched match_val   region exposed generationTime
18      xxxxxxxxx           <NA>        NA     <NA>      NA             NA
17  Baetis rodani Baetis rhodani       0.1  Eurasia       1        0.50000
1          Baetis         Baetis      -1.0  Eurasia       1        0.64564
2  Baetis rhodani Baetis rhodani      -1.0  Eurasia       1        0.50000
3      Baetis sp.     Baetis sp.      -1.0  Eurasia       1        0.50000
4     Athericidae    Athericidae      -1.0  Eurasia       1        0.68750
   sensitivity migration SPEAR
18          NA        NA     0
17     0.02159         0     0
1      0.02159         0     1
```

```
2      0.02159         0     0
3      0.02159         0     1
4     -0.35000         0     1
```

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)
> head(sp_modi$spear)

  Year           Site    SPEAR
1 2007 Sample Point A 43.16134
2 2007 Sample Point B 63.24266
3 2007 Sample Point C 34.98550
4 2007 Sample Point D 58.64163
5 2008 Sample Point A 42.31371
6 2008 Sample Point B 19.38471

> head(sp_modi$traits)

        taxa_data   taxa_matched match_val   region exposed generationTime
18      xxxxxxxxx           <NA>        NA     <NA>      NA             NA
17  Baetis rodani Baetis rhodani       0.1  Eurasia       1        0.50000
1          Baetis         Baetis      -1.0  Eurasia       1        0.64564
2  Baetis rhodani Baetis rhodani      -1.0  Eurasia       1        0.50000
3      Baetis sp.     Baetis sp.      -1.0  Eurasia       1        0.50000
4     Athericidae    Athericidae      -1.0  Eurasia       1        0.68750
   sensitivity migration SPEAR
18          NA        NA     0
17     0.02159         0     1
1      0.02159         0     1
2      0.02159         0     1
3      0.02159         0     1
4     -0.35000         0     1
```

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

4.4 Modifying SPEAR-values

TODO