

# rspear: Calculate SPEAR in R

Eduard Szoecs

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## 1 Theoretical background

## 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 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)
> str(spear_example)

'data.frame':      43 obs. of  4 variables:
 $ Taxon      : chr  "Baetis" "Baetis rhodani" "Baetis rodani" "xxxxxxxxx" ...
 $ Abundance: int   1 1 1 1 1 2 1 15 16 20 ...
 $ Year       : int   2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
 $ Site       : chr   "Sample Point A" "Sample Point A" "Sample Point A" "Sample Point A" ...
```

### 3.1 Data requirements

Like the web application rspear requires data in the long format (see `spear_example`). 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.

### 3.2 Calculating SPEAR-values

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

```
> traitdb <- "/home/edisz/Documents/Uni/Projects/rspear/data/traits.csv"
> sp <- spear(spear_example ,
+           taxa = "Taxon", group = c("Year", "Site"), abundance = "Abundance",
+           region = "Eurasia",
+           traits=traitdb)
```

`spear()` takes as first argument the `data.frame` with the abundances. Then we must specify the columns coding the taxon-names, the abundances and grouping variables. This can be done either by entering the names manually or with `names()` (the second option is less error-prone):

```
> sp <- spear(spear_example ,
+           taxa = names(spear_example)[1], group = names(spear_example)[3:4],
+           abundance = names(spear_example)[2],
+           region = "Eurasia",
+           traits=traitdb)
```

After specifying the columns,