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# Analysis of species attributes (e.g. traits or species indicator values)

## Community weighted mean (CWM)

Theory **R functions** Examples Exercise 

### library (weimea)

The package `weimea` (community weighted mean approach, Zelený 2018) is R package (currently in beta release) focused on relating community-level species attributes (traits, indicator values) to sample attribute (environmental variables). Current distribution is on GitHub (<https://github.com/zdealveindy/weimea>; see the installation instructions below - these are different for Windows and Mac OS).

- `cwm`
- `test_cwm`
- `test_fourth`
- `envfit_cwm`

### Windows

Windows binary (for R 3.6.2): [weimea\\_0.1.18.zip](#)

To directly install `weimea` in R for Windows, use the following:


```
download.file  
( 'https://anadat-r.davidzeleny.net/lib/exe/fetch.php/en:data:weimea_0.1.14.zip', 'weimea.zip' )  
install.packages (paste (getwd (), 'weimea.zip', sep = '/'), repos = NULL,  
type = 'win.binary')
```

If you get the error message that `RcppArmadillo` is missing, install it first by `install.packages ("RcppArmadillo")`.

Alternatively, you can install the package directly from GitHub. For this, make sure you have the latest version of `Rtools.exe`, compatible with your R version, installed on your computer and added to your program path, and that you installed the latest version of the package `devtools`.

```
devtools::install_github ('zdealveindy/weimea')
```

## MacOS

MacOS binary: [weimea\\_0.1.4.tar.gz](#) (thanks to Will Ou for compiling!) 

You may need to install gfortran binary (follow instructions [here](#))

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