

***enviMass* installation guide**

enviMass is a software package to be run in the R statistical environment. Since it is continuously developed and debugged, it is not yet made available as a somewhat static package from the R package repository. Instead, the latest version of *enviMass* is freely available from its development repository at *GitHub*: <https://github.com/blosloos/enviMass>. Thus, for downloading, installing and running *enviMass*, do the following (Windows, full administrator rights (!), internet access):

(1) Have the latest version of the *R statistical environment* installed on your computer: <http://cran.rstudio.com/> -> Download R for Windows -> base -> ...

(2) Install the latest version of *Google Chrome* (or *Firefox*) and set it as default browser.

(3) Install *Rtools*: <http://cran.r-project.org/bin/windows/Rtools/>. During the *Rtools* installation, make sure to check “edit system PATH” (this will enable your computer to access *Rtools* from R).

(4) Open R by clicking on its icon - the *R Console* pops up. Therein, type&enter the following:

```
> install.packages("devtools")
```

Choose any mirror you like. This installs the *devtools* package. Together with the above *Rtools*, it will download, compile¹ and install (a) *enviMass* from its *GitHub* repository and (b) all the packages *enviMass* depends on from the R packages library:

(5) Again, in the R console type&enter:

```
> library(devtools)
```

```
> install_github("blosloos/enviMass",dependencies=TRUE)
```

enviMass and all its dependency packages are thereby installed locally into the R library folder (again, freely choose a mirror for these dependencies).

(6) Now, the *enviMass* user interface (UI) should be available. Simply, in the *R console* type&enter:

```
> library(enviMass)
```

```
> webMass()
```

Repeat step **(5)** whenever you want to update *enviMass*, after running

```
> update.packages(ask=FALSE)
```

in your freshly opened R console; this will also retrieve the latest versions of all dependencies.

¹ Here, compilation means that the human-readable source code of the raw package is converted into executable=machine-readable binary code, which is platform-dependent. The *GitHub* repository only stores the *enviMass* source code.

In the unlikely case that you have received a compiled `enviMass.zip` package from us, the installation of both *Rtools* and the *devtools* package is not required. Instead, do the following after the above steps **(1)** and **(2)** (again, with internet access):

(3) Install the dependency packages of *enviMass*. In the *R console*, type&enter:

```
> install.packages(c("enviPick", "enviPat", "nontarget", "nontargetData", "shiny",  
"shinyBS", "shinyFiles", "shinyRGL"))
```

(4) Navigate to “Packages” from the *R Console* menu and proceed via “Install Package from locale .zip-file ” and navigate to the `enviMass.zip`-file which you received.

Continue with the above step **(6)**.