

## ***enviMass* installation guide**

*enviMass* is a software package to be run in the R statistical environment. Its latest development version is freely available from the GitHub repository: [https://github.com/blosloos/enviMass\\_devel](https://github.com/blosloos/enviMass_devel). For downloading, installing and running *enviMass* from GitHub 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, compile<sup>1</sup> and install (a) the development version of *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_devel")
```

*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.

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<sup>1</sup> 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)**.