

# isoMS software installation protocol

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## Introduction

isoMS software provided as an R-package. To be able to use it you need to have up-to-date R installed on your computer (R-project).

## Installing the isoMS package

- open R or R-studio window
- execute commands

```
install.packages(c("tidyverse", "devtools", "parallel", "DT", "rmarkdown"))
source("https://bioconductor.org/biocLite.R")
biocLite(mzR)
devtools::install_github("hadley/multidplyr")
devtools::install_github("snp/isoms")
```

## Checking the installation

Check the installation by executing `library(isoms)` in R window.