Preface

Here, you can learn how to use `tidyMass` to do the data processing and analysis for the LC-MS metabolomics data. It contains several parts.

If you are new to R or the `tidyverse`

We recommend that you start by learning some basics about R and the tidyverse first, then return here when you feel ready. Here are some resources to start learning:

- Finding Your Way To R, from the RStudio Education team.
- Learn the tidyverse, from the tidyverse team.

Part 1. Install `tidymass`

You can learn how to install `tidymass`, and update it. You can also find here how to download the docker version of `tidymass` and build your own docker image based on `tidymass`.

Part 2. `massdatabase` package and `mass_dataset` class

You can find here how to download the demo data and create `mass_dataset` class by yourself. And how to use `mass_dataset` class organize your omics data and process it.

Part 3. Metabolite annotation

All the metabolite annotation can be found here. You can also learn here how to construct the databases for `metid` using the `massdatabase` package.

Part 4. Whole workflow using `tidymass`

Here, you can learn how to use `tidymass` for data processing and analysis, from data converting to biological function mining.

The code, data and docker image of case study in our manuscript are provided here.