

EMSL Integration Visualization Tutorial

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Software Requirements

Below is a list of software that will be necessary for participation in the hands-on sessions. Please follow the steps below prior to the workshop. Contact me if you have any problems or questions!

1. Download and install R from <http://cran.r-project.org/>
 - a. Click on Mac or Windows
 - b. If Mac, click on R-3.6.1.pkg
 - c. If Windows, click on base, then Download R 3.6.1 for Windows
2. Download and install RStudio from <http://www.rstudio.com/products/rstudio/download>. Select the free version of RStudio Desktop.

R Requirements

Open RStudio, which opens an R session, and paste in the following commands into the Console window, depending on which data type you'd like to focus on during the tutorial. **NOTE: You may need to redo every " when copy/pasting these.**

1. Amplicon Sequencing

```
install.packages("BiocManager")
BiocManager::install("ALDEx2")
BiocManager::install("biomformat")
BiocManager::install("DESeq2")
BiocManager::install("edgeR")
BiocManager::install("pcaMethods")
install.packages("devtools")
devtools::install_github("pmartR/pmartRseq")
```

2. Fourier Transform Mass Spectrometry

```
install.packages("devtools")
devtools::install_github("EMSL-Computing/ftmsRanalysis")
OPTIONAL – devtools::install_github("EMSL-Computing/MetaCycData")
```

3. Proteomics, Metabolomics, and/or Lipidomics (LC-/GC-MS)

```
install.packages("devtools")
devtools::install_github("pmartR/pmartR")
```

Once installed, scripts will be able to utilize the package via loading which occurs each time you execute a given workflow or script. In our case, that environment loads

1. Amplicon Sequencing

```
library(pmartRseq)
```

2. Fourier Transform Mass Spectrometry

```
library(ftmsRanalysis)  
OPTIONAL – library(MetaCycData)
```

3. Proteomics, Metabolomics, and/or Lipidomics (LC-/GC-MS)

```
library(pmartR)
```

These will load the respective package(s) into our environment.

These lines should execute without error. If you encounter an error like

```
> Error in library("ftmsRanalysis") : there is no package called 'ftmsRanalysis'
```

Then that package failed to install and you can retry its installation from above and read the console for any prompts.