## **EMSL Integration Visualization Tutorial**

October 10, 2019

## 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.

- 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 <a href="http://www.rstudio.com/products/rstudio/download">http://www.rstudio.com/products/rstudio/download</a>. 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.** 

a. 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")

b. Fourier Transform Mass Spectrometry

```
install.packages("devtools")
devtools::install github("EMSL-Computing/ftmsRanalysis")
```

c. 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 packages via loading which occurs each time you execute a given workflow or script. In our case, that environment loads

a. Amplicon Sequencing

library(pmartRseq)

b. Fourier Transform Mass Spectrometry

library(ftmsRanalysis)

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

library(pmartR)

These will load the respective package 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.