

May 31st, 2023

EMERGE Webinar: Analysis of Quantitative Mass Spectrometry-based Proteomics Experiments using MSstats and MSstatsTMT

Presenter

Devon Kohler (Northeastern University)

Materials

All materials can be found in the [Google Drive](#) for the presentation:

If you would like to follow the tutorial hands-on during this presentation, please prepare the following:

- 1) A reasonably modern laptop
- 2) All data can be downloaded from the Google Drive [HERE](#)
- 3) [Install MSstatsShiny](#) using the instructions below
 - a) Download R - <https://cran.r-project.org/>. Note R version must be ≥ 4.2
 - i) Note: if on windows you must also install R Tools - <https://cran.r-project.org/bin/windows/Rtools/>
 - ii) Optionally you can also install RStudio Desktop - <https://posit.co/downloads/>
 - b) Run R or RStudio (if downloaded)
 - c) In the console run the installation code below (<https://bioconductor.org/packages/release/bioc/html/MSstatsShiny.html>)
 - d) MSstatsShiny can now be started by running `MSstatsShiny::launch_MSstatsShiny()` in the console

Installation code:

```
if (!require("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")
```

```
BiocManager::install("MSstatsShiny")
```

Example code for MSstats analysis can be found [HERE](#)

Slides

Available soon!