fragmentR *Clostridium difficile* Tutorial 1.0.0

**Running from the command line:**

What you will need:

R version 4 +

One does not need any R experience to run fragmentR! It can be run dirrectly from the command line. All you need is to download the *C. difficile* database and the FSA files from the walk lab website (https://thewalklab.com/tools). We find it is best to create a folder specifically for running fragmentR. Place the “F-RibotypingFiles” in the directory you are running fragmentR from.

Table

Description automatically generated with medium confidence

From the terminal navigate to the directory you plan on running fragmentR from. To download the required packages run the “setup\_fragmentR.R” script from the terminal. This will also create a “Files\_to\_analyze” folder.

On a mac:

Rscript Desktop/Run\_Fragment\_Analysis/setup\_fragmentR.R

On windows:

Desktop/Run\_Fragment\_Analysis/setup\_fragmentR.R

Drag and drop files you wish to match to a ribotyping database into the “Files\_to\_analyze” folder.

On a mac:

Rscript Desktop/Run\_Fragment\_Analysis/Call\_FSA.R

On windows:

Desktop/Run\_Fragment\_Analysis/Call\_FSA.R

The results will populate a folder named “Results YYYY-MM-DD Hour/Min/Sec”. As the script runs it will populate the results folder with jpegs of chromatograms and plots comparing the query and best hits in the database. At the end a SUMMARY.csv table is also produced, summarizing all the files that were in “file\_to\_analyze” folder.