Matrix Merger 1.0 2021-07-08

# What it can do

Specifically in metabolomics data there are several possibilities to combine features.

1. Reads standard format (‘Samples’, ‘Features’, some matrices in an excel file)
2. Selects one numeric matrix
3. Combines features as per user selection
4. Saves Samples, (new) Features and matrix

# Who to combine

1. Adducts: this option is called “Class Fatty Acid” since this is what they all have in common. For adducts, there is a ‘Rt tolerance’: Adducts are only combined if they are within a given tolerance. [when there are more than two adducts, the condition range = max(Rt) – min(Rt) < tol is applied]
2. ‘Class m:n’, for example PC 36:2. No Rt check is performed
3. ‘Class’, for example all PCs

# How to combine

1. Sum
2. Max
3. Median