The DeepMS1 code primarily consists of three steps. It should be run in a folder containing MS2 data, MS1 features, and the corresponding database. Step 1 is executed for data preprocessing, which includes format adjustment and data calibration. Step 2 is carried out for the initial matching with a 15 ppm mass tolerance and training of the linear regression model. Finally, step 3 is performed for protein scoring and FDR filtering to obtain the final results.





