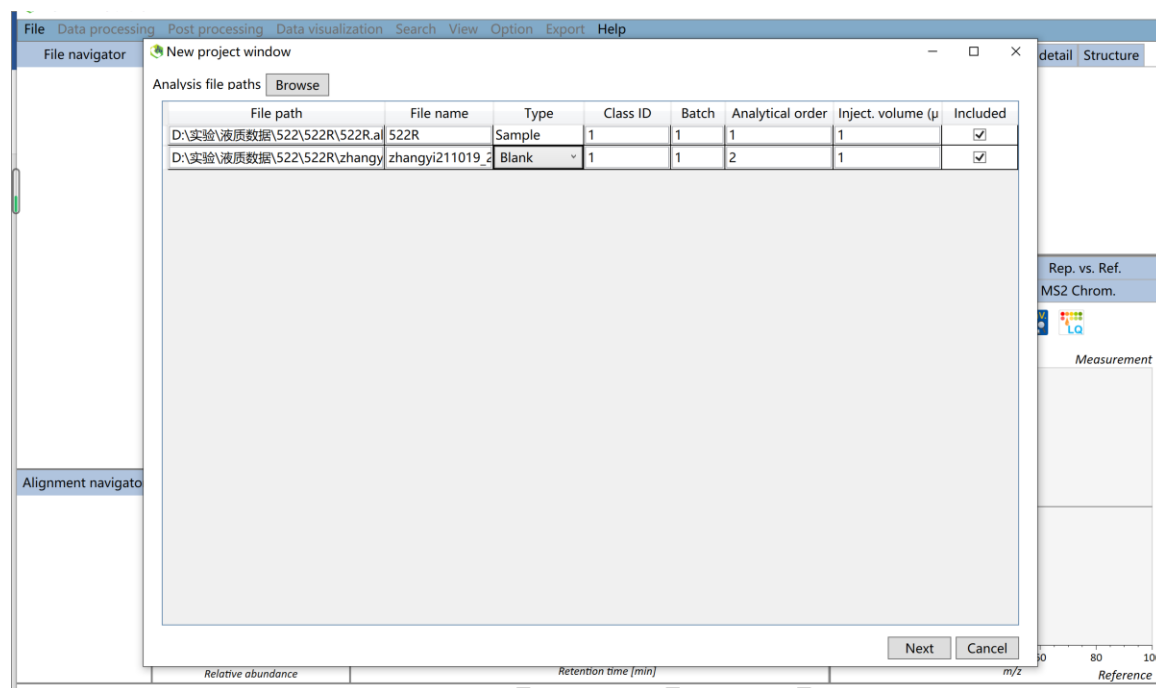
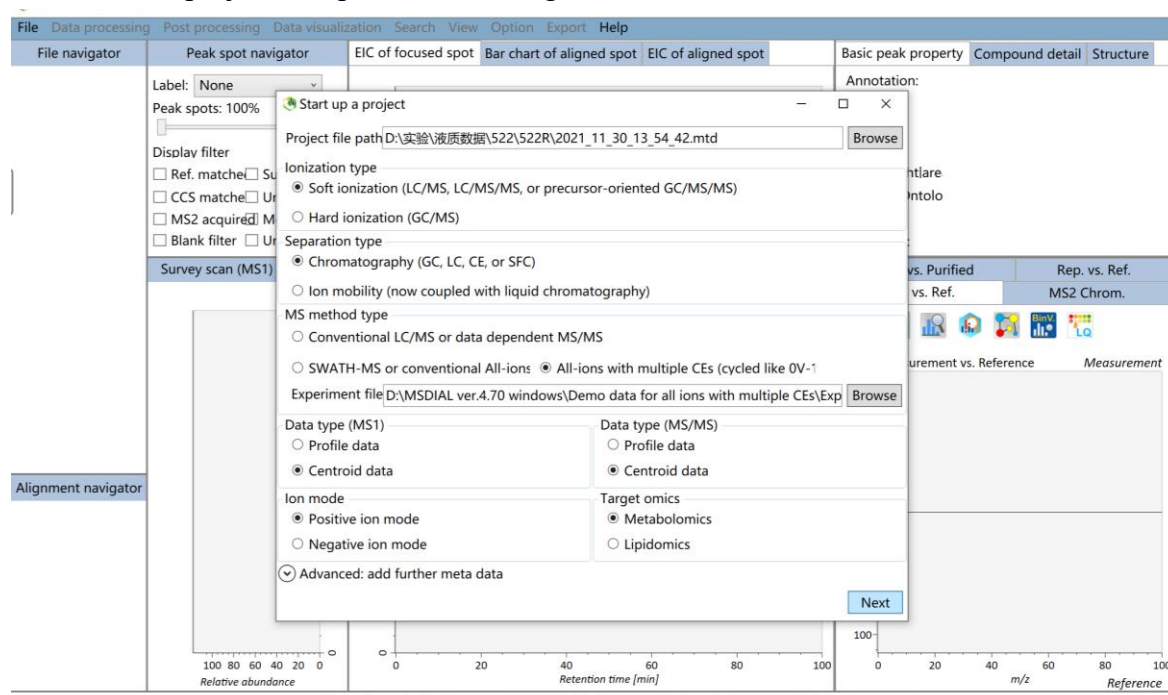
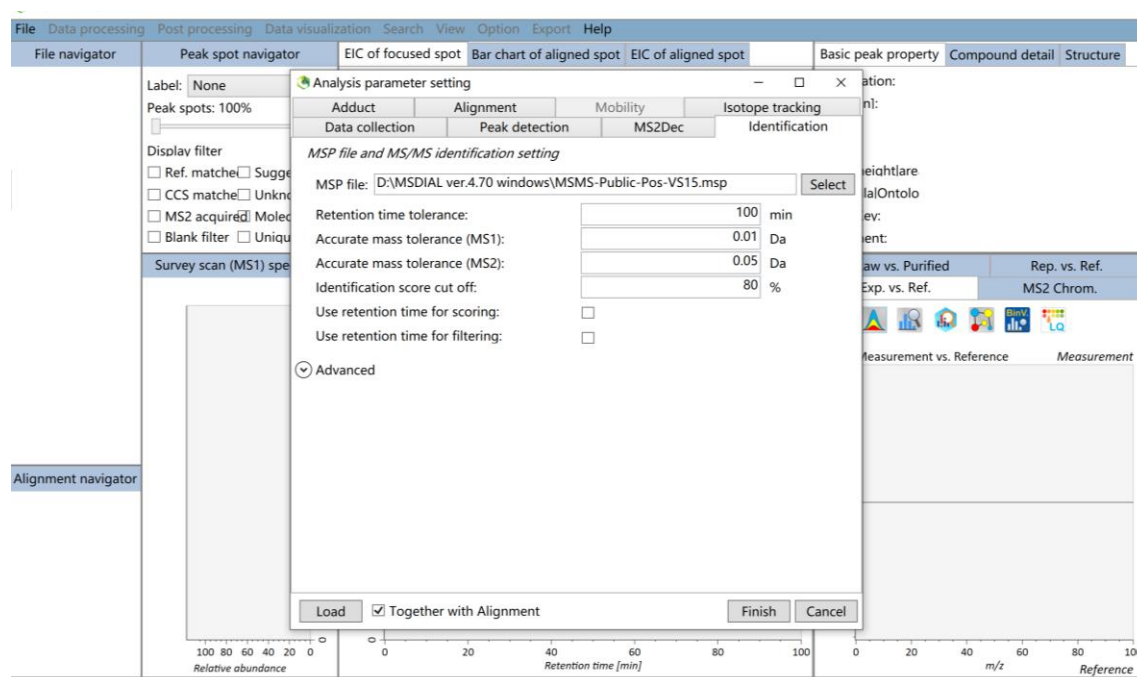


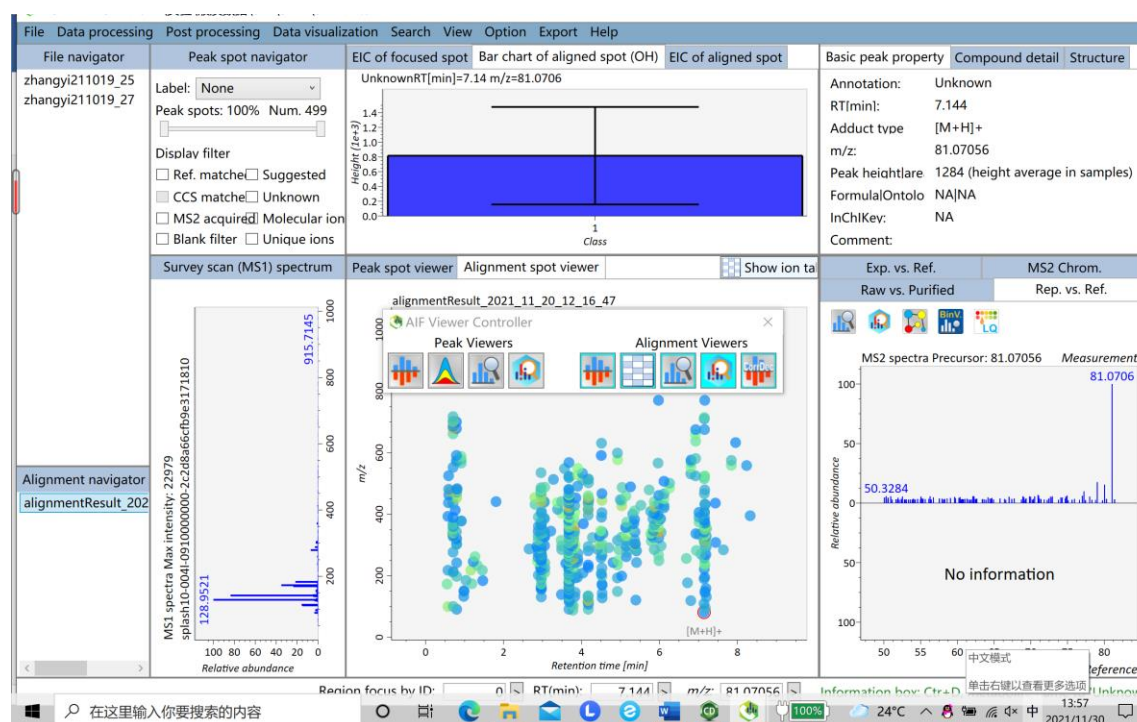
Create a new project, the parameter settings are as follows:



Analysis parameters are all default parameters except database selection.



The results are as follows:



## Export result for GNPS:

The screenshot displays the GNPS software interface during the export of alignment results. The central focus is the 'Alignment result export' dialog box, which is configured to export the data as an 'mgf' file. The dialog includes various options for data matrix types, peak identification, and filtering. The background shows a 'Bar chart of aligned spot (OH)' with a peak at 7.144 minutes and m/z 81.0706. The interface also includes a 'Peak spot navigator' and a 'Survey scan (MS1) spectrum' plot.

## This is the interface for running FBMN:

The screenshot shows the FBMN interface for file selection. The 'Select Input Files' pane on the left displays a hierarchical file structure, including folders like 'lutiantiana' and 'A', and files such as '17M.mgf', '17M.txt', '17 A5R.mgf', '17 A5R.txt', and '17C.mgf'. The 'Selected Files' pane on the right shows a list of selected files, including 'Selected MS2 File MGF/MSP(Progenesis QI)/mzML(MzTab-M)', 'Selected Feature Quantification Table', 'Selected Original mzML Files', 'Selected Sample Metadata Table', 'Selected Library Files', and 'Selected Additional Edges From External Tools'. The 'Selected Library Files' section lists several spectral libraries, including 'CCMS\_SpectralLibraries/GNPS\_Passattuto\_Libraries/decoy\_GNPS-LIBRARY.mgf' and 'CCMS\_SpectralLibraries/GNPS\_Passattuto\_Libraries/decoy\_GNPS-FAULKNERLEGACY.mgf'. The interface also includes buttons for 'Clear Selection' and 'Finish Selection'.

File Selection		
MS2 File MGF/MSP(Progenesis Q1)/mzML(MzTab-M):	Select Input Files	2 files and 0 folders are selected
Feature Quantification Table:	Select Input Files	2 files and 0 folders are selected
Original mzML Files:	Select Input Files	
Google Sheets Metadata URL (Experimental):	None	
Sample Metadata Table:	Select Input Files	

Basic Options		
Quantification Table Source:	MS-DIAL	
Precursor Ion Mass Tolerance:	0.02 Da	
Fragment Ion Mass Tolerance:	0.02 Da	

But it failed.

FEATURE-BASED-MOLECULAR-NETWORKING (version release_28.2)
<b>FAILED</b> <a href="#">[Clone]</a> <a href="#">[Clone to Latest Version]</a> <a href="#">[Restart]</a> <a href="#">[Delete]</a>
<b>MSDIAL</b> Must input exactly 1 spectrum mgf file Tool execution terminates abnormally with exit code [1]
lutiantiana (lutiantiana@163.com)
522R-522M
2021-11-29 22:03:21.0
2 minutes 52 seconds

When I put in a data, it can run successfully. But in this case, how can we compare multiple groups of data?