

mzkit

Data toolkits for processing LC-MS and GC-MS data

[View project on GitHub](#)

Mzkit

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Mzkit is an open source raw data file toolkit for mass spectrometry data analysis, provides by the **BioNovoGene** corporation. The features of mzkit includes: raw data file content viewer(XIC/TIC/Mass spectrum plot/MS-Imaging), build molecule network, formula de-novo search, de-novo annotation of the unknown metabolite features and targeted data quantification.

- [View User Manual PowerPoint](#)
- [View Mzkit Update History](#)

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Credits

This open source mass spectrometry data toolkit is developed at the [BioDeep](#) R&D laboratory and brought to you by [BioNovoGene](#) corporation.



Product Screenshots

BioNovoGene Mzkit [Raw File Viewer]

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News

连导师都不想错过的代谢组学论坛

2020-07-13

本论坛邀请 梁融、Oliver Fiehn、尹慧勇、郭登斌、吕海海、纪剑（排名仅按照会议演讲顺序）6 位国内外知名的代谢组领域科学家作为特邀嘉宾，围绕代谢组学领域进行专题探讨，以推动代谢组学领域的创新和发展。并结合同行组学研究的最新进展，剖析代谢组学整合多组学研究的切入点和在科研中的应用。

天天抽它！百万福利大放送！

2020-05-15

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诺米代谢项目文章荣登Small杂志|多组学联用

2020-05-11

发布日期：2020-05-11

周年庆首份大礼|预存优惠享不停！

2020-04-24

诺米代谢即将迎来公司7周年的生日，为答谢新老客户对诺米代谢的关爱与支持，公司将于5月1日-6月30日开展预存款活动。期间恰逢中国的传统节日

Output

Ready! Use m/z Data Toolkits 67.44 MB

BioNovoGene Mzkit [Raw File Viewer]

文件 Main Tools About Mzkit Data Tools Data Viewer Data Analysis

Imports Save Linear Linear MRM Quantify Ions Ions

Targeted Quantification Library

Start Page x BioNovoGene M/Z Data... Targeted Quantification x

Linear Reference Quantification Result Settings

Linear of Choline

$f = 0.00322 + 5.535e^{-04} \times x$
 $R^2 = 0.99545$

Peak area(AU)

Cti u mol/L

Legend: Predict, Standard Reference, Linear

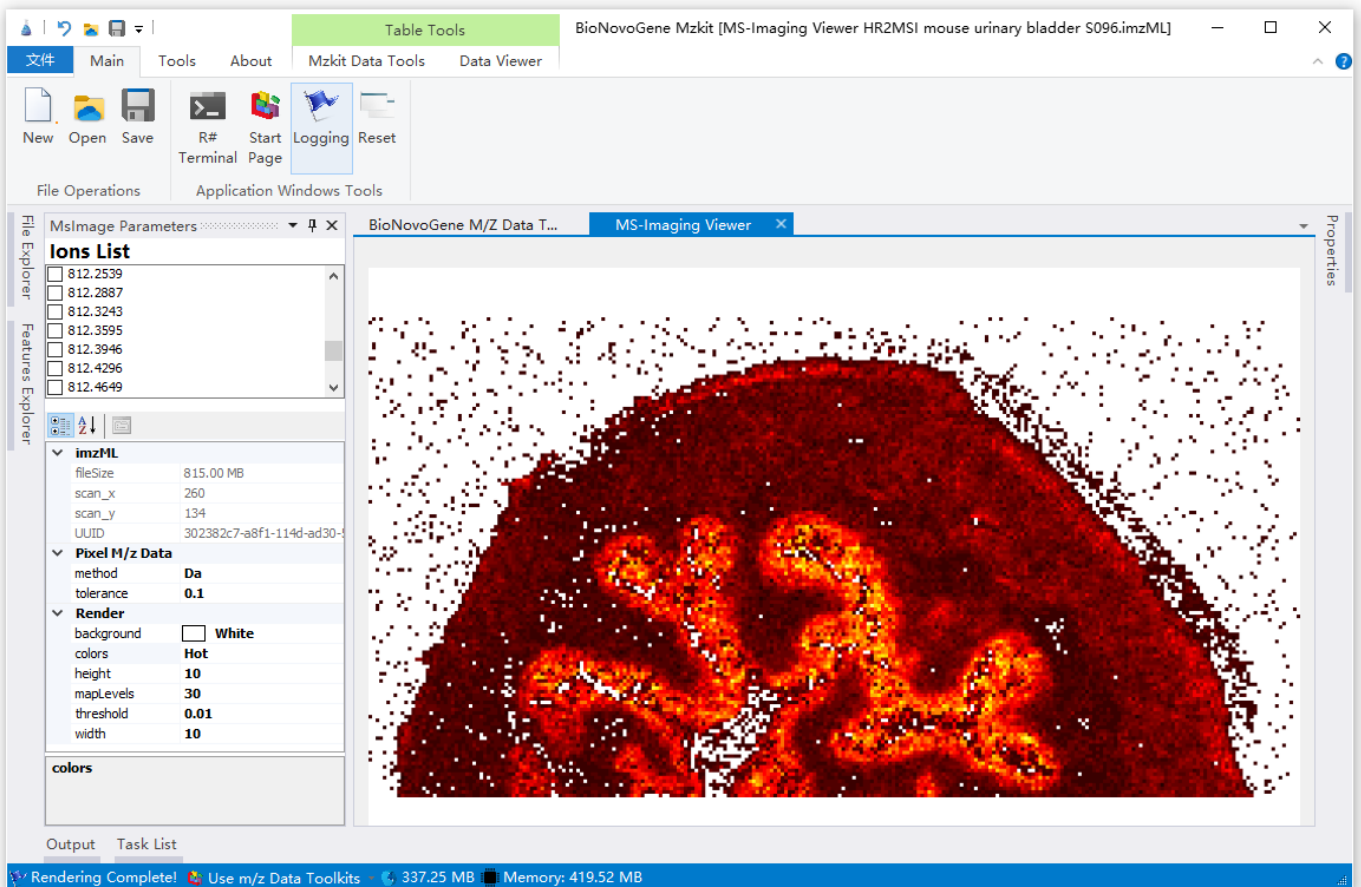
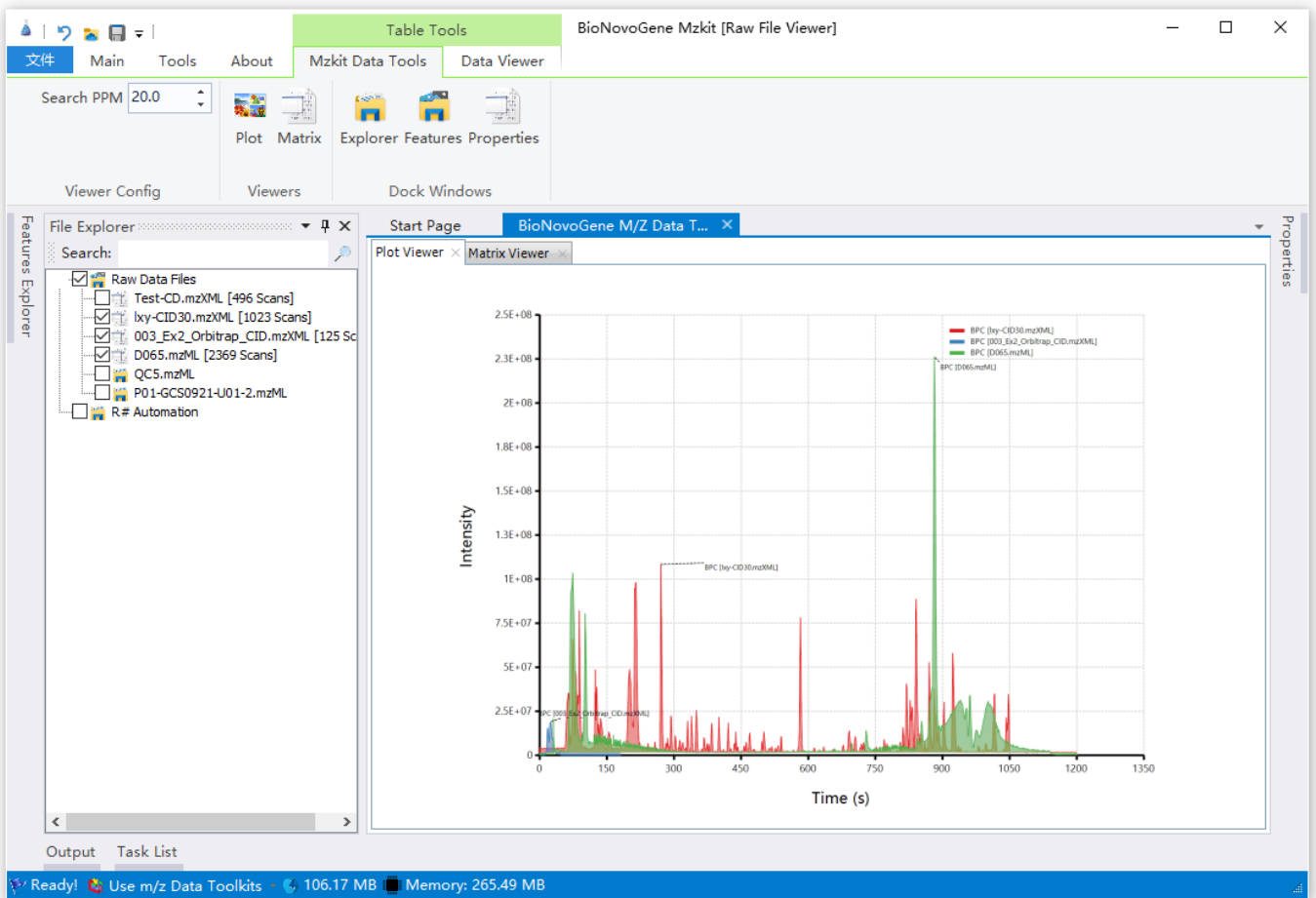
ID	Name	ALS	Alt	clS	Cti	Px	yfit	error	variant	valid	le
Choline	Choli...	368640	7070	1	400	0.0191...	404.6605	4.6605	0.0117	True	L7
Choline	Choli...	380870	16480	1	800	0.0432...	839.883...	39.8831	0.0499	True	L6
Choline	Choli...	379240	27200	1	1600	0.0717...	1353.91...	246.08...	0.1538	True	L5
Choline	Choli...	379110	67210	1	4000	0.1772...	3260.97...	739.02...	0.1848	False	L4
Choline	Choli...	368890	1631...	1	8000	0.4421...	8046.79...	46.7928	0.0058	True	L3
Choline	Choli...	349380	4133...	1	20000	1.1830...	21431.4...	1431.4...	0.0716	True	L2
Choline	Choli...	306730	6882...	1	40000	2.2438...	40595.1...	595.12...	0.0149	True	L1

Select Library Profile: DBS

Features	IS	L1-3	L2-3	L3-3	L4-3	L5-3	L6-3	L7-3
Choline	Choline d9	40000	20000	8000	4000	1600	800	400
Choline d9		0	0	0	0	0	0	0
Betaine	Betaine d9	50000	25000	10000	5000	2000	1000	500
Betaine d9		0	0	0	0	0	0	0
TMAO	TMAO d9	1000	500	200	100	40	20	10

Output Task List

Ready! Use m/z Data Toolkits 106.17 MB Memory: 516.87 MB

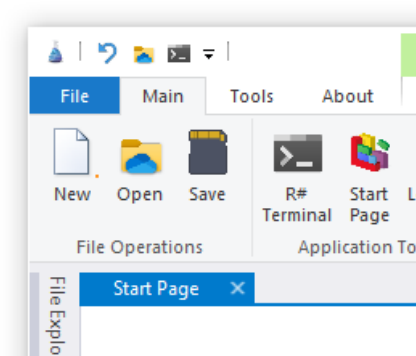


I. Raw Data Viewer Instruction

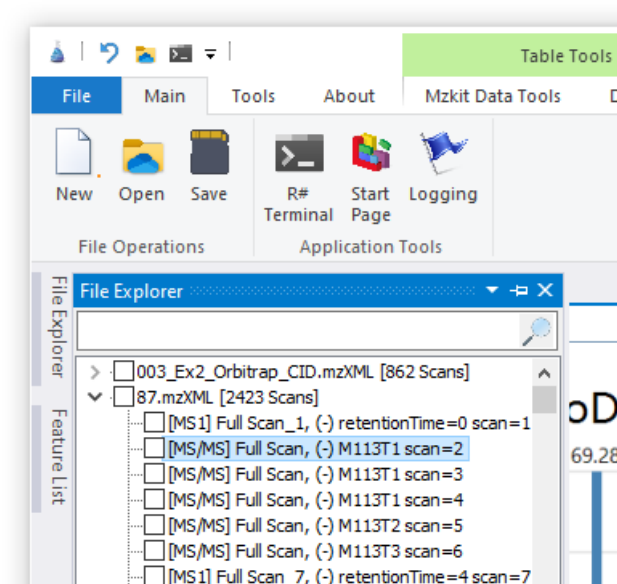
Important Note: this application only supports the open source [mzXML/mzML/imzML](#) raw data file formats. For view the data in the vendor format file like the [Thermo *.Raw](#) required convert to the [mzXML](#) file format at first. It is recommended that convert the vendor format file to [mzXML](#) via [ProteoWizard](#).

1.1. Imports raw data file

For view the file content of the [mzXML](#) or [mzML](#) datafile in [mzkit](#), you must imports the raw data file into the [mzkit](#) at first. Here is how: select the [Main](#) tabpage of [mzkit](#) you will see the [Open](#) command for the raw data imports operation. Then you are going to click this [Open](#) command button, choose the raw data file for imports and wait for it finished.











Then you should see the files that you've imports into [mzkit](#) on the [File Explorer](#) dock panel if there is no error occurs during the raw data file imports progress. Now you can click on the raw data file tree to expend it and click one of the feature in your raw file to view the content data.



1.1.1. Background Task

For improvements of the user experience when you are using the [mzkit](#) application, the raw data files is imports to [mzkit](#) application under a background task. You can see the background task progress throught the [Task List](#) window:

Task List

Task	Content	Start Time	Status	Progress
 Imports Raw Data	D:\B-D10.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D18.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D21.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D12.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D15.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D22.mzXML	10/15/2020 8:10:02 PM	Pending	...
 Imports Raw Data	D:\B-D17.mzXML	10/15/2020 8:10:02 PM	Running...	[MS1] Full Scan_3388, (-) retentionTime=589 scan=1241
 Imports Raw Data	D:\B-D24.mzXML	10/15/2020 8:10:02 PM	Finished	

Output

Ready! Use m/z Data Toolkits 12.15 MB Memory: 304.63 MB

1.2. Search Feature

the search bar on the top of the file tree is the **m/z** search input: you can input a specific **m/z** value or **formula** expression in the search bar for search the matched features in your raw data file. This operation is usually apply for the **xic** data search.

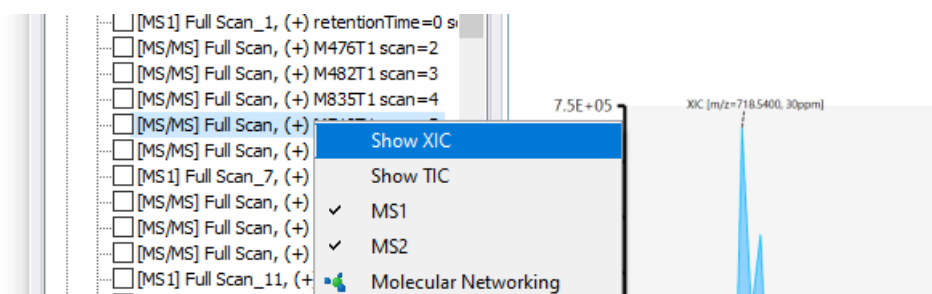
When you have click on the search button, then all of the **m/z** feature in your raw data file that match the **ppm** condition will be listed in the **Feature List** dock panel:

BioNovoGene M/Z Data Toolkit									
Feature Search Result									
Raw Data File/Feature	#Features	M/z	rt	PPM	Polarity	Charge	BPC	TIC	
003_Ex2_Orbitrap_CID.mzXML	59								
21.mzXML	0								
37.mzXML	0								
38.mzXML	0								
86.mzXML	0								
87.mzXML	0								
B-D10.mzXML	0								
B-D12.mzXML	0								
B-D13.mzXML	0								
B-D15.mzXML	0								
B-D16.mzXML	0								
B-D17.mzXML	0								
B-D18.mzXML	0								
B-D20.mzXML	0								
B-D21.mzXML	0								
B-D22.mzXML	0								
B-D24.mzXML	0								
P-2.mzXML	0								

An example of search m/z 834.6 with tolerance error 30ppm. the result in the **Feature List** is usually used for create a XCI plot.

1.3. XIC plot

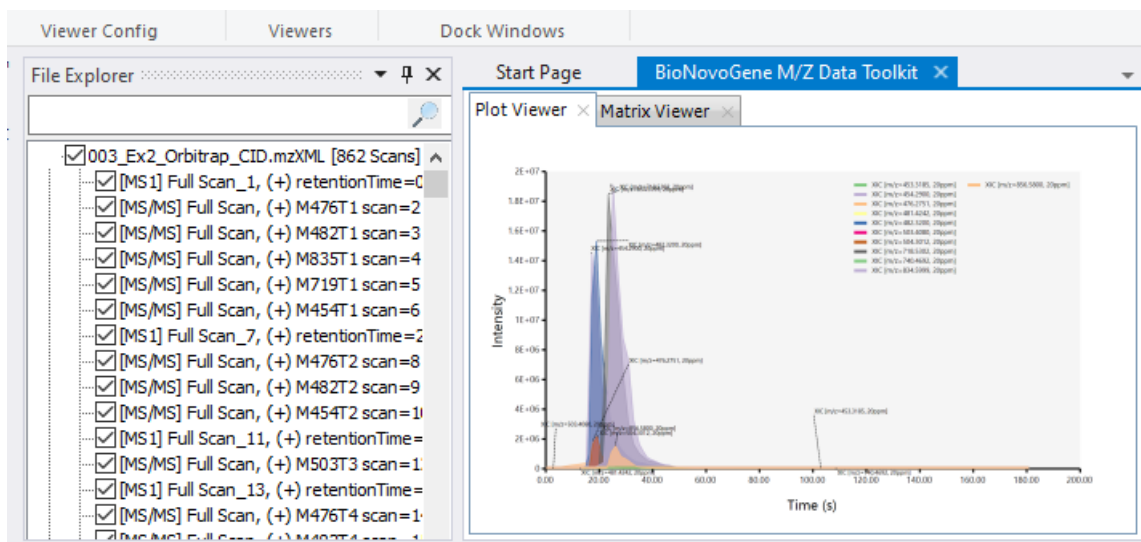
Expend the file content tree in the **File Explorer**, and then mouse right click on one MS2 feature in your file, select **xic** for create a XIC plot for a specific ion feature:



The XIC plot is a kind of time-signal chromatography plot of a specific m/z ion.

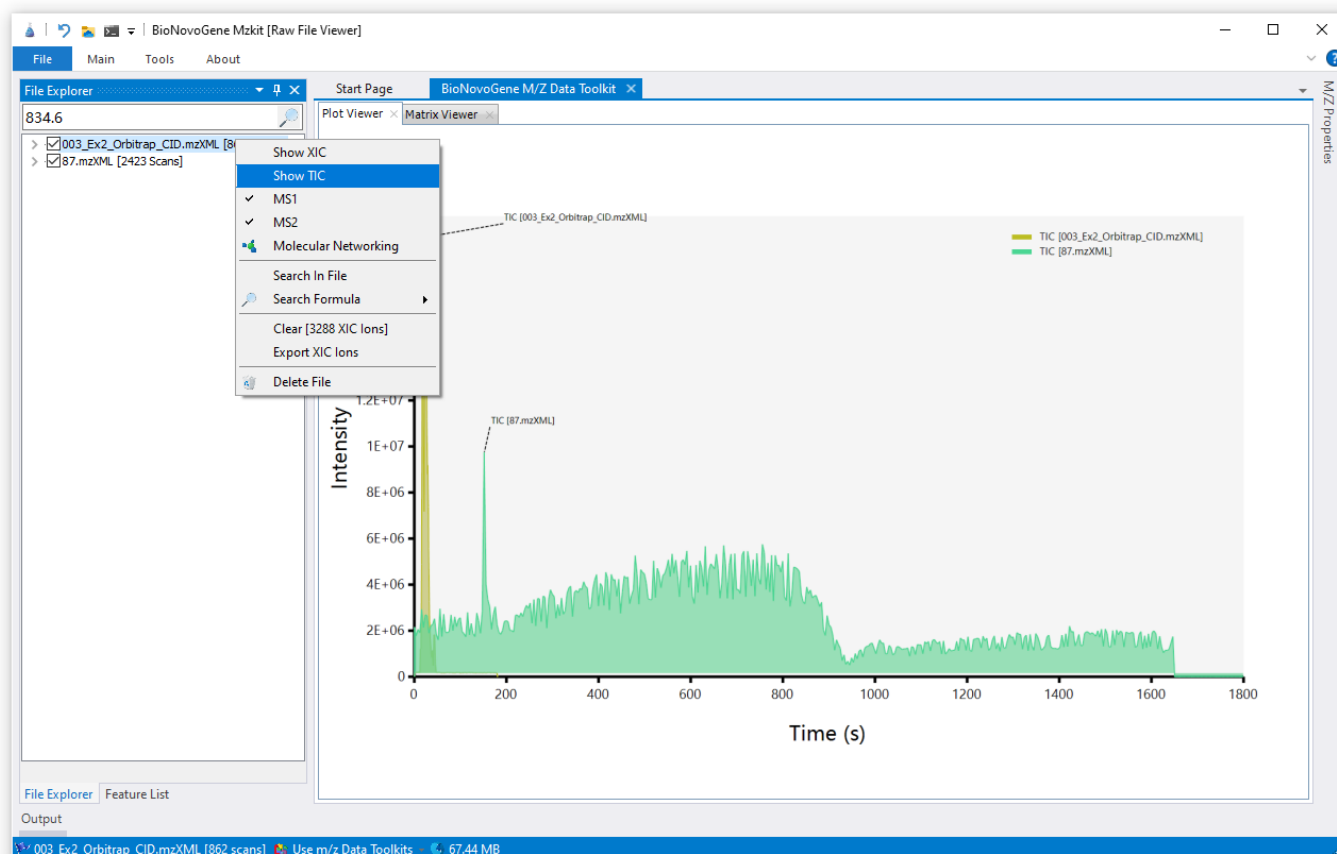
1.3.1. XIC overlay

you can click on the checkbox besides the Ms2 feature for select different ion feature for create the XIC overlay plot:



1.4. TIC plot

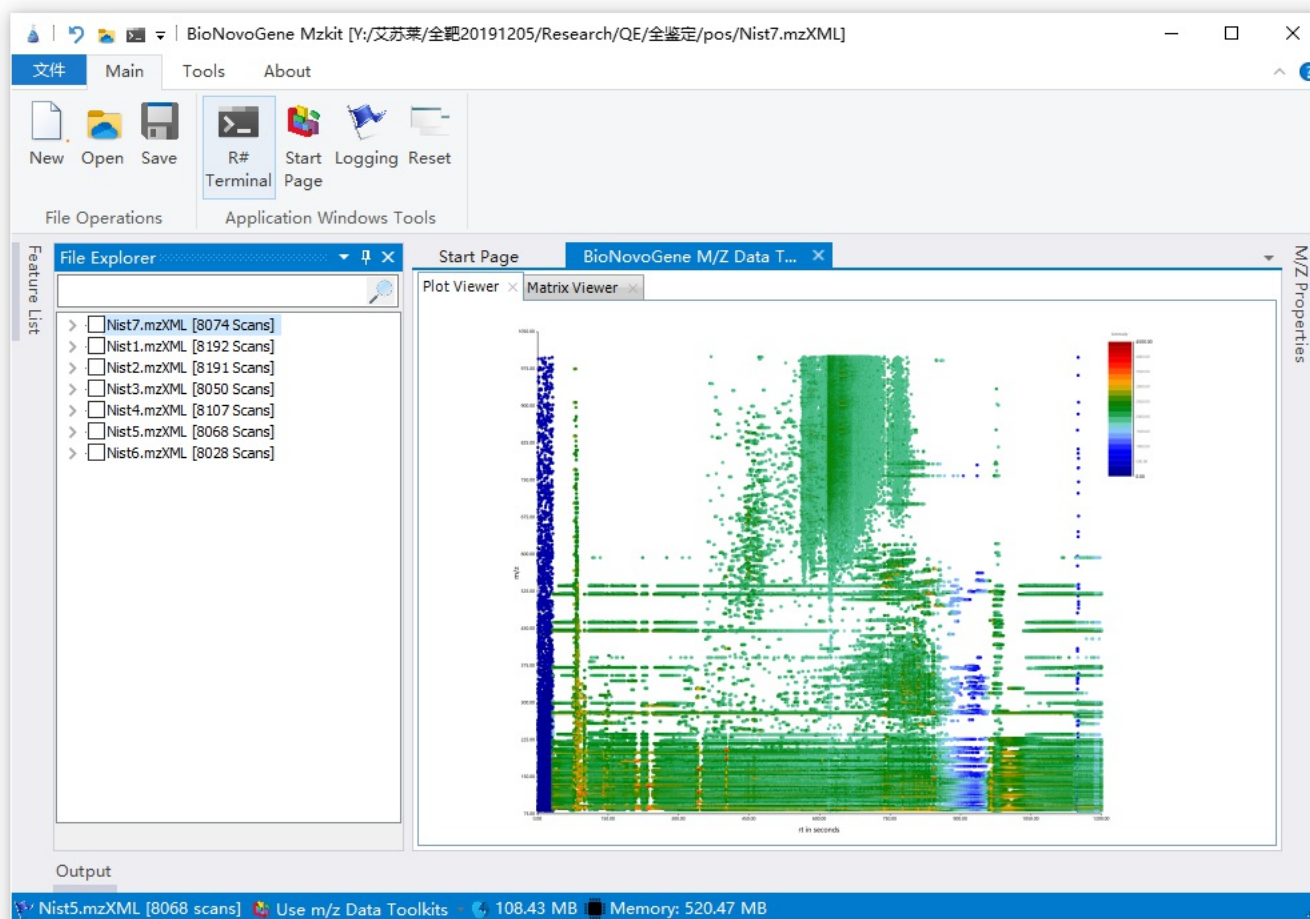
as the same as create a XIC plot, you also can create TIC plot for a single file or multiple file by select multiple file by check on checkbox:



The TIC plot is similar to the XIC plot, data is generated from all ions.

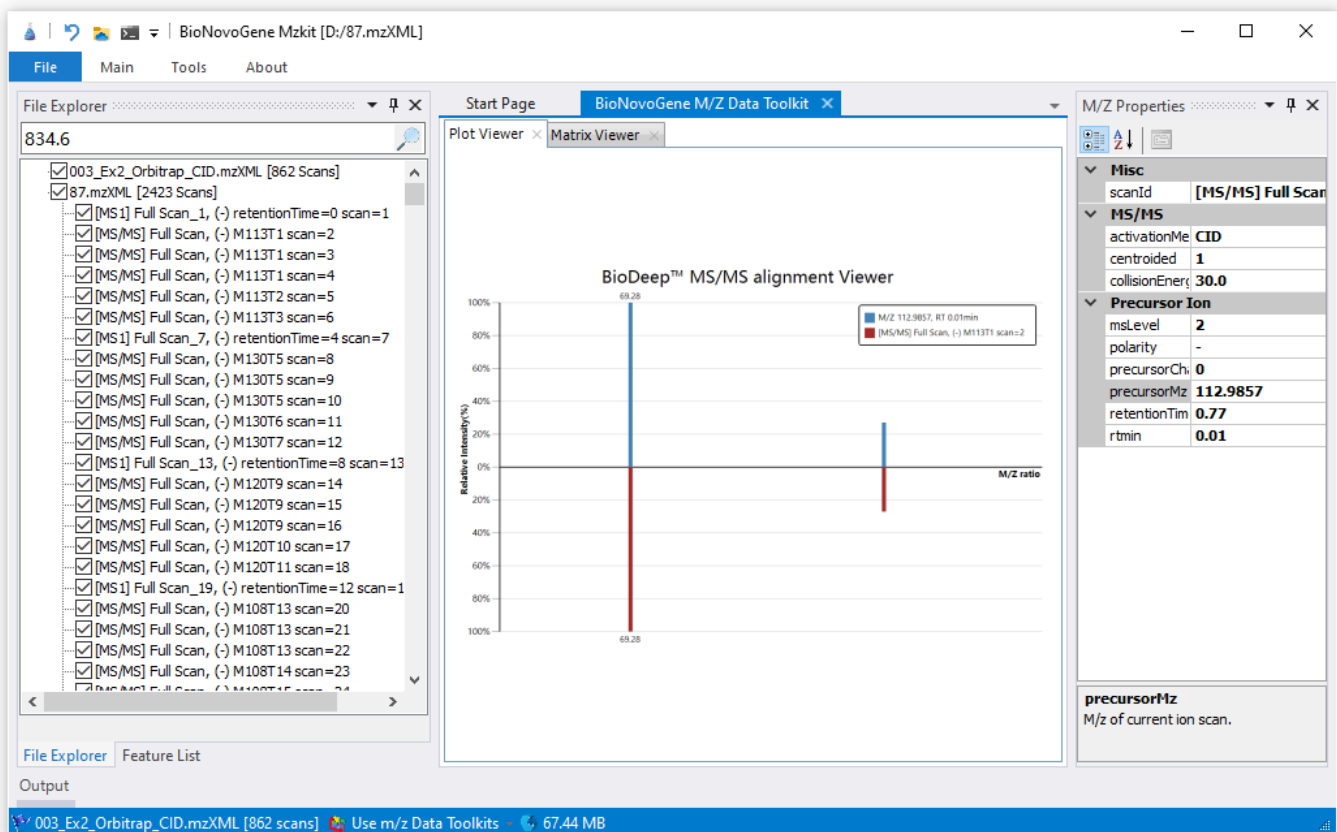
1.5. Raw Scatter

just click on the node of the raw file, then you will open the raw scatter plot of your specific raw data file, example as:



1.6. View Mass spectra

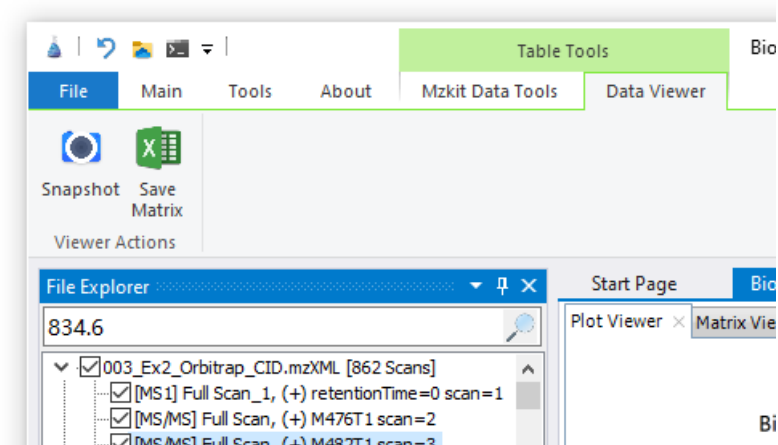
For view the mass spectra data in your file, just click on one of the scan feature in your raw data file:



1.7. Save Plot and Export matrix

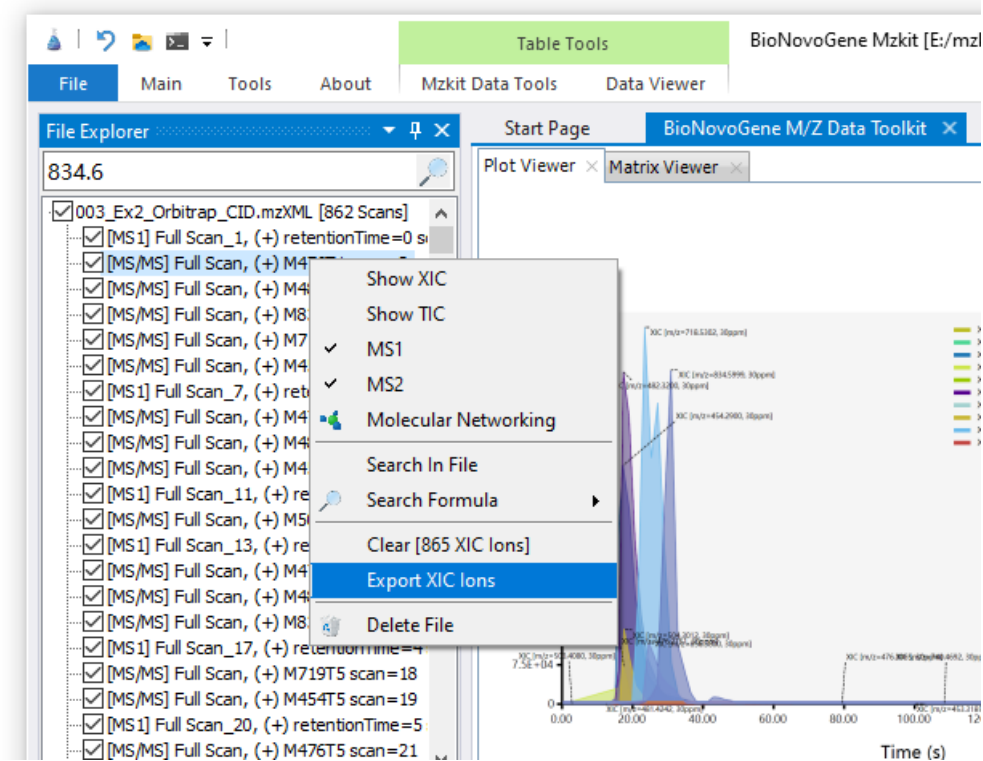
The mzkit application provides the function for save the plot image and the plot data in your raw data file. for example, select the **Data Viewer** tab page in mzkit, you will see two viewer action buttons in the menu:

1. **[Snapshot]** for export the XIC/TIC/MS2 data plot image to a specific file.
2. **[Save Matrix]** for export the Mass spectra or Chromatography data to a specific Excel table file.



1.7.1. Export XIC

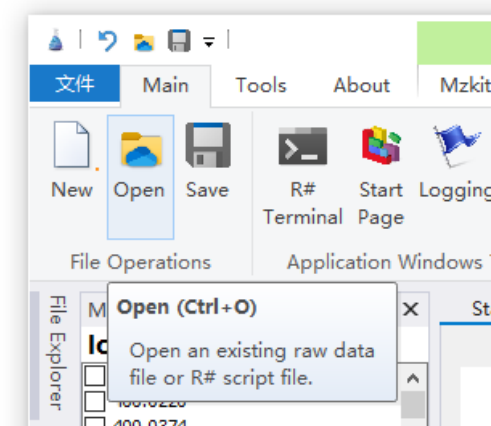
Export the XIC data to a specific file is also keeps simple, just mouse right click on the file content tree and then choose **Export XIC Ions**.



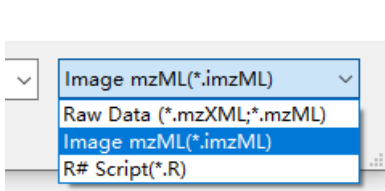
1.8. Ms-Imaging

mzkit software is also supports the **imzML** file format for run ms-imaging rendering, here is how to view the imzML raw data file in mzkit application:

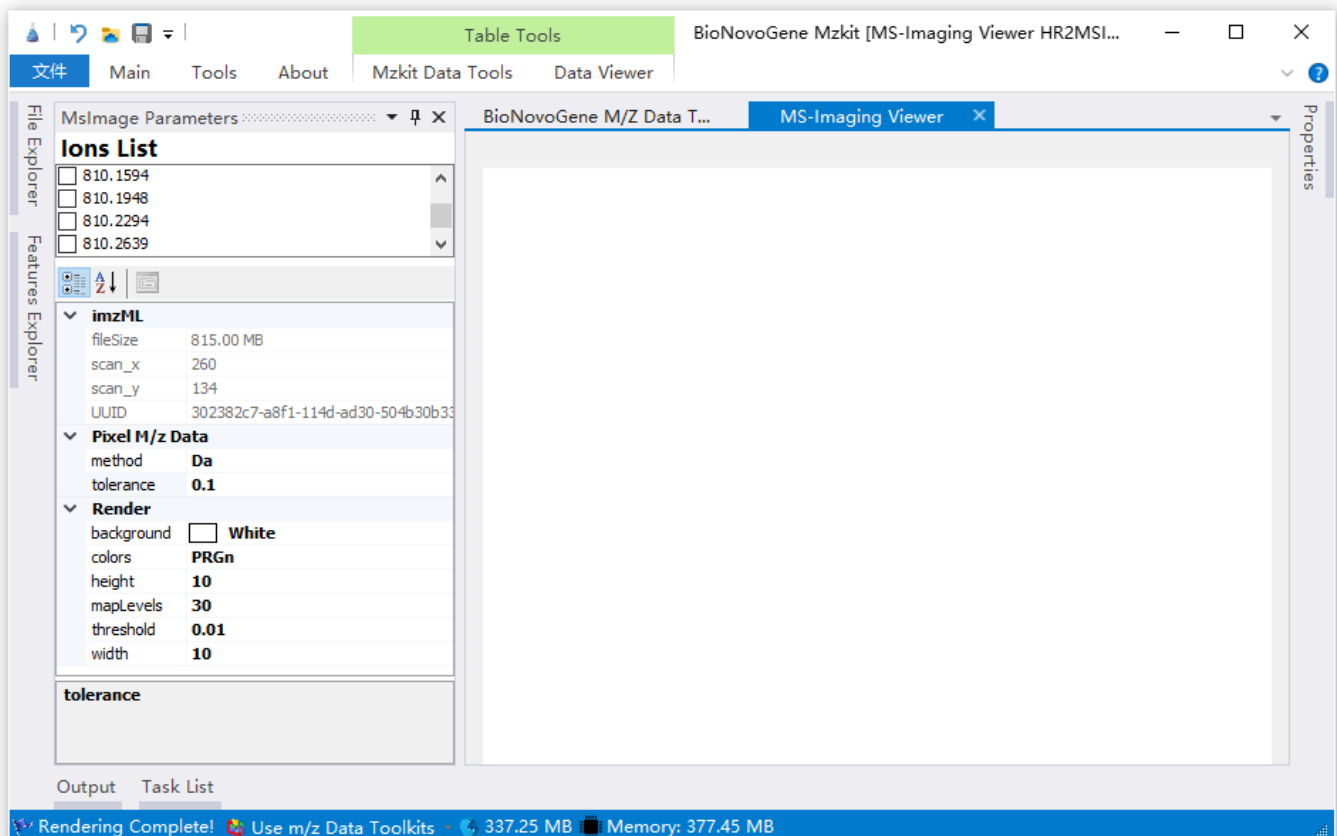
a. click of the open button on the file menu:



b. then you will see a pop out dialog for select raw data file, select the **imzML** file format in the file filter, like:



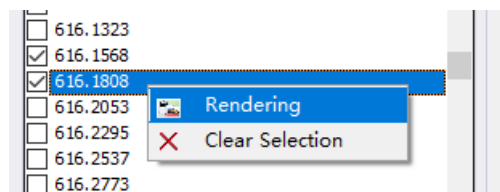
c. after the imzML raw data file has been imported into mzkit, then a raw data view for ms-imaging will be open, it looks like:



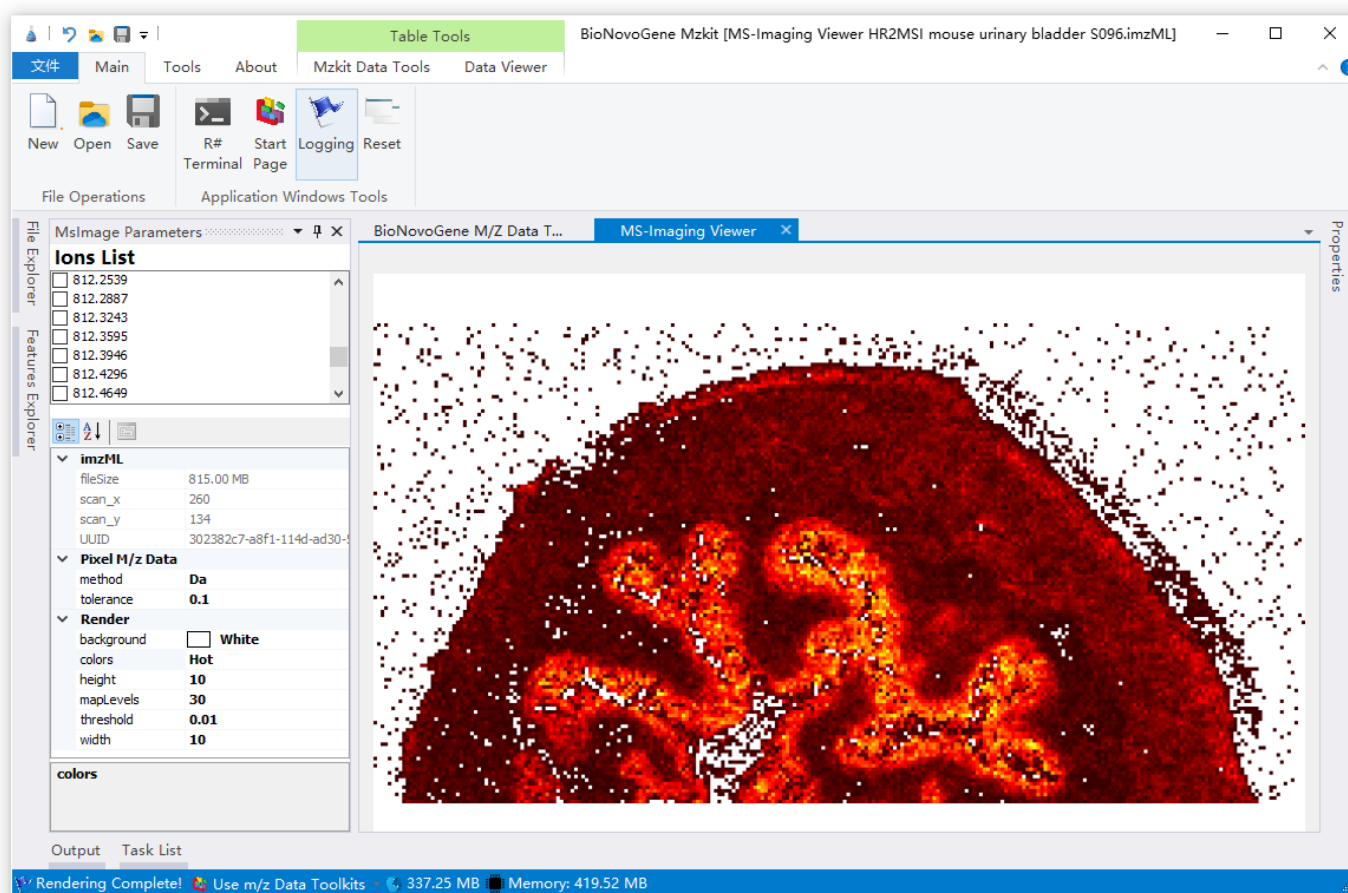
two components for view ms-imaging contains:

- [MsImaging Parameters] Panel for select ions and adjust rendering parameters.
- [MS-Imaging Viewer] tab page for show the rendering image output of the selected ions.

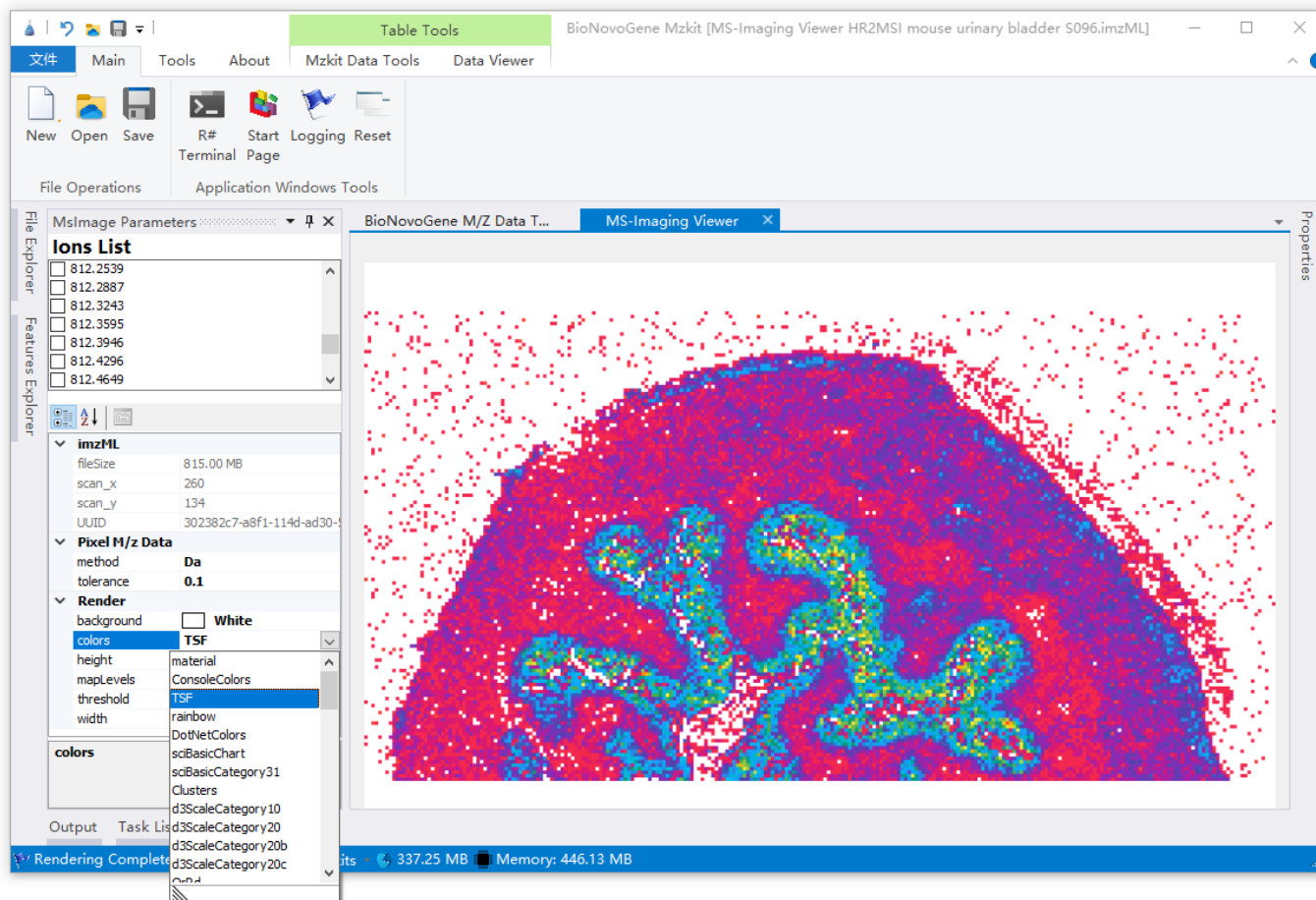
d. select target ions in the explorer panel, and then mouse right click on the ions, select **rendering** menu item for run ms-imaging rendering:



e. finally, you will see the imaging on the [MS-Imaging viewer] tab page after loading pixels data from the related **ibd** data files:



f. you can tweaks of the image from the [MsImaging Parameters] Panel.

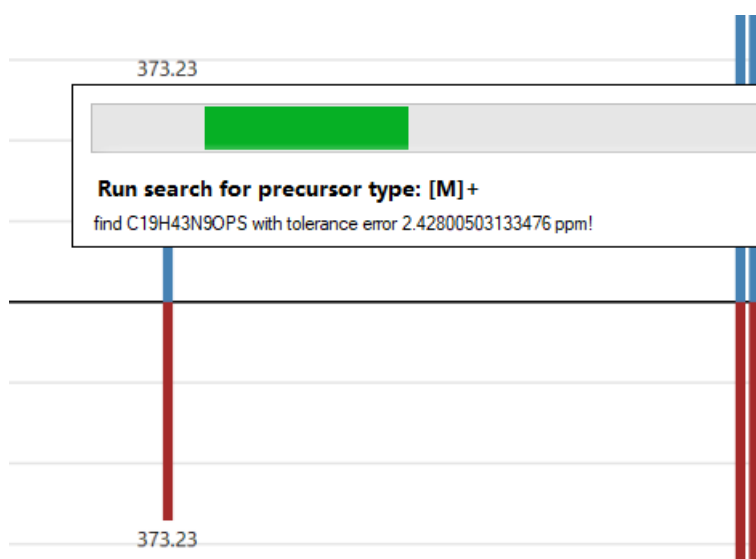


change different color schema for rendering the MS-image in mzkit application.

2. Data Annotations

2.1. Formula search

You can search for the formula of one feature in your raw data file with mzkit for do some de-novo annotation with just simply mouse right click on one of the feature and then select **Search Formula**, and then wait for a while to let mzkit for search all of the candidate formula by enumerates all of the possible element combinations:



Once the mzkit have been done of formula search, then all of the matched formula will be shown on the result page. there are some information about the each formula search result is listed in the result table, includes: formula result, its corresponding exact mass value, mass error of the searched m/z and the m/z calculated from the exact mass, ion charge value from your raw file, precursor type information, etc.

The screenshot displays the BioNovoGene M/z Data Toolkit interface. The main window is titled "Formula De-novo Search". It features an input field for "Input m/z:" and a "Search Formula" button. The "Formula Search Profile" is set to "Custom". Below the search bar is a table of results with the following columns: Formula, Exact Mass, PPM, Charge, Adducts, M, and Precursor Type. The table lists 15 candidate formulas, all with a charge of 1 and an adduct of 1.007276. The precursor type for all entries is "[M+H]+".

Formula	Exact Mass	PPM	Charge	Adducts	M	Precursor Type
C10H60N4O3PS5	475.30064	3.96745530050556	1	1.007276	1	[M+H]+
C11H38N15O4P	475.2968678	3.96902668275556	1	1.007276	1	[M+H]+
C11H43N10O8S	475.2985898	0.346042224054862	1	1.007276	1	[M+H]+
C11H45N10O6P2	475.299863	2.33269402027553	1	1.007276	1	[M+H]+
C11H46N11O3PS2	475.2963976	4.95829921045409	1	1.007276	1	[M+H]+
C11H48N11OP3S	475.2976708	2.2795629660041	1	1.007276	1	[M+H]+
C11H51N6O7S3	475.2981196	1.33531475163379	1	1.007276	1	[M+H]+
C11H53N6O5P2S2	475.2993928	1.34342149269659	1	1.007276	1	[M+H]+
C11H55N6O3P4S	475.300666	4.02215773726617	1	1.007276	1	[M+H]+
C11H56N7P3S3	475.2972006	3.26883549358304	1	1.007276	1	[M+H]+
C11H58NO9PS3	475.3011148	4.96640595163648	1	1.007276	1	[M+H]+
C11H59N2O6S5	475.2976494	2.32458727921273	1	1.007276	1	[M+H]+
C11H60O8P5	475.297611	2.40537857038609	1	1.007276	1	[M+H]+

At the bottom of the window, a status bar indicates: "Run formula search for m/z 476.306030273438 with tolerance error 5 ppm, have 591 formula found! Use m/z Data Toolkits 67.44 MB".

You also can search of the formula by input any **m/z** value in the input box of the search result page. Click on the formula then you could submit the candidate formula into the biodeep database for search of the metabolite information.

This is a partial screenshot of the BioNovoGene M/z Data Toolkit interface, showing the "Formula De-novo Search" header and the "Export" button.

2.1.1. Export Formula Search Result

Export the formula search result just like other data that we've introduced before, just click on the **Formula Result** tab page and then click on the Export button. this command will let you save the formula search result into a specific Excel table file.

2.2. Molecular Networking

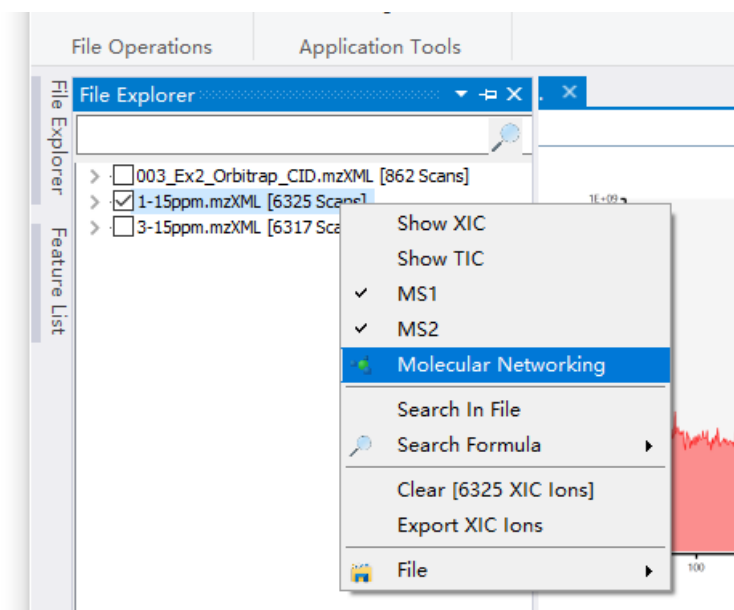
The molecular networking in mass spectrum data is a kind of spectrum similarity network. You can build a molecule network use mzkit in a very easy way:

2.2.1. step1 select ions

For create a spectrum similarity network, it required some ms2 ions data provides to mzkit for run spectrum matrix alignment and evaluate the simialrity scores between these spectrum matrix data. select the ions data just like plot XIC operation it does in mzkit: check on the ms2 feature in the **file explorer** dock panel.

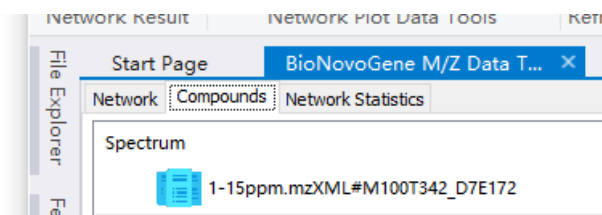
2.2.2. step2 build network

Once we have the mass spectrum data selected, then we could run the matrix similarity between these matrix for build a network. now we mouse right click of the file tree in the **file explorer**, and then choose the **Molecular Networking** menu item:



2.2.3. step3 view network data

once the networking progress have been done, then we could view the network result data in the **Molecular Networking** tool page. there are three tables in the tool page for show your network data: **Network**, **Compounds** and **Network Statistics**.



- the **Network** tab page contains the edges data in your network, which is the spectrum cluster simialrity result. all of the spectrum alignment its simialrity value is less than the **Spectrum Similarity** threshold value that will be removes from the network.

File Explorer Feature List

Start Page BioNovoGene M/Z Data T... Application Settings Molecular Networking Vie... Molecular Networking Vie...

Network Compounds Network Statistics

CompoundA	CompoundB	similarity	forward	reverse	View
m.mzXML#M148T160_2	m.mzXML#M150T94_B0	0.9741	0.9912	0.9741	View Alignment
m.mzXML#M148T160_2	m.mzXML#M150T70_2F	0.9739	0.9848	0.9739	View Alignment
m.mzXML#M148T160_2	m.mzXML#M190T180_B	0.9496	0.9496	0.9683	View Alignment
m.mzXML#M150T70_2F	m.mzXML#M391T800_C	0.9144	0.9144	0.9770	View Alignment
m.mzXML#M706T831_8	m.mzXML#M718T818_3	0.9985	0.9987	0.9985	View Alignment
m.mzXML#M706T831_8	m.mzXML#M718T818_B	1.0000	1.0000	1.0000	View Alignment
m.mzXML#M706T831_8	m.mzXML#M719T726_C	0.9982	0.9982	1.0000	View Alignment
m.mzXML#M706T831_8	m.mzXML#M719T693_9	0.9964	0.9964	1.0000	View Alignment
m.mzXML#M706T831_8	m.mzXML#M720T790_4	0.9979	0.9979	1.0000	View Alignment
m.mzXML#M706T831_8	m.mzXML#M732T796_E	0.9985	1.0000	0.9985	View Alignment
m.mzXML#M706T831_8	m.mzXML#M733T804_0	1.0000	1.0000	1.0000	View Alignment
m.mzXML#M706T831_8	m.mzXML#M833T706_5	0.9947	0.9947	0.9985	View Alignment
m.mzXML#M706T831_8	m.mzXML#M837T758_7	0.9917	0.9917	0.9980	View Alignment
m.mzXML#M706T831_8	m.mzXML#M861T816_2	0.9974	0.9974	0.9988	View Alignment

Output

The network size is huge for create layout, entire progress will be very slow... Use m/z Data Toolkits 266.72 MB Memory: 331.03 MB

there are columns in the edge table: **CompoundA** and **CompoundB** is the spectrum reference id in this edge connected. and the **similarity**, **forward** and **reverse** column is the similarity score value of the two spectrum matrix and the last **view** column contains the button that let you view the spectrum matrix alignment result visual plot.

4. the **Compounds** tab page contains the spectrum cluster (**network nodes**) information in your network.

File Explorer Feature List

Start Page BioNovoGene M/Z Data T... Application Settings Molecular Networking Vie... Molecular Networking Vie...

Network Compounds Network Statistics

Spectrum	Cluster/File	Scans/Frag...	m/z	rt	rtmin
1-15ppm.mzXML#M100T342_D7E172	6	2	100.0763125	341.78	313.94
1-15ppm.mzXML#M100T366_50B663	6	11	100.0763125	366.48	366.48
1-15ppm.mzXML#M100T48_05DBBC	6	3	100.0763125	48.05	18.7
1-15ppm.mzXML#[MS/MS] Full Scan, (+) M100T19 scan=150	1-15ppm.mzXML	7	100.0763	18.7	n/a
1-15ppm.mzXML#[MS/MS] Full Scan, (+) M100T239 scan=1815	1-15ppm.mzXML	12	100.0763	239.4	n/a
1-15ppm.mzXML#[MS/MS] Full Scan, (+) M100T48 scan=384	1-15ppm.mzXML	16	100.0763	48.05	n/a
1-15ppm.mzXML#M100T516_F54A12	6	18	99.5317777777778	515.99	71.56
1-15ppm.mzXML#M100T649_497514	6	1	99.5129	649.3	649.3
1-15ppm.mzXML#M101T175_64365B	6	17	101.060330434783	174.99	49.12
1-15ppm.mzXML#M101T481_F06DBC	6	1	101.060330434783	480.82	480.82
1-15ppm.mzXML#M101T635_FED0A0	6	5	101.060330434783	634.53	505.95

Output

The network size is huge for create layout, entire progress will be very slow... Use m/z Data Toolkits 266.72 MB Memory: 330.77 MB

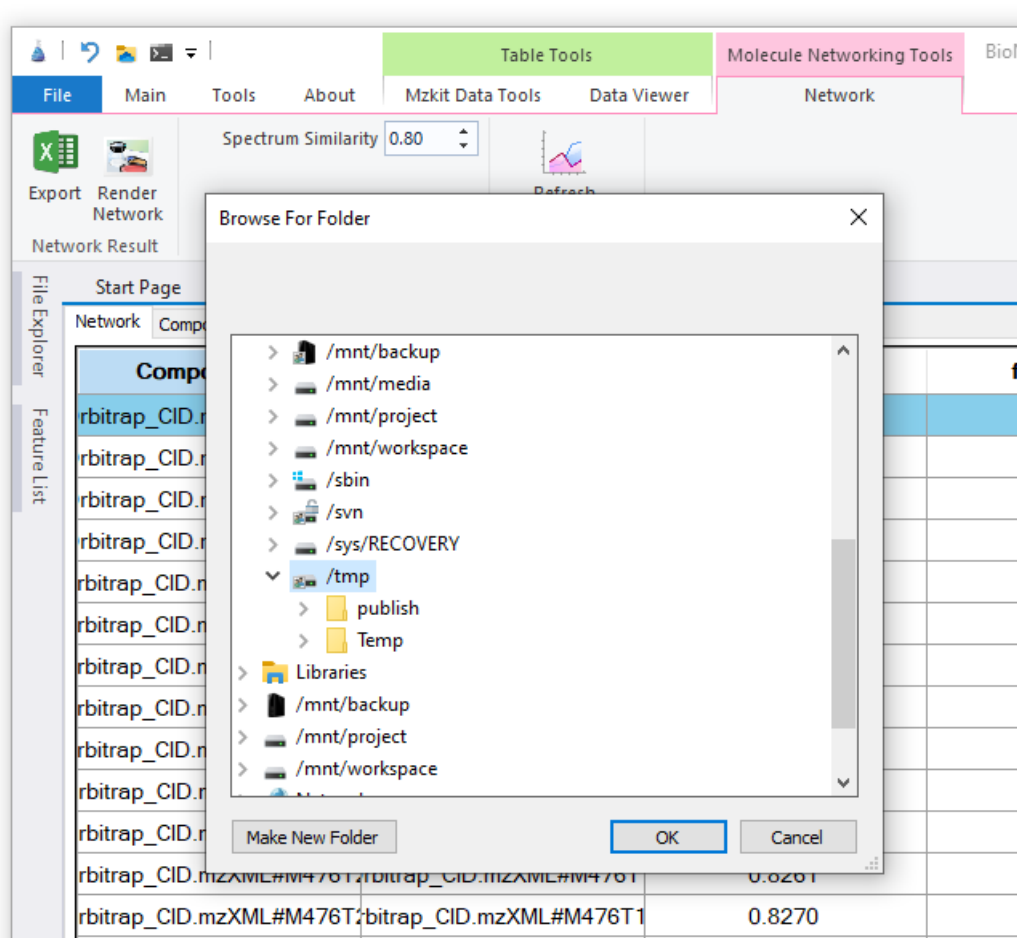
2.2.4. step4 network visualization

The mzkit program provides a small build-in network visualization engine that could let you visual the resulted molecular network with just a simple mouse click. As you can see in the previous screenshot, there is a **Render Network** command button on the top menu when the **Network** tab is activated. Now we just click on it, and wait for the network layout calculation progress complete, and then we will see a new tag page which is named **Molecular Networking Viewer** will be shown in the document area of the mzkit program.

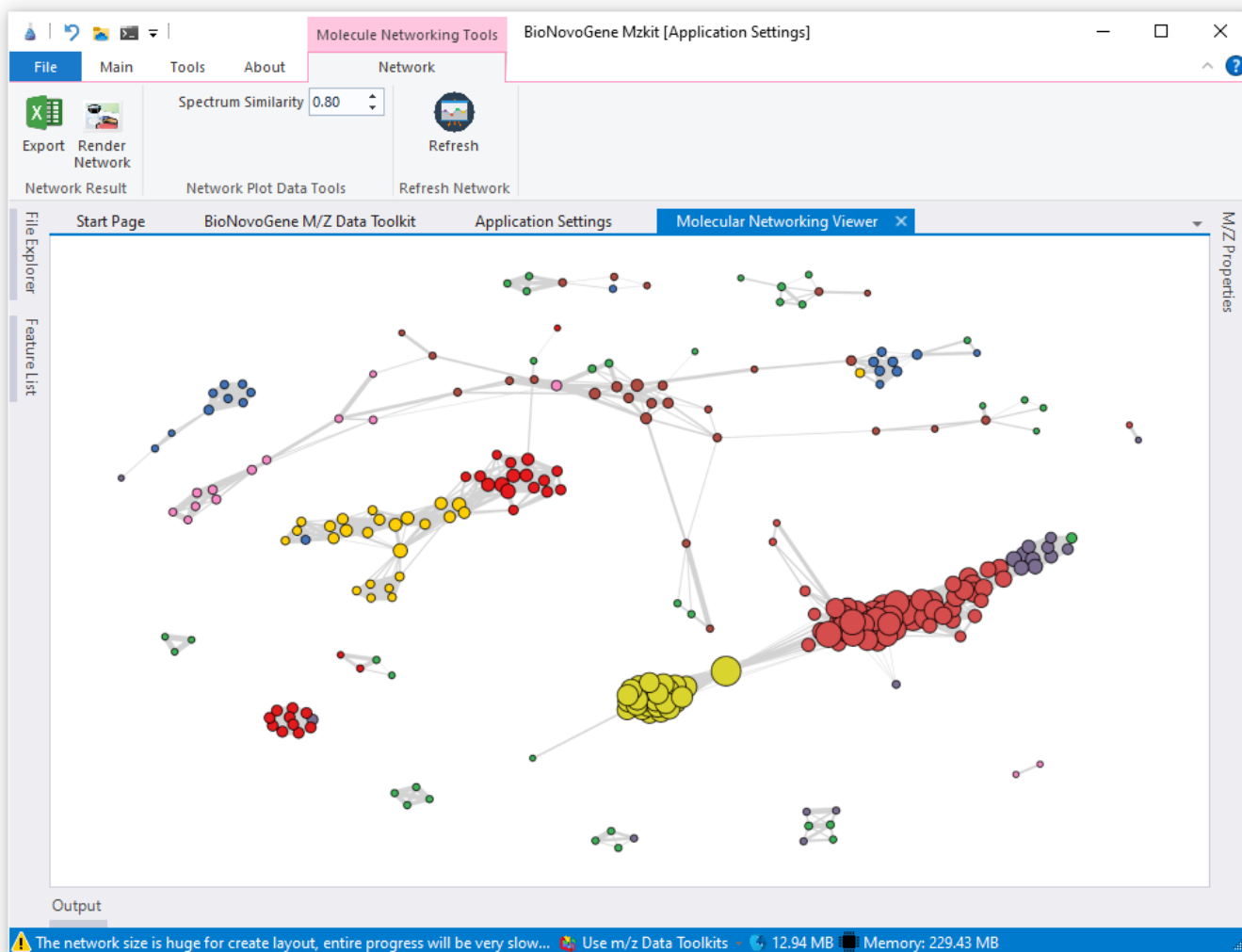
2.2.5. Export Network Data

There is not too much style tweaking in the mzkit build-in network visualizer, so that you may want to export the network data into table and then visualize it in other network visualization software like the famous **Cytoscape**.

Just click on the **Export** command button beside the **Render Network** button in the **Network** menu tab, then a dialog of save network data will be triggered and opened. Select a location in the dialog and then you can save the network table data into a given location for visualization in other software.



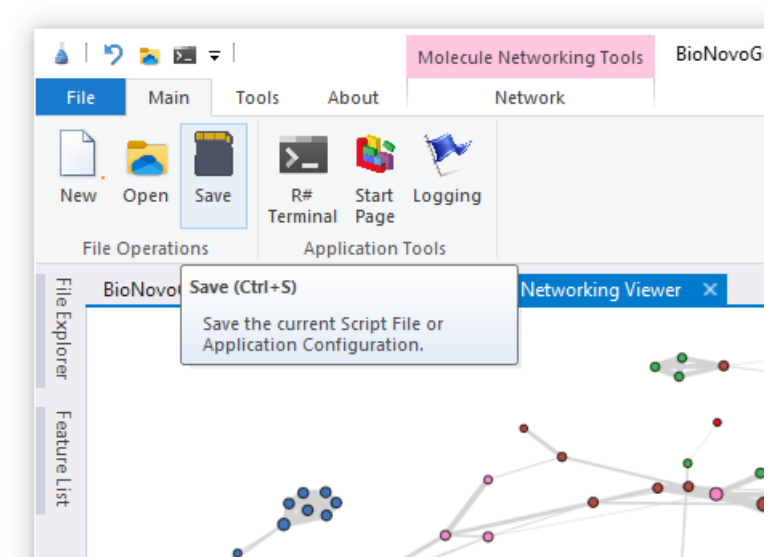
2.2.6. Save Network Visual



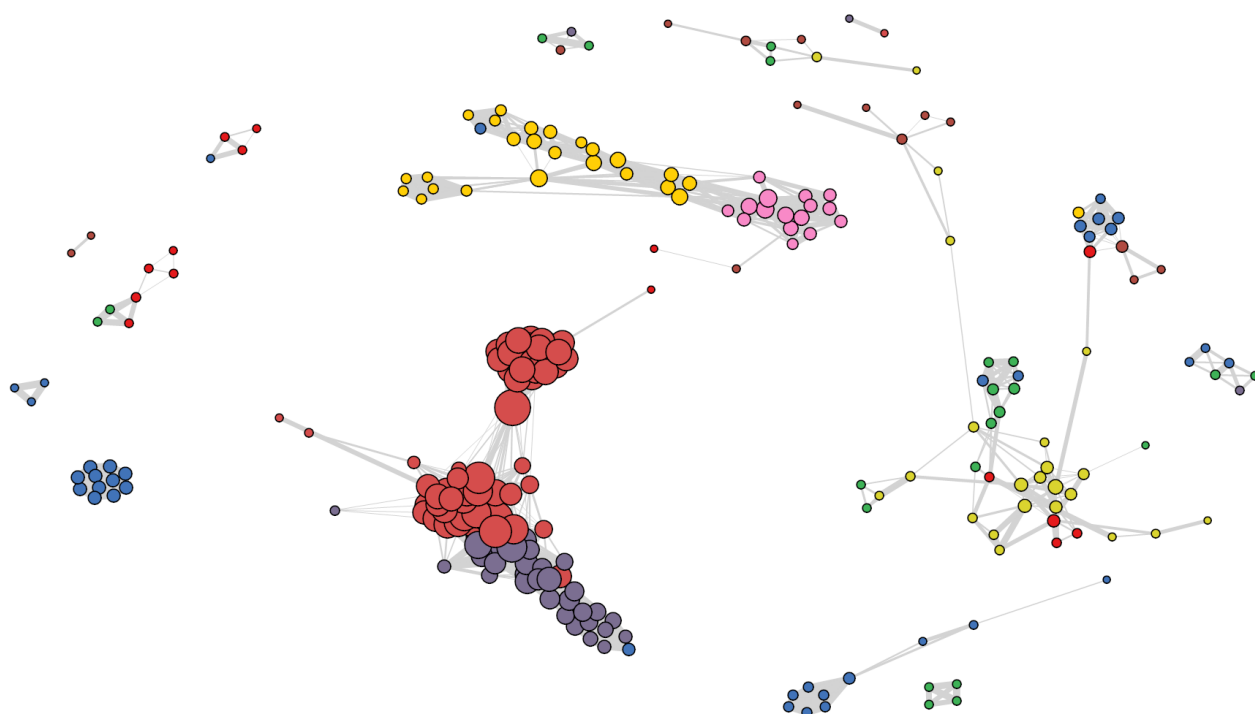
For export the network image, just mouse right click on the viewer panel, then you could see a popout menu **Save Image** that could use for viewer image saved.



You also can save the network image via **Save** command in the **Main** menu tab page when the molecular networking viewer is current active document page in mzkit program.



Now you can use the saved network image for your publications:



Targeted Data Quantification

Introduce Ions Library

Use the Quantify Analysis Tools

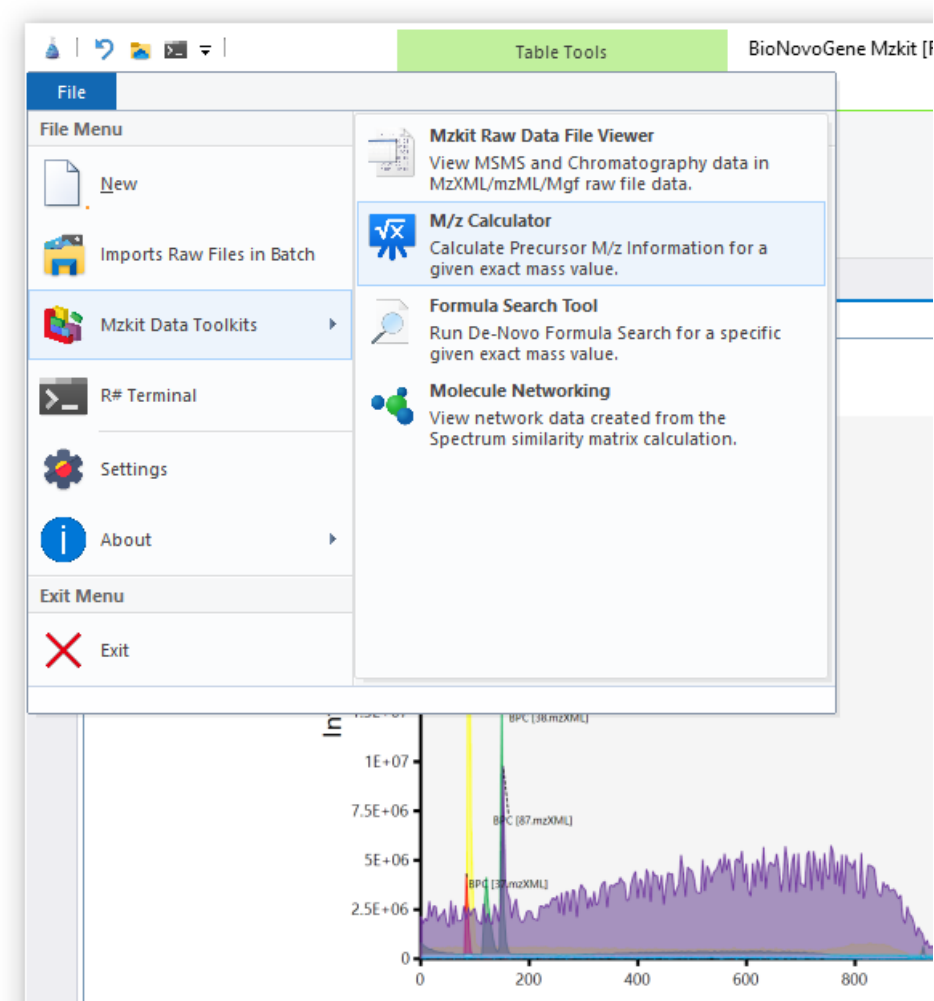
Linear Modelling

Sample Quantify

3. Appendix

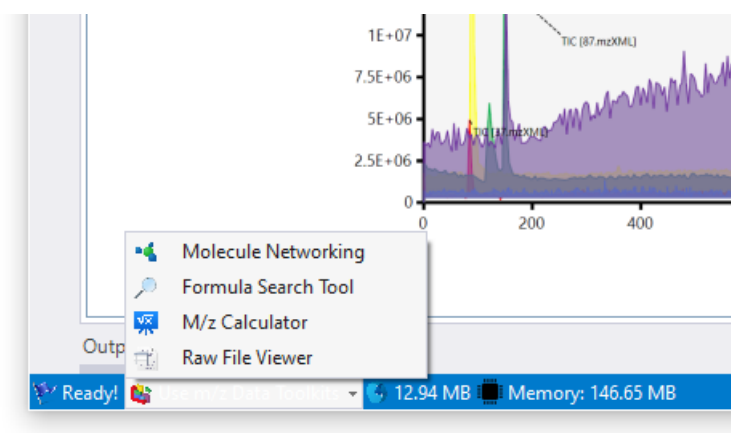
3.1. Switch Between Toolkit

You can switch between toolkit pages via the start menu of mzkit:



click **[File]** -> **[Mzkit Data Toolkits]**, and then click on one toolkit item then you can switch to the required toolkit page.

or just select a page from the app switcher toolstrip menu:

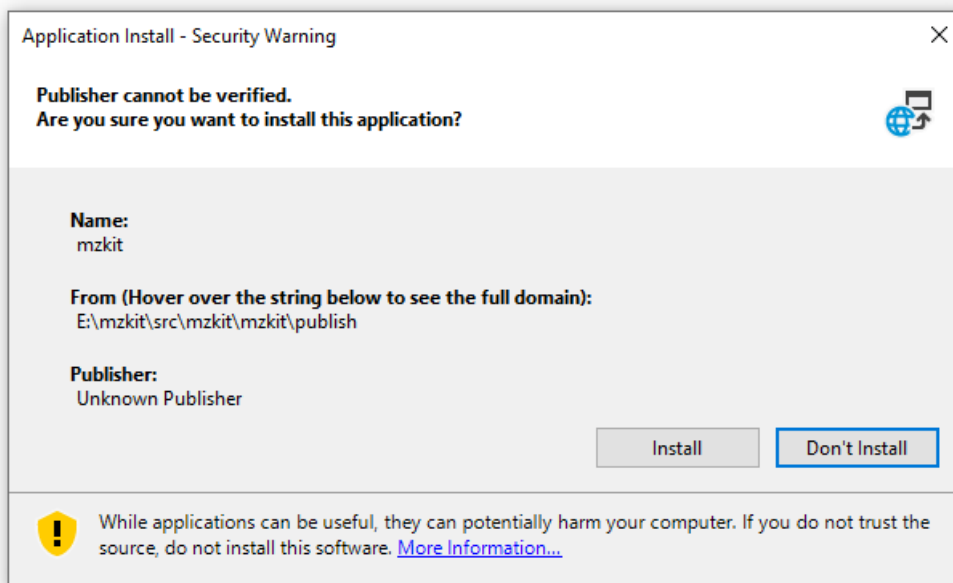


3.2. Install Mzkit

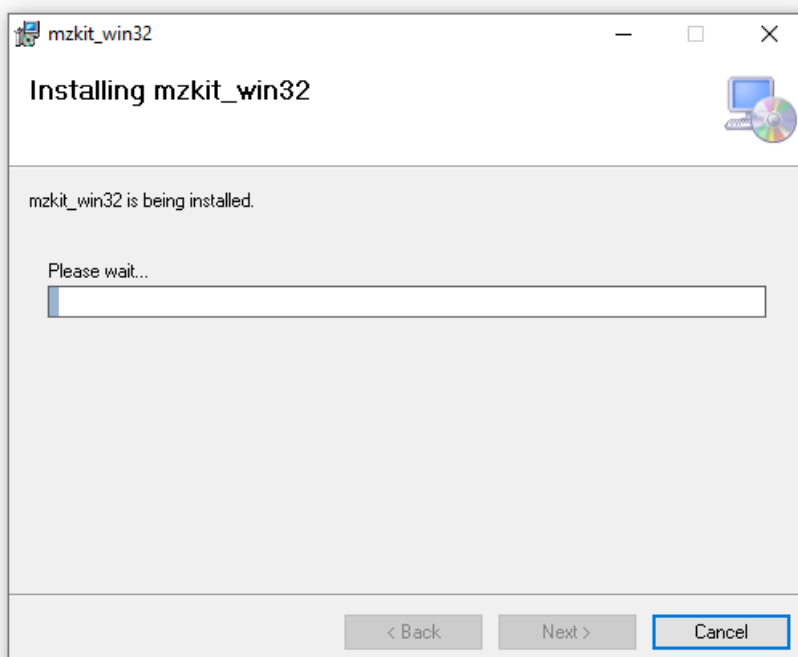
If you have already installed the mzkit application, please uninstall the previous version before you install the new version of the mzkit application.



When you have extract the zip package of the mzkit compression package, then you could found a `setup.exe` install application in the top of folder. Click on this setup application, then your will going to install mzkit program into your computer system.



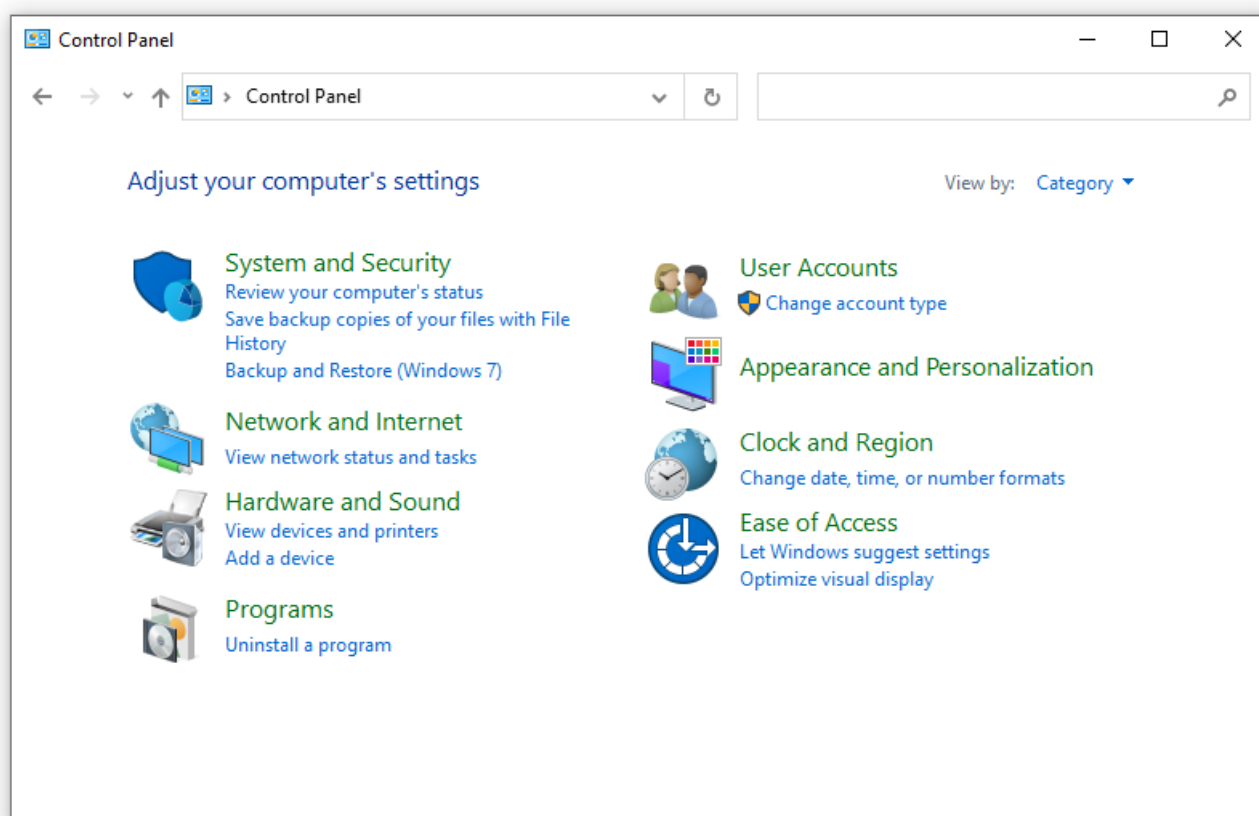
When you have launch the mzkit installer, then you will see a security warning dialog from your windows system, just click on the `Install` for start the install progress, and then just needs to wait for the installer finish the progress of copy the mzkit application files.



3.3. Uninstall Mzkit

if you want to removes mzkit from your computer system, then you could follow this instruction for uninstall:

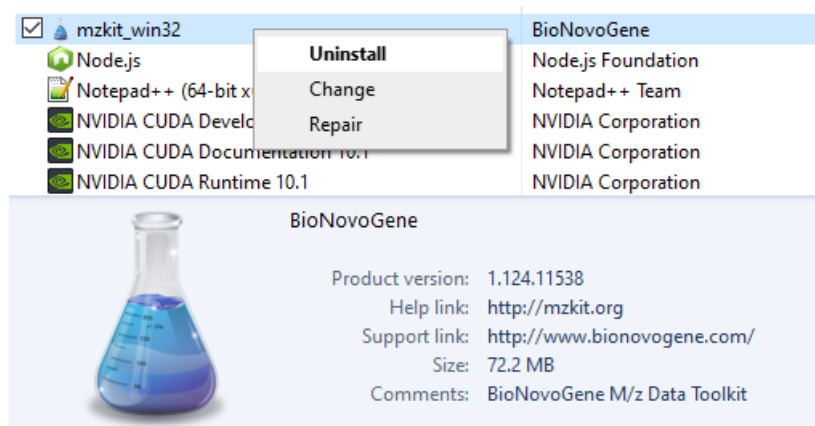
1. Open the control panel of your windows system, and then click of the link `uninstall a program`



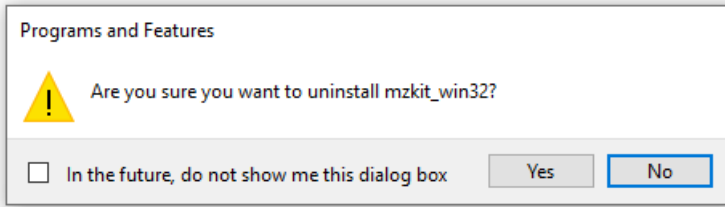
1. Then you will see a list of program that installed on your windows, located the mzkit application

	MySQL Installer - Community	Oracle Corporation	5/12/2018	17.4 MB	1.4.25.0
	MySQL Server 8.0	Oracle Corporation	6/7/2019	392 MB	8.0.11
	MySQL Workbench 6.3 CE	Oracle Corporation	5/12/2018	148 MB	6.3.10
	mzkit	BioNovoGene	9/8/2020		1.12.1.16
	Node.js	Node.js Foundation	8/3/2018	52.8 MB	8.11.3
	Notepad++ (64-bit x64)	Notepad++ Team	6/26/2020	14.3 MB	7.8.5
	NVIDIA CUDA Development 10.1	NVIDIA Corporation	7/12/2019		10.1
	NVIDIA CUDA Documentation 10.1	NVIDIA Corporation	7/12/2019		10.1

1. Then right click on the mzkit, select `uninstall`, then you can removes mzkit from your windows system



Just click `OK` on the dialog:



[mokit](#) is maintained by [xieguigang](#).

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