1 General Introduction

WTV2.0 is an open-source software platform with an intuitive graphical interface which provides users with a convenient one-stop solution for the whole process of widely targeted GC-MS data. WTV2.0 provides a complete metabolomics workflow encompassing the integration of metabolite libraries, the generation of widely targeted acquisition methods, qualitative and semi-quantitative analysis of data.

1.1 *library builder* - Metabolite Library Integration

library builder is a module focusing on integrating mass spectra libraries and retention time information. Initially, the imported libraries, RT information and retention index (RI) calibration data were integrated. After format standardization of compound names (e.g., replace ".beta." with "beta") and removes of invalid mass spectrum, the redundant information was excluded based on compound names, synonyms, and CAS numbers. The RTs were calculated or calibrated using RI calibration data. A feature of *library builder* is in addition to alkane standards, it is compatible with the use of RT and RI from other compounds in the RI calibration dataset, thus broadening calibration coverage. For example, due to the inconvenience in obtaining C4 and C5 alkanes, ethanol (RI = 427) and ethanethiol (RI = 517) can be incorporated to the dataset for the RT calibration of compounds with RI < 500. Afterward, the non-redundant RT list and library were exported. An additional function of the *library builder* is the integration of unknown signals in untargeted or cSIM data to the library, thereby expanding the detection coverage of acquisition method. However, the imported unknown signals might be compounds already existing in the library. To avoid redundancy, the integrated and non-redundant library was used as background, and imported unknowns are compared for spectral similarity with compounds having adjacent RTs. Only when the similarity score between an unknown signal and all its neighboring compounds falls below the user-defined threshold is the unknown integrated into the library. This ensures the accuracy and consistency of the

metabolite library, laying a reliable foundation for subsequent processes, such as widely targeted acquisition method generation and data analysis.

1.2 *method generator* - Widely Targeted Acquisition Method Generation

method generator, another key component of WTV2.0, is responsible for generating widely targeted acquisition methods. The software first picks the minimum group of characteristic ions for each compound based on metabolite library, which are sufficient to characterize from all compounds within a user-set window to form the highest sensitivity detected ion segmentation. However, due to the instrument detection's certain limitation on the number of SIM segments, in order to generate an acquisition method file that the instrument can read, we need to adjust the segment information according to the requirements of each manufacturer. We do this by automatically merging the segments that have the least sensitivity reduction to meet the instrument requirements, that is, adding the minimum number of ions to be detected.

The scope of this program is very broad. For high-throughput detection of high-coverage libraries, the software generates comprehensive SIM (cSIM) detection methods through the above algorithm. While for low-throughput detection, whether it is a low-coverage library or a high-coverage library, the program can assist in generating high-sensitivity detection method and accurate qualitative analysis of targeted metabolites by comparing the mass-to-charge ratio and corresponding intensity of compounds in the mass spectrum and selecting an appropriate number of detection ions.

1.3 *data analyzer* - Data Qualitative and Semi-Quantitative Analysis

data analyzer is tailored for qualitative and semi-quantitative analysis of GC-MS cSIM data. Raw data was first performed the missing value imputation, followed by data smoothing using a linearly weighted smoothing average method. For each data point, its first derivative (fd), the second derivative (sd), and the abundance difference (ad) were calculated, and used to calculate the first derivative filter (ff), second derivative filter (sf) and abundance difference filter (af). Utilizing these filters, the software identifies the left boundary, apex and right boundary of a peak. Afterward, the software conducts the baseline correction and adjusts the RT and intensity of the apex

point. For each peak, the software utilizing the ad and sd value to identify the apex point of co-eluted peaks, and recovers the peak shape using least square method. The sharpness value (SV) of each peak was calculated and added to the subintervals of scans. A second derivative Gaussian filter was applied to identify the component. For identification, the standard mass spectrum retains only the ions detected by the acquisition method and compared with the spectra of component to calculates the match score and reverse match score. The RT or RI penalty score was also calculated. These scores are collectively used to calculate the final similarity score. Annotation results with similarity score greater than the user-defined threshold are listed. Finally, semi-quantitative analysis was carried out by calculation of the peak area and peak height of quantitative ion.
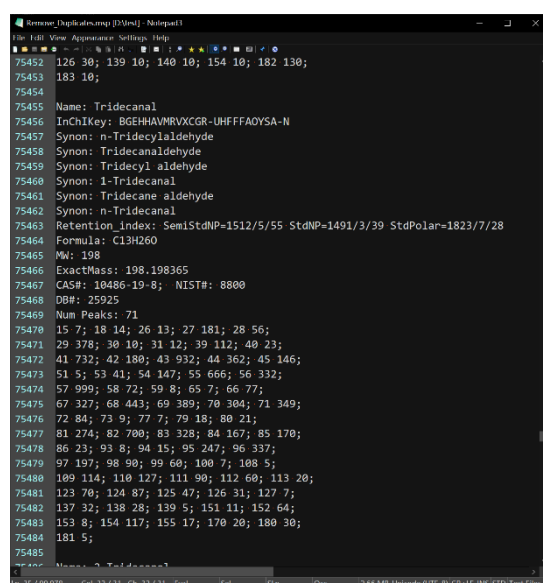
For more detailed information, read on in the documentation, checkout the paper.

2 Using the Software

2.1 Building a Compound Library (MSP) for Detection and Identification（the *library builder* module）

2.1.1 Data Preparation
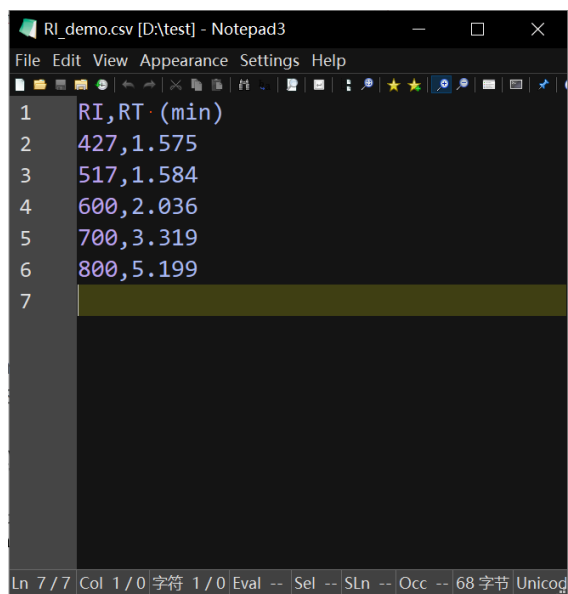
MSP file(s)

Prepare MSP files that contains mass spectrometry information and theoretical retention times for substances.

Retention Time Information

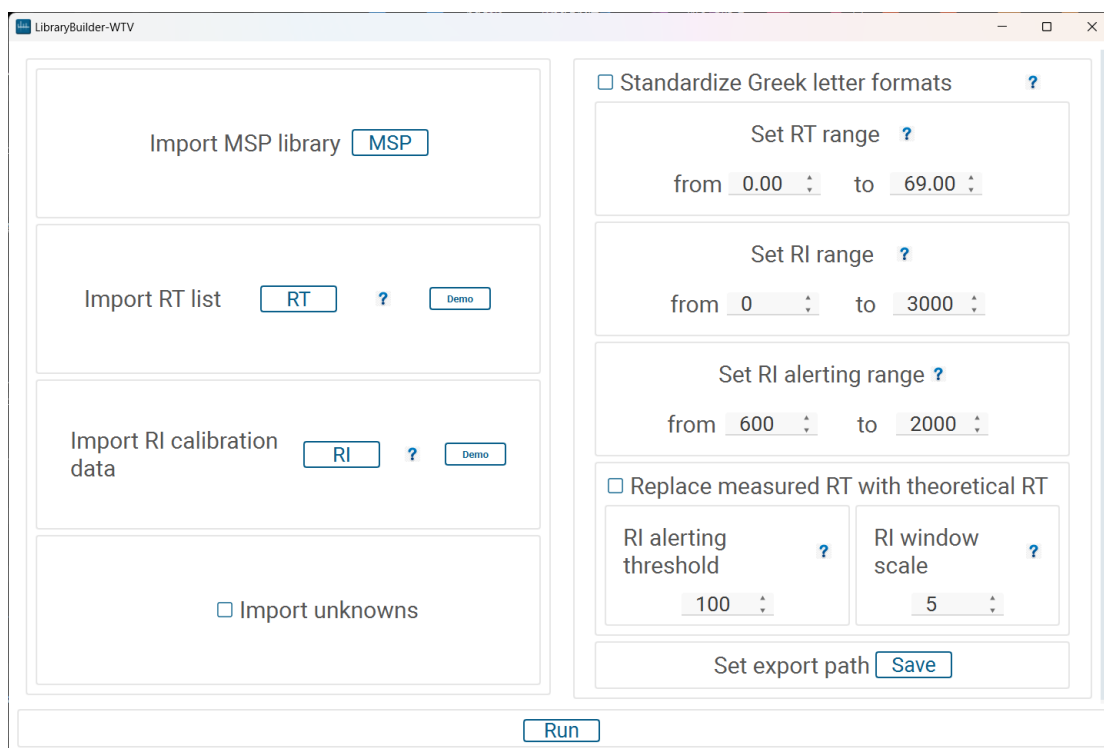Using actual measured retention times (RT)

Or / And RI calibration

2.1.2 Parameter Configuration
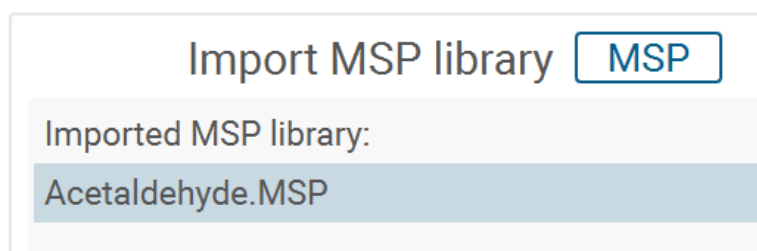

Import MSP library

To input an MSP file, simply click the 'MSP' button and select the desired MSP file.

Once selected, the interface will display all the selected file directories, confirming a successful input.
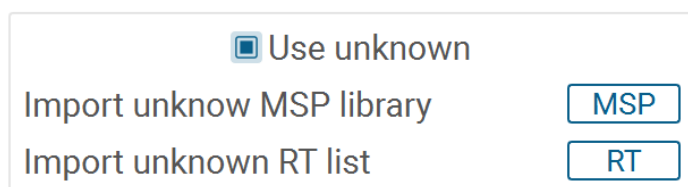

Import RT list: Import a list of compounds and their RT.

Import RI calibration data: Import RI calibration data.

Use unknown: Users can use this feature when users need to enhance signals from compounds that cannot be qualitatively identified.

When users wish to use this feature, simply select the white box to highlight it, and the hidden menu will become visible. Within the hidden menu, input the corresponding information for the unknown item.

Similarity is calculated between unknowns and compounds within the user-defined retention time (RT) window. Only when the similarity is below the set threshold with all nearby compounds will the unknown be integrated into the database.

Standardize Greek letter formats: This option allows for a unified representation of Greek letters. Eg: ".alpha." -> "alpha"

Set RT range: Once configured, the output retention times will be constrained within this range.

Set RI range: Once configured, the output retention index will be constrained within this range.

Set RI alerting range: Only unreasonable RT (Retention Time) values outside the configured range will trigger a warning.

Replace measured RT with theoretical RT: Selecting this option will replace measured retention times outside the set theoretical retention time window with the theoretical retention time.

RI alerting threshold: Compound will be marked if the difference between the measured RI and the database Rl exceeds this threshold.

RI window scale: The larger this value, the larger the Rl error threshold when the RI is larger. Setting it to 0 disables this feature. For more specific and detailed information, please refer to the official documentation of the AMDIS software.
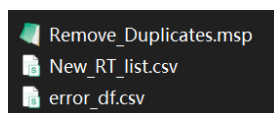
Set export path: Click the 'Save' button, choose a saving path, and the processed results will be saved to this directory.
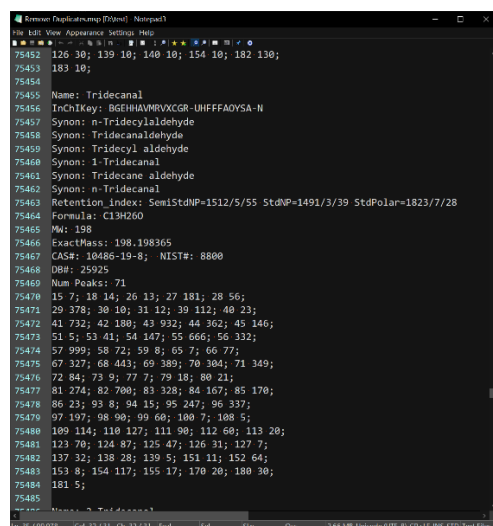
Tips:

1. Any file directory entered can be deleted by double-clicking the entered entry.
2. Clicking the corresponding "demo" button allows viewing the required format.

2.1.3 Results and Reports

After configuring all parameters, click the 'Run' button. The program will automatically generate three result files.

The MSP result file:

The RT (Retention Time) result file

	A (Name)	B (RT)	C (RI_msp)	D (RI_input)	E (Alert)
842	5-Nonanol	21.528	1092	1095	
843	2-Furanmethanol, propar	21.5884	1096	The content of the retention time actually detected was not retrieved	rt_is_in_silico
844	Fenchone	21.5884	1096	The content of the retention time actually detected was not retrieved	rt_is_in_silico
845	Pyrazine, 2-methoxy-3-(1	21.6555	1097	The content of the retention time actually detected was not retrieved	rt_is_in_silico
846	2-Undecene, (E)-	21.6555	1097	The content of the retention time actually detected was not retrieved	rt_is_in_silico
847	7-Octen-4-ol, 2-methyl-	21.6555	1097	The content of the retention time actually detected was not retrieved	rt_is_in_silico
848	o-Guaiacol	21.689		1097	
849	Guaiacol	21.7		1098	
850	Pentanoic acid, butyl este	21.7227	1098	The content of the retention time actually detected was not retrieved	rt_is_in_silico
851	3-(Methylthio)propanoic	21.7227	1098	The content of the retention time actually detected was not retrieved	rt_is_in_silico
852	trans-Linalool oxide (fura	21.743	1086	1098	
853	3-Nonanol	21.754	1095	1098	
854	4-Nonanol	21.808	1088	1099	
855	2H-Pyran-2-one, tetrahy	21.817	1092	1099	
856	Methyl benzoate	21.87		1100	
857	Benzoic acid, methyl ester	21.915	1094	1101	
858	Butanoic acid, 2-methyl-,	21.9263	1101	The content of the retention time actually detected was not retrieved	rt_is_in_silico
859	6-Nonenal, (Z)-	21.9263	1101	The content of the retention time actually detected was not retrieved	rt_is_in_silico
860	2-Cyclohexen-1-one, 4,4	21.9263	1101	The content of the retention time actually detected was not retrieved	rt_is_in_silico
861	Furan, 3-(4-methyl-3-pe	21.9263	1101	The content of the retention time actually detected was not retrieved	rt_is_in_silico
862	2-Nonanone	21.94	1092	1101	
863	Caryophyllenyl alcohol	21.95		1101	
864	3-Hexen-1-ol, propanoa	21.962	1100	The content of the retention time actually detected was not retrieved	rt_is_in_silico
865	(Z,Z)-3,6-Nonadienal	21.962	1100	The content of the retention time actually detected was not retrieved	rt_is_in_silico
866	2-Undecene, (Z)-	21.9955	1102	The content of the retention time actually detected was not retrieved	rt_is_in_silico
867	Diallyl disulphide	21.999	1081	1102	
868	Thujone	22.0648	1103	The content of the retention time actually detected was not retrieved	rt_is_in_silico
869	(E)-1-Allyl-2-(prop-1-en	22.0648	1103	The content of the retention time actually detected was not retrieved	rt_is_in_silico
870	1-Nonen-4-ol	22.0648	1103	The content of the retention time actually detected was not retrieved	rt_is_in_silico
871	Decane, 2,6,8-trimethyl-	22.134	1104	The content of the retention time actually detected was not retrieved	rt_is_in_silico
872	2,2,6-Trimethyl-3-keto-6	22.186		1105	
873	Butanoic acid, 2-methyl-,	22.2033	1105	The content of the retention time actually detected was not retrieved	rt_is_in_silico
874	Ethanone, 1-(4,5-dihydro	22.2726	1106	The content of the retention time actually detected was not retrieved	rt_is_in_silico
875	3-Cyclohexene-1-metha	22.2726	1106	The content of the retention time actually detected was not retrieved	rt_is_in_silico
876	Disulfide, dipropyl	22.3418	1107	The content of the retention time actually detected was not retrieved	rt_is_in_silico
877	1,3,8-p-Menthatriene	22.353	1119	1107	
878	Unknown S	22.376		1107	
879	Propanoic acid, hexyl este	22.4111	1108	The content of the retention time actually detected was not retrieved	rt_is_in_silico
880	2H-Pyran-3(4H)-one, 6-e	22.4111	1108	The content of the retention time actually detected was not retrieved	rt_is_in_silico
881	2,6,6-Trimethylbicyclo[3.2	22.4111	1108	The content of the retention time actually detected was not retrieved	rt_is_in_silico
882	Phenol, 2,6-dimethyl-	22.4111	1108	The content of the retention time actually detected was not retrieved	rt_is_in_silico
883	Pentanoic acid, 3-methyl	22.4111	1108	The content of the retention time actually detected was not retrieved	rt_is_in_silico
884	Filifolone	22.42		1108	
885	Hexanoic acid, propyl est	22.445	1094	1108	

The warning information file

	A (Name)	B (reason)
1	Name	reason
2	n-Hexadecanoic acid	WARNING: This compound already exists in the database. Duplicates are not allowed.
3	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
4	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
5	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
6	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
7	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
8	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
9	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.
10	Phenylethyl Alcohol	WARNING: This compound already exists in the database. Duplicates are not allowed.

Warning information including:

WARNING: The compound was not found in the provided MSP file.

WARNING: This compound already exists in the database. Duplicates are not allowed.

WARNING: The RT value is out of the valid range.

WARNING: The synonym name has been changed to NIST Preferred Name.

2.2 Generating a Widely-Targeted SIM Method for Compound Detection（the *method generator* module）
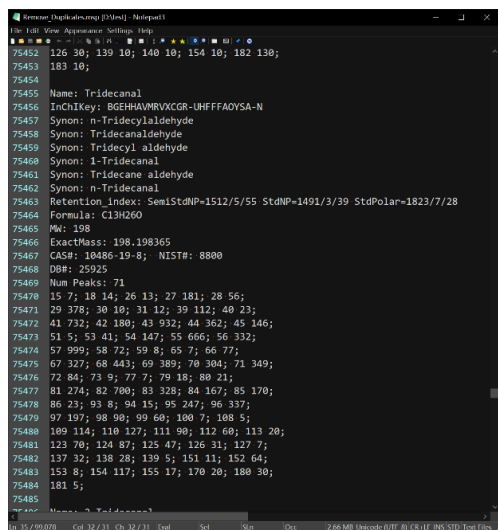
2.2.1 Data Preparation

Before using this software, it is necessary to prepare two input files. The input files can directly utilize the corresponding result files generated by the *library builder* module.
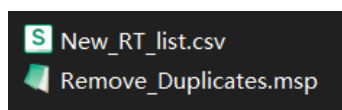
These input files should include the compound names and their corresponding RT (Retention Time) information.

	A	B
1	Name	RT
2	Acetaldehyde	1.496
3	Methanethiol	1.526
4	Ethane	1.5523
5	Ethyl Chloride	1.555
6	Formaldehyde	1.559
7	Propene	1.5612
8	Methyl Alcohol	1.5677
9	Methyl formate	1.5695
10	Ethylene oxide	1.5727
11	Dimethylamine	1.5753
12	Ethylamine	1.5773

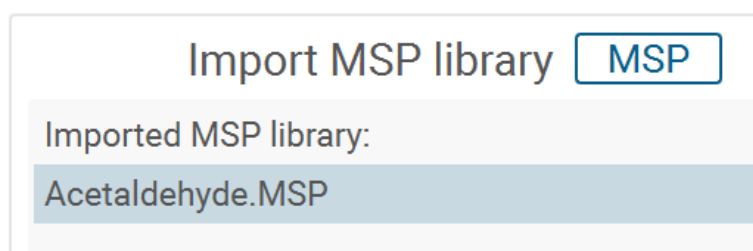In addition, you should also have a Mass Spectrometry (MS) information file in the MSP format.

2.2.2 Parameter Configuration

Import MSP library

To input an MSP file, simply click the 'MSP' button and select the desired MSP file.

Once selected, the interface will display all the selected file directories, confirming a successful input.

Import RT list: Import a list of compounds and their RT.

Set compound list: When "set compound list" is selected and a compound list is imported, the generated collection method will only contain qualitative ions of compounds in the list.

Maximum RT: Enter the end time of the temperature ramp program.

Solvent delay: Enter the start time for mass spectrometry detection, also known as the solvent delay time.

m/z range: The qualitative ions will be selected from within this range.

Ion intensity threshold: Ions with abundances lower than the maximum ion abundance multiplied by this threshold value will be excluded from the selection of qualitative ions.

RT window: When selecting qualitative ions, target compounds are compared for similarity with substances within the user-defined RT (Retention Time) window.

Similarity score threshold: When the similarity score is below the threshold of 0.85, two spectra are considered distinguishable. The default threshold is set to 0.85.

Prefer m/z threshold: M/Z values below this threshold will be assigned a lower weight in the calculation of the weighted score. The default threshold is set to 60.

Minimum ions number: This represents the minimum number of ions required for the selection of qualitative ions.

F_R factor : The 'Ratio of Peak Pairs' term is considered in the similarity score calculation only if the number of ions is greater than the specified threshold. The F_R factor is typically set to be consistent with the minimum number of ions. For more specific and detailed information, please refer to the official documentation of the AMDIS software.

SIM segmentation parameters:

Maximum SIM segments: The maximum number of segments allowed in the SIM (Selected Ion Monitoring) acquisition method. Default: 99.

Minimum dwell time (ms): The allowed minimum dwell time. Default: 10 ms.

Data points per second: Adjust the number of data points per second. If the calculated dwell time based on the specified data points per second falls below the minimum dwell time, the data points per second will be decreased to ensure that the dwell time remains greater than or equal to the minimum dwell time. The default setting is 2.

Export to Agilent data acquisition method (xml format file): Select this option to export the XML-formatted file used by Agilent data acquisition software.

Set export path: Click the 'Save' button, choose a saving path, and the processed results will be saved to this directory.

2.2.3 Generated Widely-Targeted SIM Method
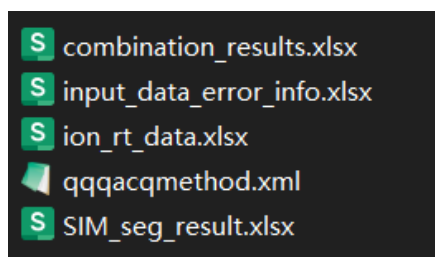
combination_results: This displays the combined information of target compounds after merging.

	RT	Ion_Combination	Note	Similar_Compound_List	SCL_Note
Acetaldehyde	1.496	[43, 44]		['Methyl formate']	
Methanethiol	1.526	[47, 48]		[]	

input_data_error_info: This file highlights discrepancies in the input data that led to improper identification and analysis.

ion_rt_data: This file displays the results of the final compounds and their qualitative ions.

The content of this file is identical to the 'combination_results' file, but it is in a different format to make it more user-friendly for other purposes.

	RT	ion
Acetaldehyde	1.496	43
Acetaldehyde	1.496	44
Methanethiol	1.526	47
Methanethiol	1.526	48
Ethyl Chloride	1.555	64
Ethyl Chloride	1.555	66
Propene	1.5612	41
Propene	1.5612	40
Propene	1.5612	37
Propene	1.5612	39

SIM_seg_result: This file presents the results of the SIM segments.

qqqacqmethod.xml: The XML-formatted file used by Agilent data acquisition software.

2.3 Data Analysis (the *data analyzer* module)

2.3.1 Data Preparation

2.3.1.1 Mass Spectrometry File Format Conversion

Before data analysis, we need converse raw data to open formats (.mzML/.cdf) by open access application.

Data conversion to open format (.mzML)

Conversion with MSConvert

Download and install ProteoWizard from here (http://proteowizard.sourceforge.net/downloads.shtml) .

After installation, from the Start Menu, click the ProteoWizard folder and open MSConvert.

Click Browse and select file(s) for conversion. Then click Add to add them to the MSConvert workflow.

Choose an Output Directory.

Under Options, choose mzML (prefered) or mzXML for output format, 32-bit for binary encoding precision, SIM as spectra and uncheck Use zlib compression.

Click Add to add the filter.

Save the parameters for the next conversion. This will save you some time and prevent misconfiguration. In Presets (left bottom), click on Save Presets, and select "Save as default for the format".

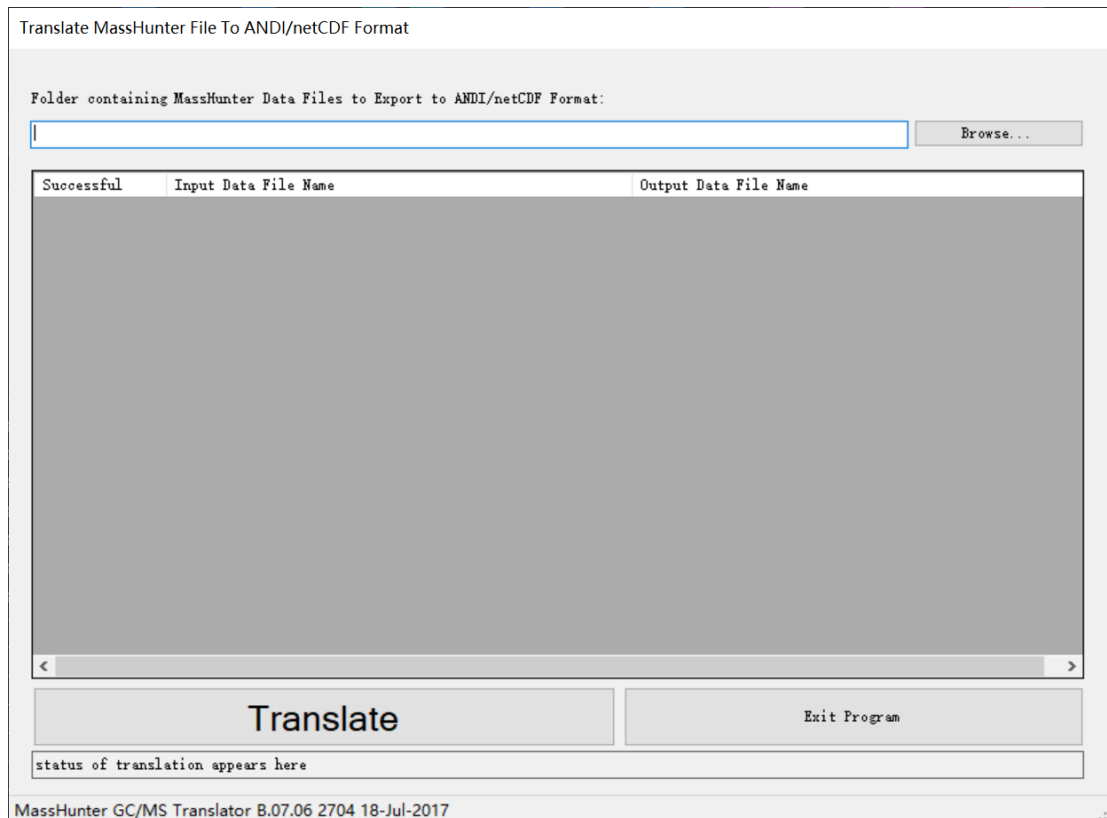Click on Start. Check your folder for the new .mzML files. Verify that these files open properly in Insilicos or TOPP View (OpenMS http://www.openms.de/).
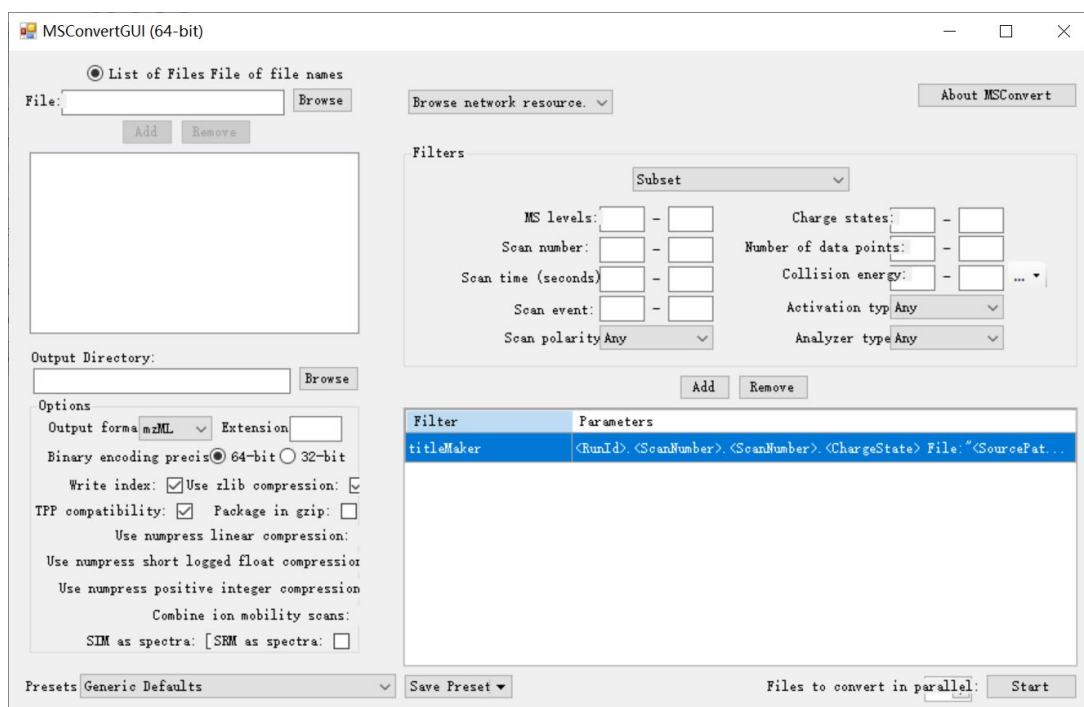
Data conversion to open format (.cdf)

Agilent: Click Browse and select folder containing file(s) for conversion.
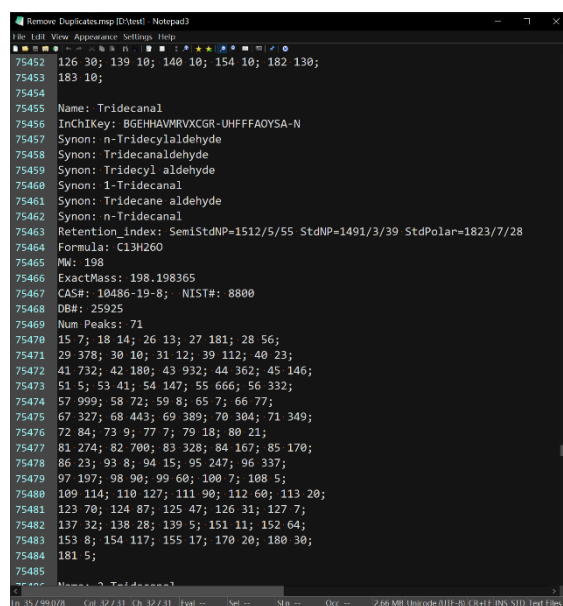
Click Translate

The CDF files are generated in the same folder as the raw data files.

For data processing methods from other vendors, please refer to the relevant data conversion instructions.

2.3.1.2 Compound Library (MSP) for identification

Input an MSP file that contains all the target metabolites. The input files can directly utilize the corresponding result files generated by the *library builder* module.

2.3.1.3 Optional: Retention Time Information

To identify compounds using actual measured retention times (RT), you will need the required files. The input files can directly utilize the corresponding result files generated by the *library builder* module.

	A	B
1	Name	RT
2	Acetaldehyde	1.496
3	Methanethiol	1.526
4	Ethane	1.5523
5	Ethyl Chloride	1.555
6	Formaldehyde	1.559
7	Propene	1.5612
8	Methyl Alcohol	1.5677
9	Methyl formate	1.5695
10	Ethylene oxide	1.5727
11	Dimethylamine	1.5753
12	Ethylamine	1.5773
13	2-Propenal	1.5779
14	Ethyl formate	1.5791
15	Butane, 2-methyl-	1.5798
16	Ethyl ether	1.5808

To identify compounds using Kovats Index calculation, you will need the necessary files.

	A	B
1	Num	RT (min)
2	8	5.219
3	9	9.34
4	10	15.177
5	11	21.877
6	12	28.764
7	13	35.514
8	14	41.988
9	15	48.144
10	16	53.937
11	17	59.401
12	18	63.787
13	19	64.851
14	20	65.484

2.3.2 Parameter Configuration

2.3.2.1 Data Import

Select the appropriate option based on the transformed file format.

File   Re-analysis

Open data   ▶   mzML

Open project   cdf
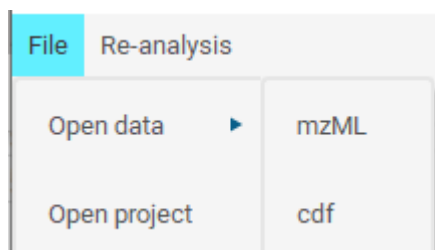
2.3.2.2 Peak Detection

DataAnalyzer   ×

Peak detection and compound perception

Smoothing factor: 5 ⏶⏷   ?

Peak filter factor: 10.0 ⏶⏷   ?

Bin number: 0.5 ⏶⏷   ?

Next

Smoothing factor: A high smooth factor can make the peaks smoother, but it may also lead to the loss of low-abundance peaks. The default value is set to 5.

Peak filter factor: A high peak filter factor can remove low-abundance peaks. If this value exceeds 10, it will significantly extend the program's runtime. The default setting is 10.

Bin number: When using a low data point acquisition mode, such as two points per second, it is recommended to set a wide peak grouping width, for example, 0.5. For more specific and detailed information, please refer to the official documentation of the AMDIS software.

2.3.2.3 Qualitative Analysis

In RI mode

Library search window: Configure the retrieval target compound window in RI mode. The program will compare all compounds within the specified matching window.

Maximum RI: The maximum RI (Retention Index) value.

Peak group Match weight: Peak group forward retrieval matching score weight.

Peak group Reverse Match weight: Peak group reverse retrieval matching score weight

Minimum ions number in peak group for identification: The minimum number of ions required for a peak group.

Similarity score threshold: The integrated similarity score threshold, where only compounds with scores above this threshold will be considered as candidate compounds.

Calculate RI penalty: Selecting this option will penalize candidate compounds with a significant difference in RI values.

RI window: Set the RI window range in which no penalty will be applied.

RI window scale: The RI penalty window will be scaled linearly by this factor. Setting it to 0 disables this feature. The default value is 2.

Level factor: A higher number indicates a more severe penalty.

Maximum penalty: Set the maximum penalty score.

No RI penalty: Peak groups without RI (Retention Index) will receive a penalty.

Inaccurate RI threshold: RI values below this threshold will be affected by the Inaccurate RI level factor.

Inaccurate RI level factor: The specified range for the Inaccurate RI threshold mentioned above is used for the following purposes.

In RT mode

Library search window: Configure the retrieval target compound window in RT mode. The program will compare all compounds within the specified matching window.

Peak group Match weight: Peak group forward retrieval matching score weight.

Peak group Reverse Match weight: Peak group reverse retrieval matching score weight.

Minimum ions number in peak group for identification: The minimum number of ions required for a peak group.

Similarity score threshold: The integrated similarity score threshold, where only compounds with scores above this threshold will be considered as candidate compounds.

Calculate RT penalty: Selecting this option will penalize candidate compounds with a significant difference in RT values.

RT window: Set the RT window range in which no penalty will be applied.

Level factor: A higher number indicates a more severe penalty.

Maximum penalty: Set the maximum penalty score.

No RT penalty: Peak groups with retention times (RT) lower than this value will not receive a penalty for mismatch.

Choose the mode for not entering retention time information.

Peak group Match weight: Peak group forward retrieval matching score weight.

Peak group Reverse Match weight: Peak group reverse retrieval matching score weight.

Minimum ions number in peak group for identification:

The minimum number of ions required for a peak group.

Similarity score threshold: The integrated similarity score threshold, where only compounds with scores above this threshold will be considered as candidate compounds.

2.3.3 Main Workspace Overview
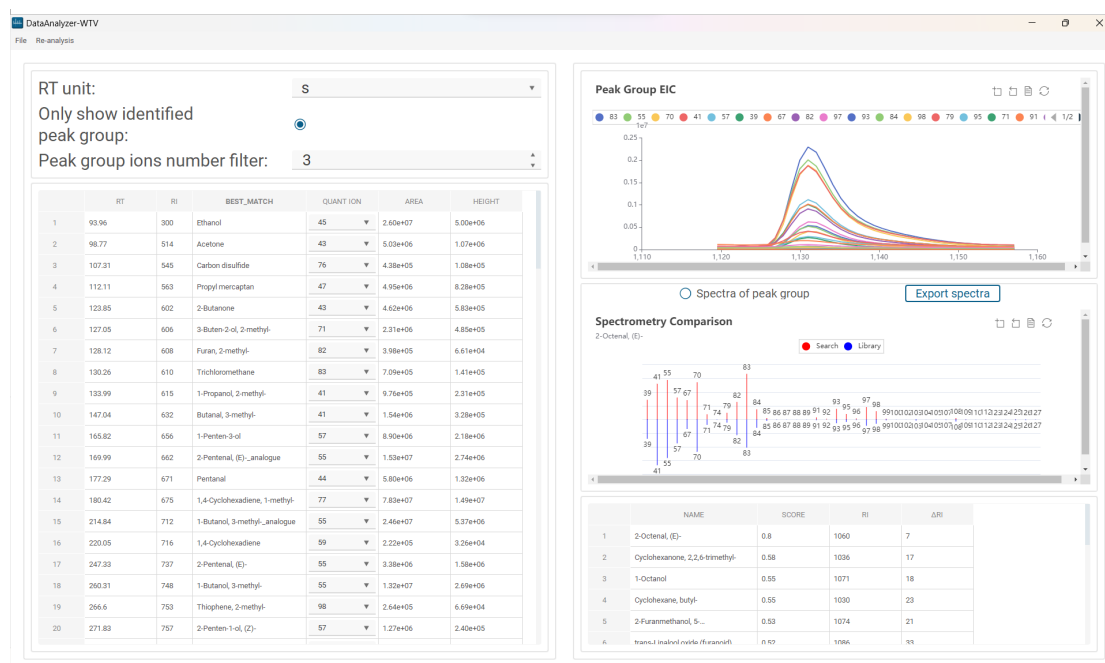
RT unit: Users can use this option to switch the RT unit between min and s.

Only show identified peak group: After the user makes a selection, the result interface will only display peak groups that can match candidate compounds under the current threshold.

Peak group ions number filter: Users can use this feature to filter peak groups that contain a number of ions not less than the current setting.

Results window:

The left panel displays the detected components, including their RT, RI, annotation results, quantitative ions, peak areas and heights. Users can also define the unit of

displayed RT, whether to show only qualified compounds, and the minimum ion number for showed components. The right panel displays the extraction ion currents (EICs), spectra comparison, and possible qualitative results for the selected component. Users can export qualitative results as a CSV file.

3 Acknowledgements