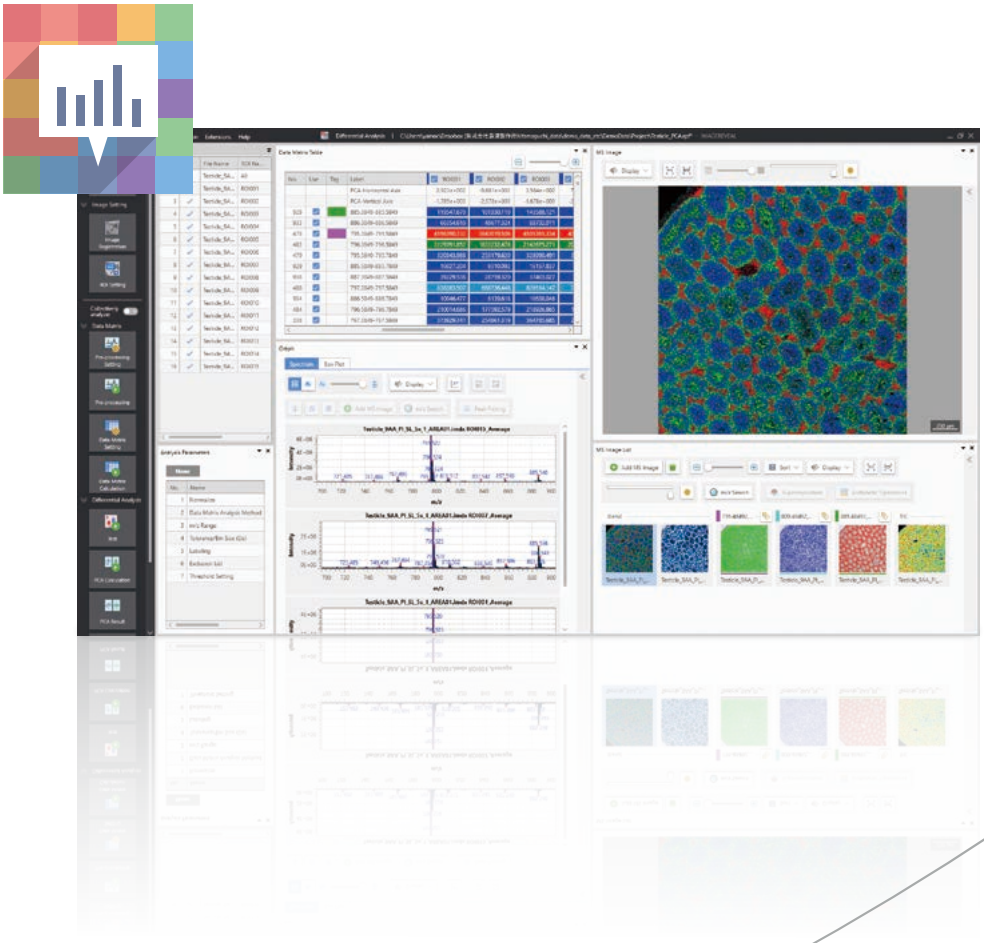
SHIMADZU
Excellence in Science

C146-E400

Mass Spectrometry Imaging Data Analysis Software

IMAGEREVEAL MS Ver.1.1



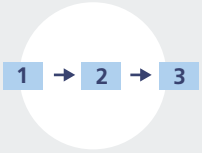
Simplifying Routine Analysis

Are you worried about wasting time or valuable data?
Automatically uncover important information from
large amounts of data with IMAGEREVEAL MS.

IMAGEREVEAL™ MS Workflow

The results can be checked after each analysis, so that e.g. the parameters can be changed and the analysis re-run if the results are not as desired.

Key Features



Simple data processing in as few as 3 steps

"Collective Analysis" function consisting of differential analysis and image analysis. Optimal for daily routine work.

Multiple analysis modes

Choose an analysis method using up to 5 analysis modes. Data can be analyzed in multiple ways through a simple workflow.

Analysis of data in general formats

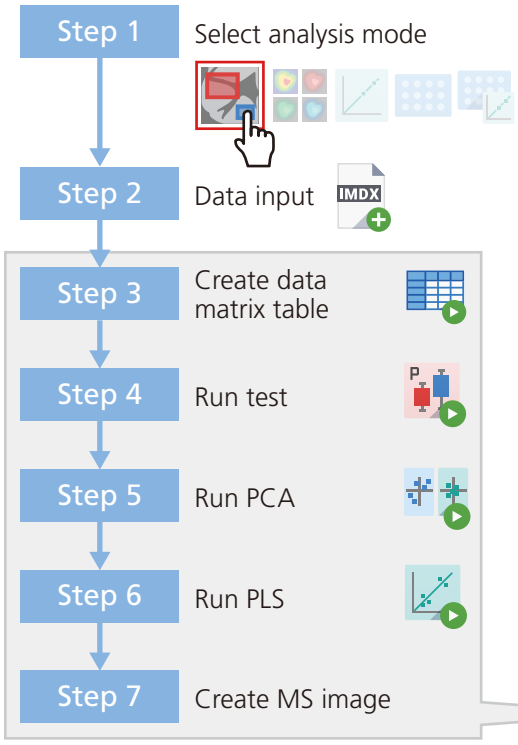
～ Includes common data formats used in MS imaging ～

Using the included data conversion tool "IMDX Converter", analysis can be carried out on data in the common MS imaging formats imzML and Analyze7.5.

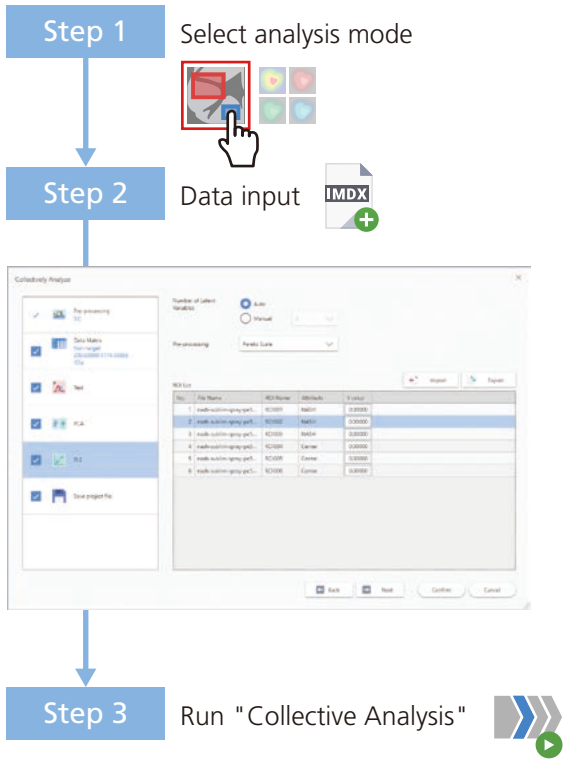
Processing in as few as 3 steps with the "Collective Analysis" mode

Automatically obtain MS images with distinctive characteristics thanks to the "Collective Analysis" mode with pre-set parameters. This is a highly convenient feature when you need to process a lot of data in the same way. The user can create data matrix tables from differential analysis and/or image analysis, carry out statistical data analysis, and obtain MS images all in one step.

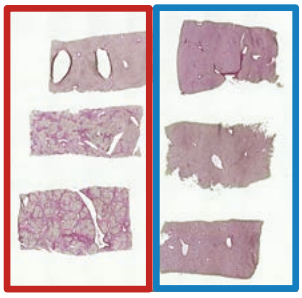
Conventional analysis workflow



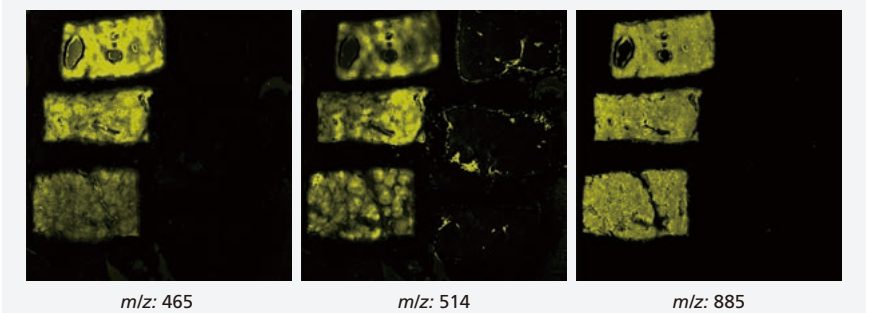
Workflow with "Collective Analysis"



Examples using "Collective Analysis"



Sections to be analyzed



Automatically selected MS images

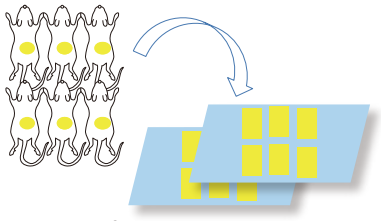
Using the "Collective Analysis" mode, MS images where the NASH tissue shows peculiarities with respect to normal tissue are automatically selected

Multiple analysis modes Introducing 3 examples of analysis modes

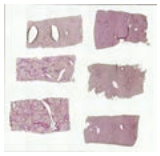
Analysis of mouse liver for NASH (Non-Alcoholic Steatohepatitis)

What is NASH?

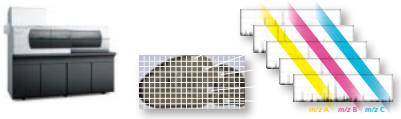
NASH (Non-Alcoholic Steatohepatitis) refers to one type of fatty liver disease that is not related to alcohol consumption.



The livers of mice with NASH are cut into serial sections



A stained image is created from the serial sections

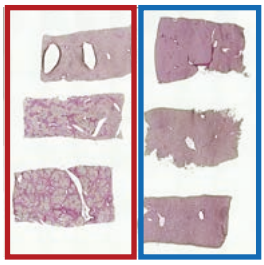


MS imaging data is obtained from the serial sections

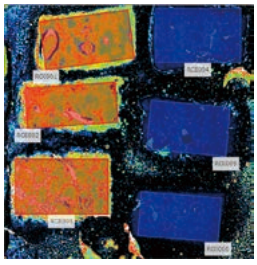
1 Finding molecules unique to NASH tissue

Differential Analysis

Using statistical methods and comparing the average spectra of the ROIs, find molecules that are causing the differences between the ROIs.



NASH tissue Normal tissue

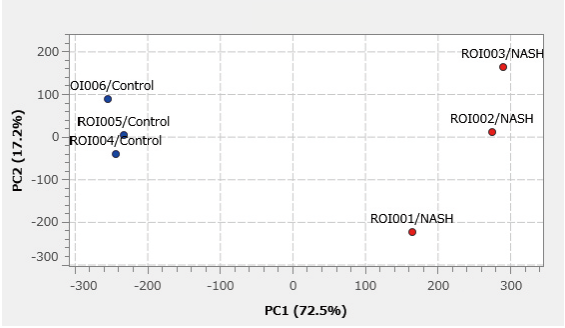


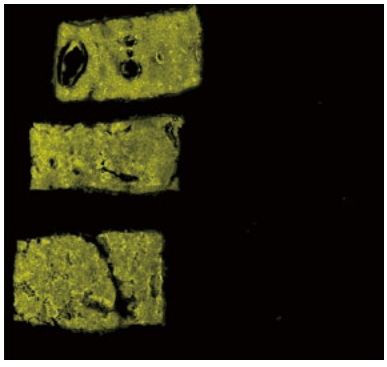
Apply settings to separate ROIs according to attributes

Run PCA (principal component analysis)

※Method to visualize characteristics of the ROI

Scatter graph:





MS image of a compound which only appears in large quantities in the NASH tissue

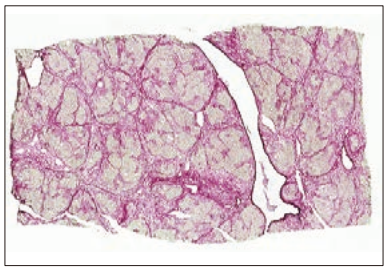
MS images are obtained where NASH tissue and normal tissue show a different distribution

Further analysis can be carried out using the test functions, PLS (partial least squares) function, etc.

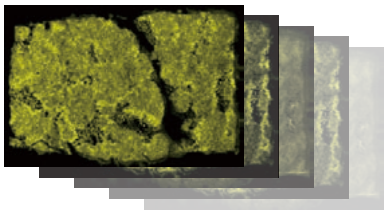
2 Finding molecules with similar distributions to the stained image

Image Analysis

Using statistical methods and comparing each *m/z* distribution, find molecules with distinctive distributions.



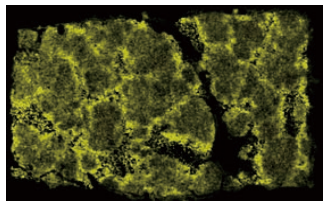
Stained image (Sirius Red stain)



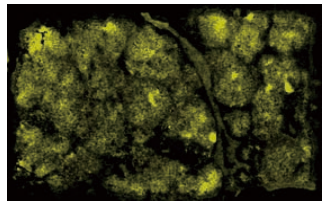
MS image data

Run Similar Image Extraction

※"Similar image extraction" is a method to search through MS image data and find MS images showing similar distributions to the stained image



MS image showing a compound abundant in a fibrotic area



MS image showing a compound abundant in a normal area

MS images resembling the stained image are obtained

Further data analysis can be carried out using "Image Classification", "Segmentation", etc.

3 Creating an MS image showing the concentration distribution of the target molecule

Quantitative Analysis

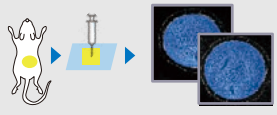
Using calibration curves, convert the intensity of the target molecule in the ROI into a concentration value.

【Preparing the unknown sample】

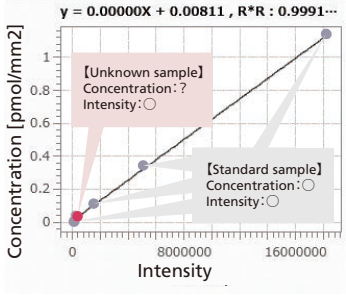
Liver section from a mouse that has been administered a drug

Sample provided by the Tottori University Chromosome Engineering Research Center

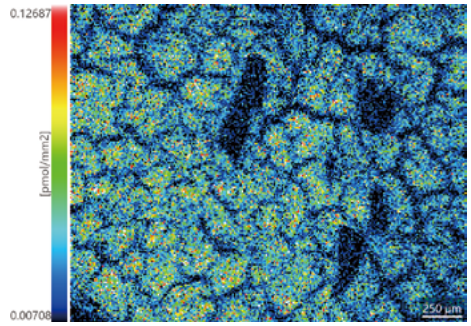
【Preparing the standard sample】



Dripping the same drug onto a liver section from a mouse that did not receive the drug



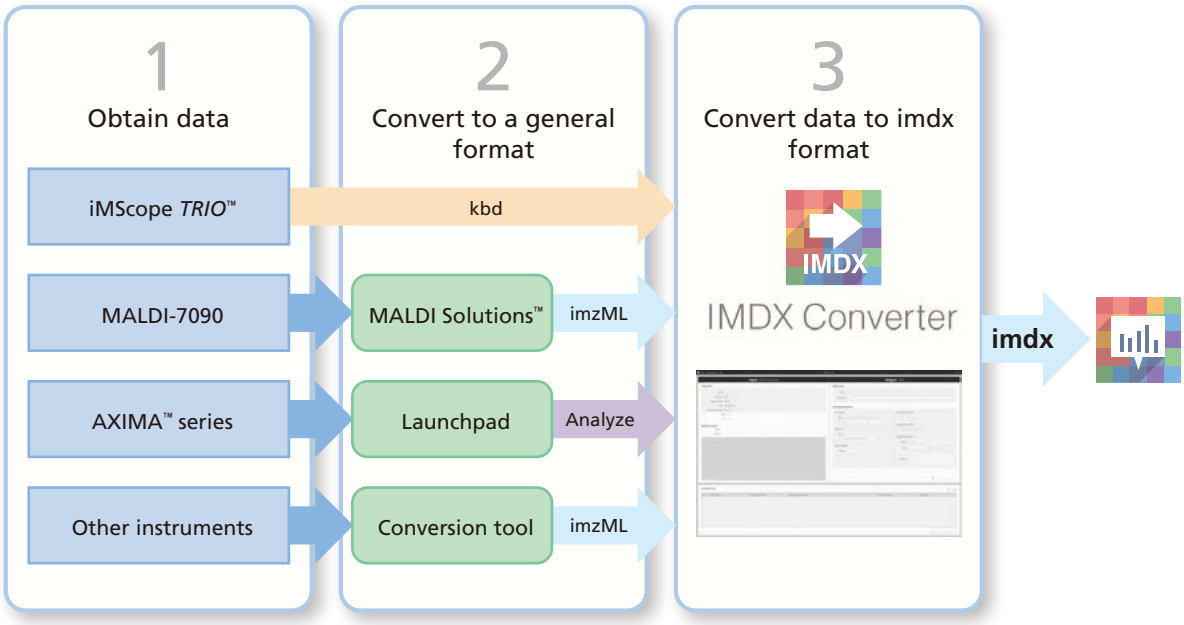
Create a calibration curve using liver sections with known concentrations of the drug



MS image with intensities converted into concentrations

An MS image is obtained showing the amount of the drug that has reached the liver

Processing of general data formats with IMDX Converter



Other features

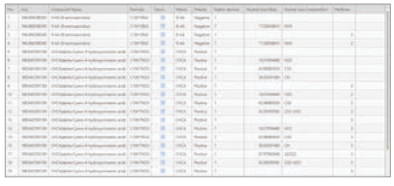
Target analysis / Non-target analysis

Target analysis Analysis of only target *m/z* values based on a list of e.g. lipids or metabolites. It is also possible to create a custom list.

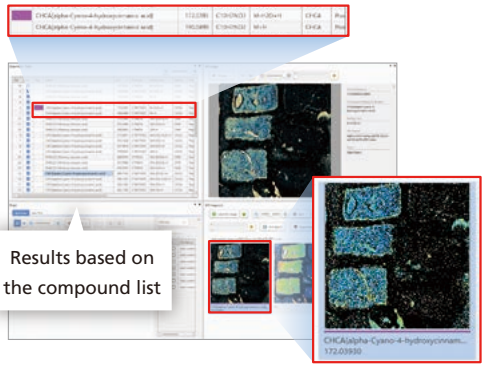
Non-target analysis Analysis over all *m/z* within the specified MS range. Useful for checking which distinctive *m/z* values are contained within the range.

Compound list

This is a table containing information such as compound names, *m/z* values, and adduct ions. Using this table, you can associate compounds with *m/z* values to carry out MS image analysis.



Compound list



Simultaneous processing of multiple MS image data files

It is possible to process multiple data files all together, and by inputting all the data at once, it is simple to compare the images. Data analysis can be carried out on up to a few hundred GB without splitting up the data.

License and feature comparison

		Basic analysis	Quantitative analysis	Differential analysis	Image analysis	Screening/ Screening (quantitative)*
	Basic license					
	Imaging license					
	Screening license					
	Full license					
Statistical analysis	t-test/u-test/ANOVA/basic statistics	○	—	○	—	○
	PCA	—	—	○	—	○
	PLS					
	Similar image extraction	—	—	—	○	—
	Image classification					
	Segmentation					
Spectral processing	Peak picking	○	—	○	○	○
	Normalization	○	○	○	○	○
	MS/MS spectrum normalization					
	Mass correction					
	Target analysis/ Non-target analysis	○	—	○	○	○
MS image	Filtering	○	○	○	○	○
	Interpolation					
	Arithmetic operations					
	Superimposition					
Image settings	Alignment (Linear/Non-linear)					
	ROI settings					
Other	Simultaneous processing of multiple data sets					
	Collective analysis	—	—	○	○	—
	Calibration curves	—	○	—	—	○
	Tagging	○	—	○	○	○
	Data conversion: imzML→imdx/Imdx→imzML	○	○	○	○	○

It is possible to upgrade from the basic license to any of the other 3 licenses, or from an imaging license or a screening license to a full license.

Screening/Screening (quantitative) is an analysis mode which automatically sets 1 ROI to 1 measurement point. It is convenient when measuring samples which differ at each measurement point. Differential analysis between measurement points can be carried out with "screening" and quantitative analysis between measurement points can be carried out with "screening (quantitative)".

A 30-day trial version of IMAGEREVEAL MS with all functions is available for download at the below website.
https://www.shimadzu.com/an/lifescience/imaging/reveal.html

Shimadzu IMAGEREVEAL Search

Operating environment

OS	Windows® 10 Professiona 64 bit English/Japanese
CPU	Intel® Core™ i7 or Intel® Xeon®
Memory	32 GB
Storage	The software uses both data files and temporary data storage. Storage equivalent to at least 5 times the size of the file being processed is required.

For more details about recommended PC specifications, please make an inquiry

Compatible formats

It is possible to convert from iMScope data files in kbd format, or from the general MS imaging formats imzML or Analyze7.5, to .imdx files that can be read by IMAGEREVEAL MS.

Caution: Certain pretreatment methods or creation of samples to obtain or process data with this software may require license permission from a third-party patent holder. (Installation of this software does not constitute such permission.) As regards the necessity of licensing from third-party patent holders, we recommend consultation with an expert or the holder of the patent rights.

This software was developed as a result of collaborative research with Kyushu University's Innovation Center for Medical Redox Navigation and Mitsubishi Tanabe Pharma Corporation.

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