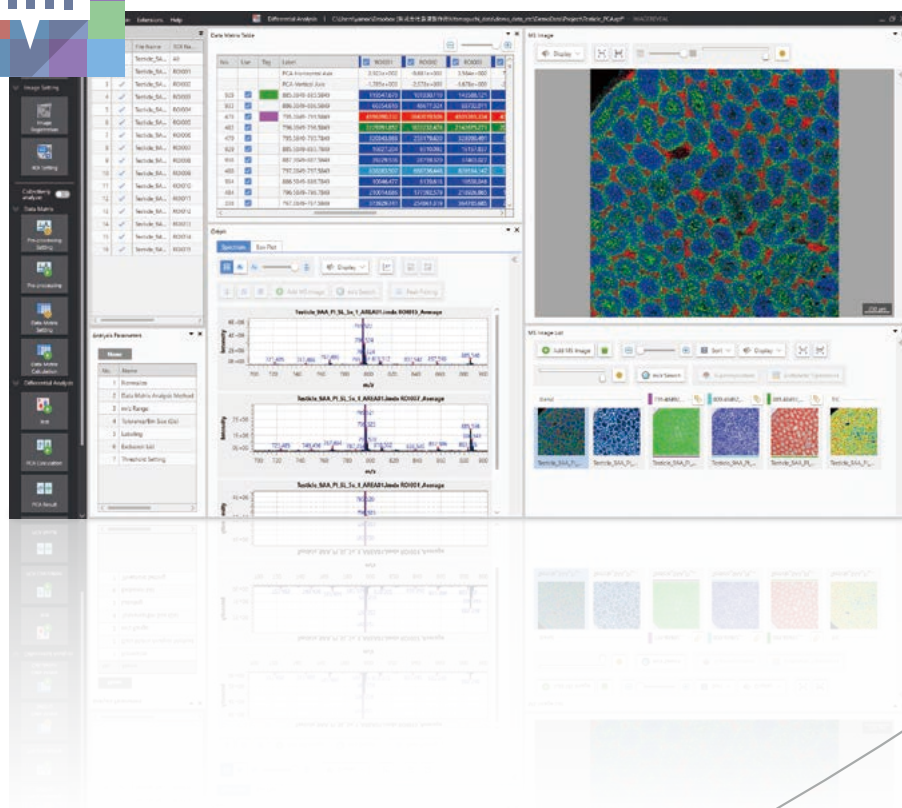


Mass Spectrometry Imaging Data Analysis Software

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.

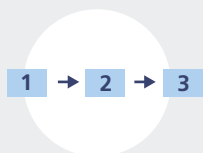


IMAGEREVEAL™ MS Workflow



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.



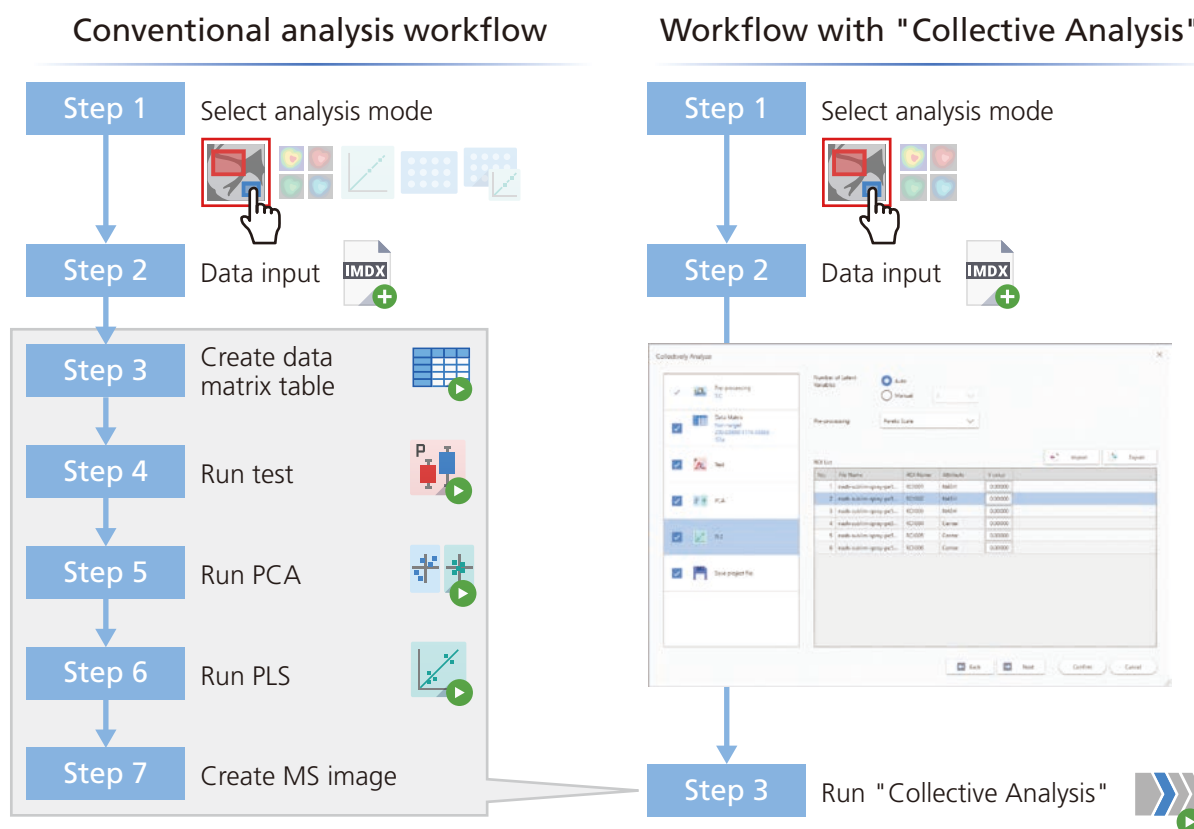
Analysis of data in general formats

~ Includes common data formats used in MS imaging ~

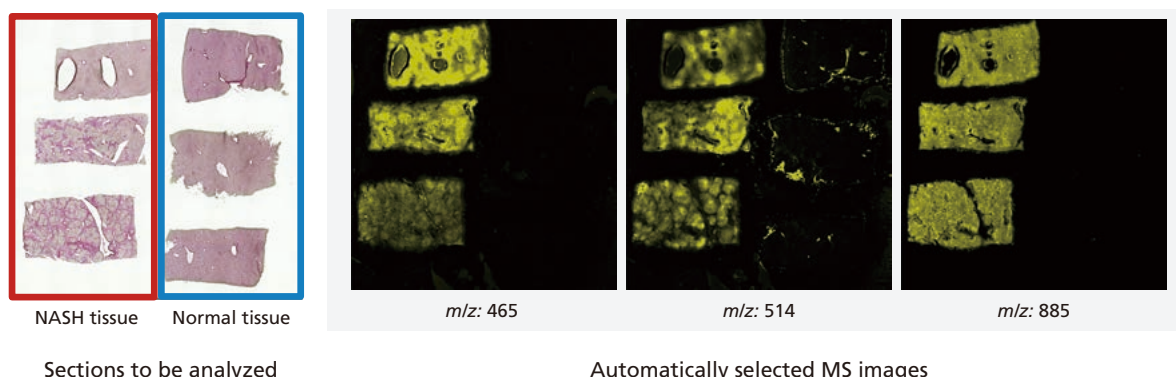
Using the included data conversion tool "IMDX Converter", analysis can be carried out on data in the common MS imaging formats imzML and Analyze7.5.

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.



Examples using "Collective Analysis"



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

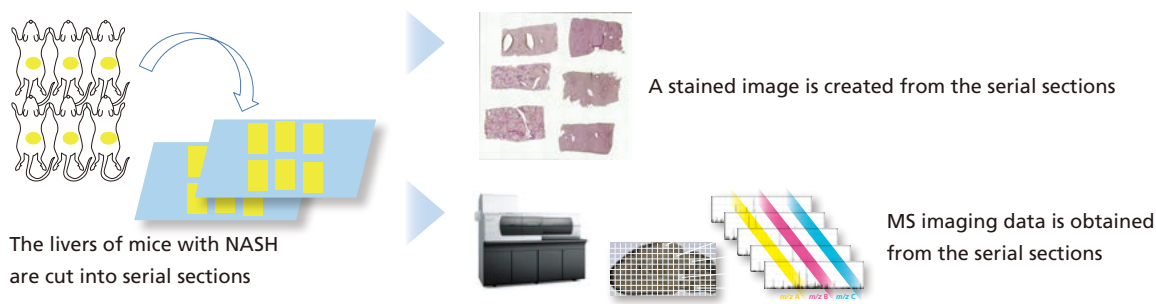
Multiple analysis modes

Introducing 3 examples of analysis modes

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

What is NASH?

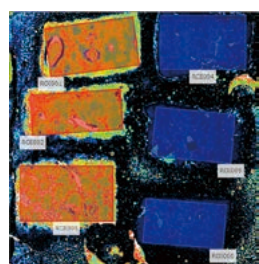
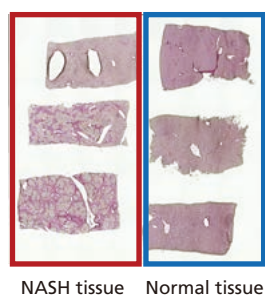
NASH (Non-Alcoholic Steatohepatitis) refers to one type of fatty liver disease that is not related to alcohol consumption.



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.

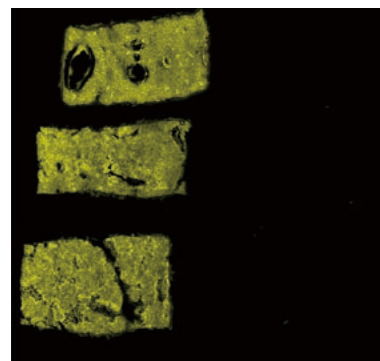


Apply settings to separate ROIs according to attributes



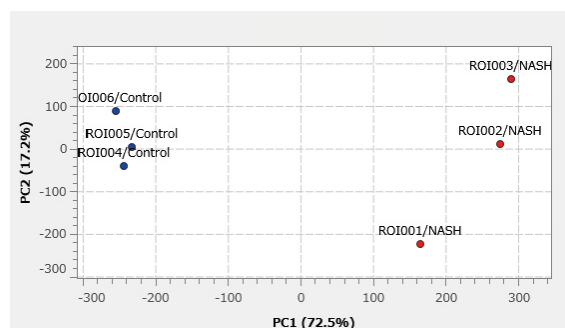
Run PCA (principal component analysis)

※ Method to visualize characteristics of the ROI



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

Scatter graph:



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

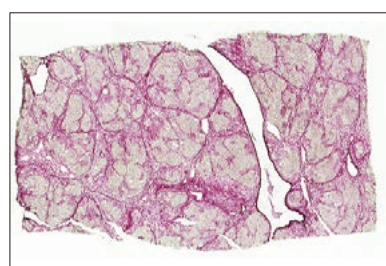
Further analysis can be carried out using the test functions, PLS (partial least squares) function, etc.



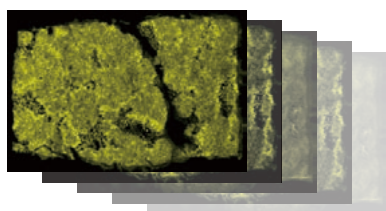
2 Finding molecules with similar distributions to the stained image

Image Analysis

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



Stained image (Sirius Red stain)

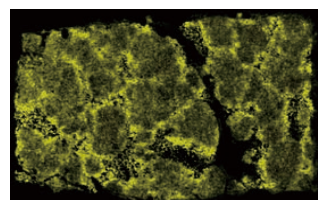


MS image data

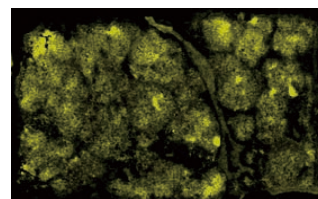


Run Similar Image Extraction

※ "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

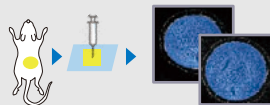
Using calibration curves, convert the intensity of the target molecule in the ROI into a concentration value.

【Preparing the unknown sample】



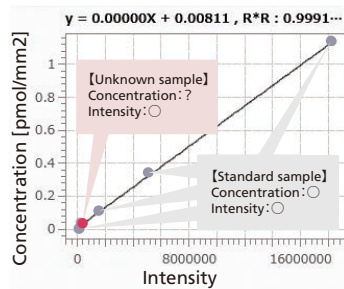
Liver section from a mouse that has been administered a drug

【Preparing the standard sample】

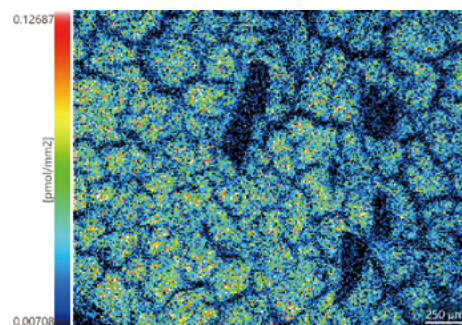


Dripping the same drug onto a liver section from a mouse that did not receive the drug

Sample provided by the Tottori University Chromosome Engineering Research Center



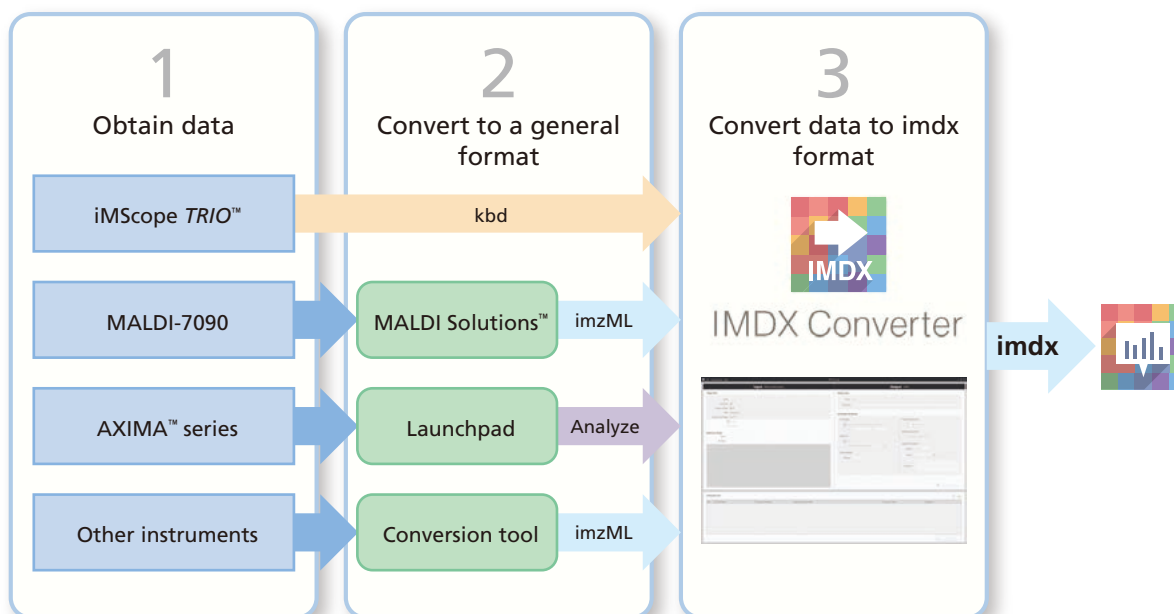
Create a calibration curve using liver sections with known concentrations of the drug



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

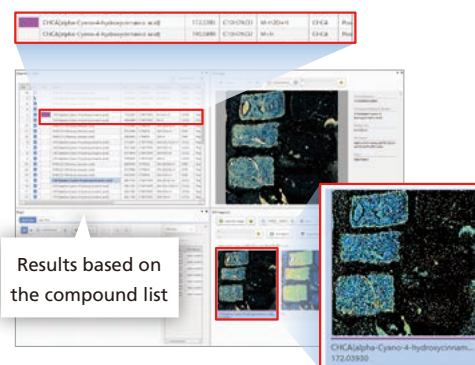
Analysis over all m/z within the specified MS range. Useful for checking which distinctive m/z values are contained within the range.

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 Name	m/z	Adduct	Other Parameters
CHCA/Alpha-Cyano-4-hydroxycinnam...	173.09959	[M+H] ⁺	...
...	...	...	...

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 license										
	Imaging license										
	Screening license										
	Full license										
		Basic analysis	Quantitative analysis	Differential analysis	Image analysis	Screening/ Screening (quantitative)*					
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 Professional 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.

IMAGEREVEAL, iMScope TRIO, AXIMA and MALDI Solutions are trademarks of Shimadzu Corporation.
 Windows is a registered trademark or trademark of Microsoft Corporation in the USA and other countries.
 Intel, Intel Core and Xeon are trademarks of Intel Corporation or its subsidiaries.

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.



Shimadzu Corporation

www.shimadzu.com/an/

For Research Use Only. Not for use in diagnostic procedures.

This publication may contain references to products that are not available in your country. Please contact us to check the availability of these products in your country.

Company names, products/service names and logos used in this publication are trademarks and trade names of Shimadzu Corporation, its subsidiaries or its affiliates, whether or not they are used with trademark symbol "TM" or "®".

Third-party trademarks and trade names may be used in this publication to refer to either the entities or their products/services, whether or not they are used with trademark symbol "TM" or "®".

Shimadzu disclaims any proprietary interest in trademarks and trade names other than its own.

The contents of this publication are provided to you "as is" without warranty of any kind, and are subject to change without notice. Shimadzu does not assume any responsibility or liability for any damage, whether direct or indirect, relating to the use of this publication.