

MarkerView™ Software for Metabolomic and Biomarker Profiling Analysis

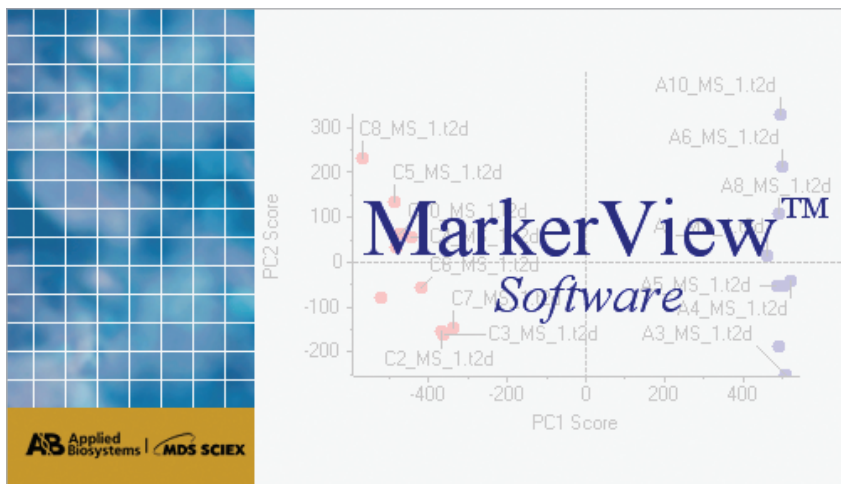
Overview

MarkerView software is a novel program designed for metabolomic applications and biomarker profiling workflows.

Using sophisticated statistical analysis and graphics tools, MarkerView software allows you to rapidly review data acquired on all Applied Biosystems/MDS SCIEX mass spectrometers to determine up- and down-regulation of endogenous species in complex samples. With statistics capabilities including principal component analysis and t-tests, you can easily mine data resulting from experiments where the sample groupings are known ahead of time (classified), experiments where you have no knowledge of the inherent sample groupings prior to analysis (non-classified), or a combination of the two. After data analysis, MarkerView software provides report generation capabilities so that you can easily track your work and record putative biomarkers that have been found.

Key Features

- Import multiple types of data acquired on any Applied Biosystems/MDS SCIEX mass spectrometer, including both ESI- and MALDI-based platforms



- Perform chromatographic and spectral peak picking to find true peaks in complex samples
- Align mass and retention time automatically to compensate for minor variations, ensuring that identical compounds in different samples are accurately compared
- Process data using classified and/or non-classified workflows with principal component analysis as well as t-tests to accelerate your discovery of new biomarkers
- Link back to raw mass spectra and extracted ion chromatograms to support identification of found putative biomarkers
- Automatically create reports on potential biomarkers and export data to third-party statistical packages for additional data-mining

Peak Picking and Alignment

MarkerView software uses sophisticated processing algorithms that accurately find peaks in complex data sets. Data alignment by the software compensates for minor variations in both mass and retention time values, ensuring that identical compounds in different samples are accurately compared to one another (Figure 1). Subsequent normalization of the data accounts for sample to sample variation, such as sample size or injection volume, and provides more precise results. MarkerView software can process data acquired by LC/MS, MALDI/MS, LC/MALDI/MS, flow injection, and/or direct infusion from all Applied Biosystems/MDS SCIEX mass spectrometers.

Statistical Analysis Tools

Principal Component Analysis

For data acquired using non-classified workflows, MarkerView™ software allows processing using principal component analysis (PCA).

Additionally, it offers the flexibility to use different scaling algorithms, such as Mean Centering, Autoscaling, and Pareto scaling, providing more flexibility in data analysis. PCA is an unsupervised multivariate statistical analysis method that compares data across multiple samples, revealing groupings among data sets and then

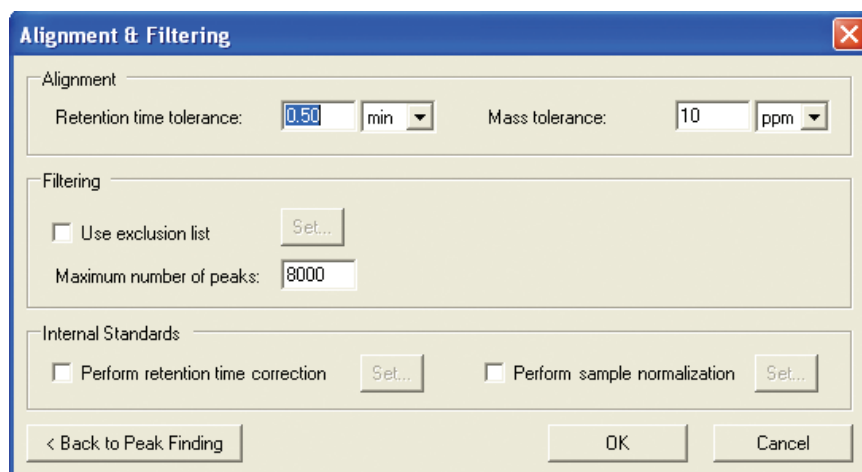


Figure 1. The Alignment & Filtering dialog box minimizes spectral interference and compensates for minor variations in mass and retention time, automatically ensuring that identical compounds in different samples are accurately compared.

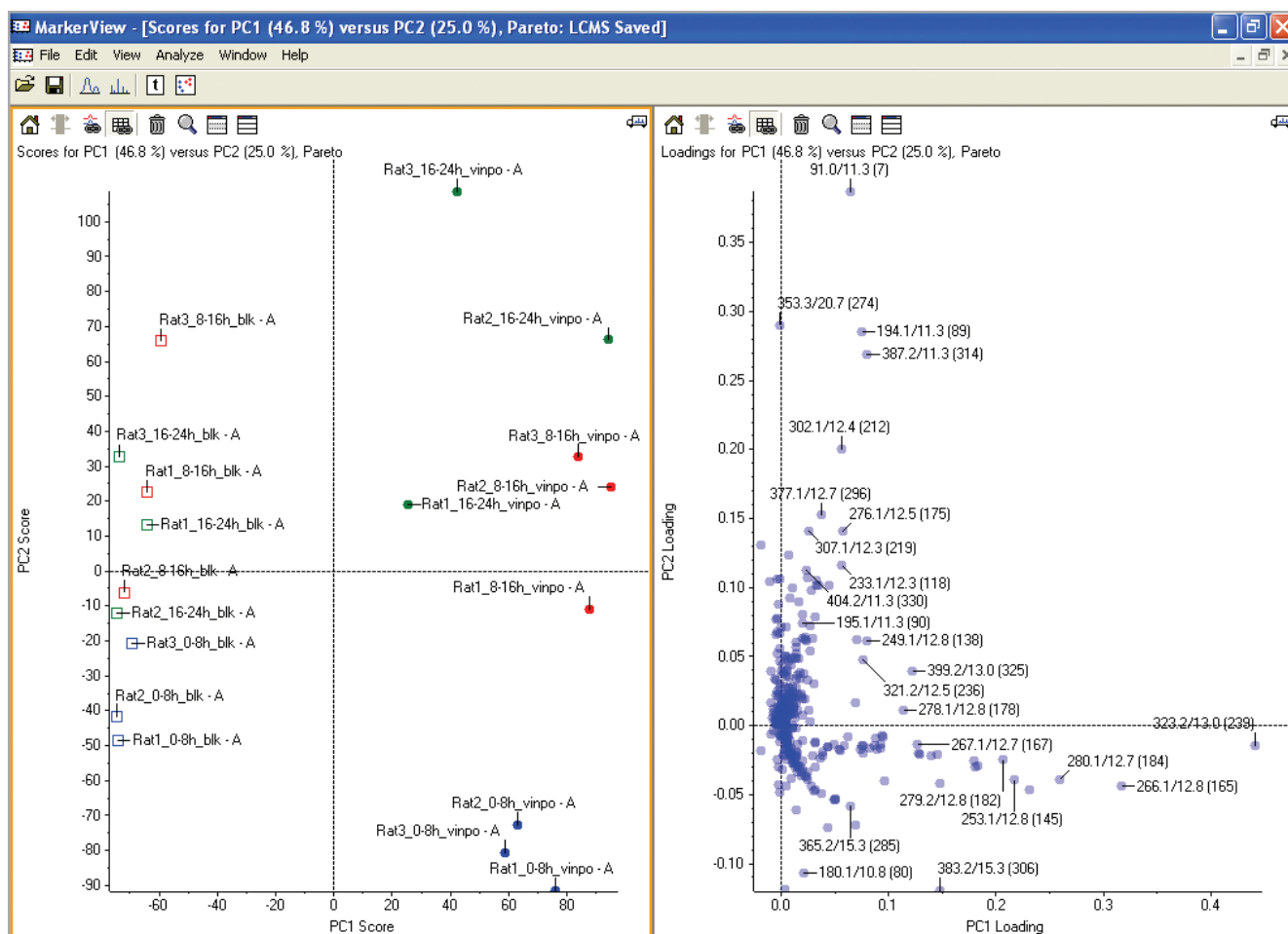


Figure 2. Principal Component Analysis shows groupings in samples based on drug dosing. In the Scores plot shown at left, open rectangles are from animals that were not dosed and closed circles are from drug-dosed animals. These samples clearly separate on the basis of drug dosing. Additionally, the animals that received the drug also showed separation on the basis of inherent diurnal differences. The Loadings plot shown on the right highlights the compounds responsible for the groupings within the samples.

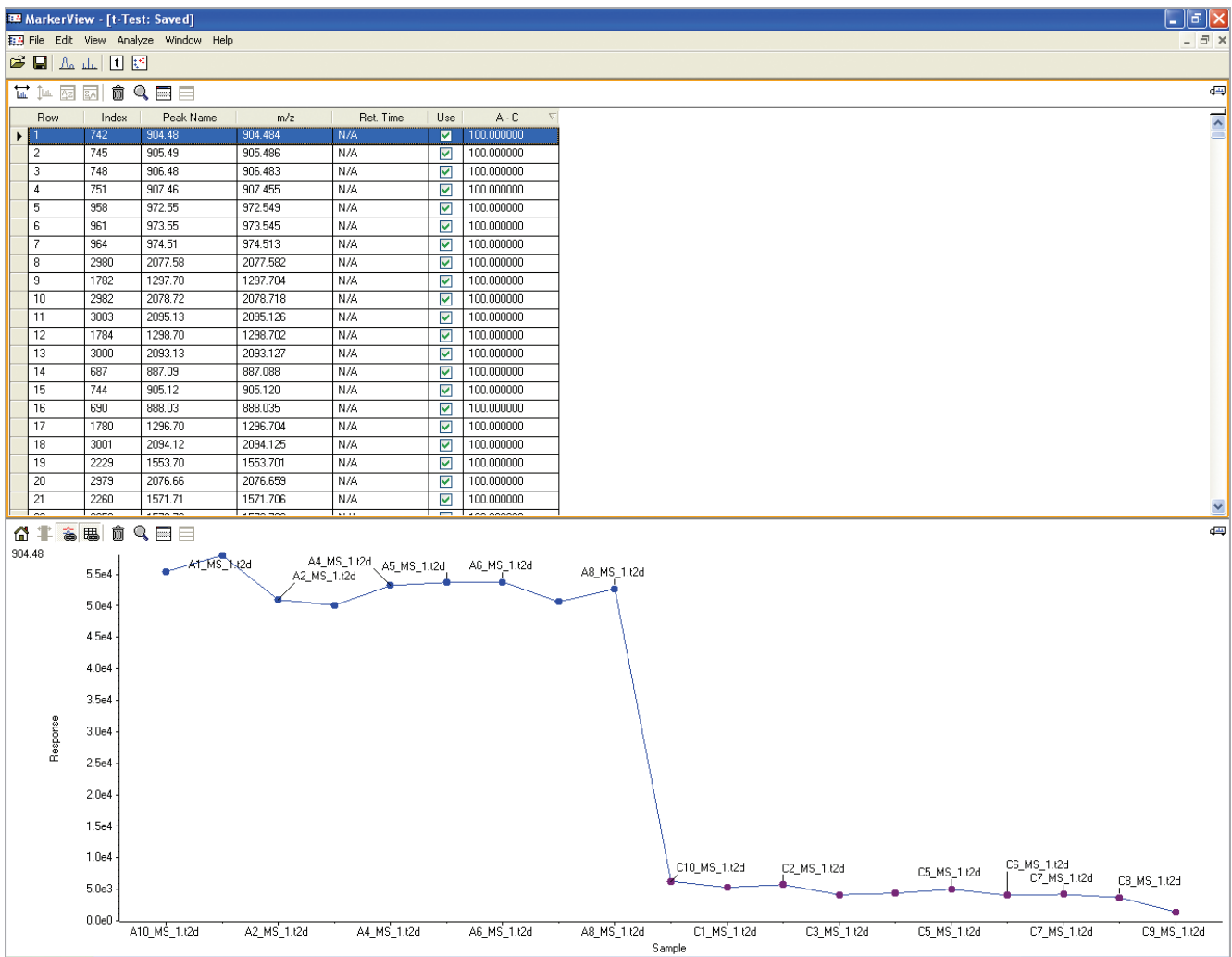


Figure 3. The Profile plot shows the selected peak from the t-test table across all samples. In this case, the peak with m/z 904.48 clearly distinguishes the group A samples from the group C samples.

graphically presents these groupings in a Scores plot. Reviewing the Loadings plot provides insight into variables that lead to sample clustering. For example, when comparing samples from animals treated with a drug versus untreated control samples, it is expected that two distinct groups would be formed in the Scores plot. The Loadings plot would then illustrate which compounds, such as metabolites or peptides, are up- or down-regulated as a result of the dosed drug (Figure 2).

T-Test

The t-test is a supervised analysis technique and is useful when two or more predetermined classes of samples are present (Figure 3). MarkerView™ software will perform a pairwise comparison of all the classes or alternatively, compare one class to all others. The results of the t-test indicate the probability that the difference between two groups is significant.

Data Visualization

When analyzing complex data sets, tools that allow visualization and manipulation of the data to discover true patterns and correlations within the data are critical. In MarkerView software, not only can you see the traditional Scores and Loadings plots generated from PCA, you can directly link to mass spectra and chromatographic data (Figure 4). Being able to interact directly with the raw data provides you with a simple way to go through multiple data files simultaneously to confirm your findings. Profile plots show the

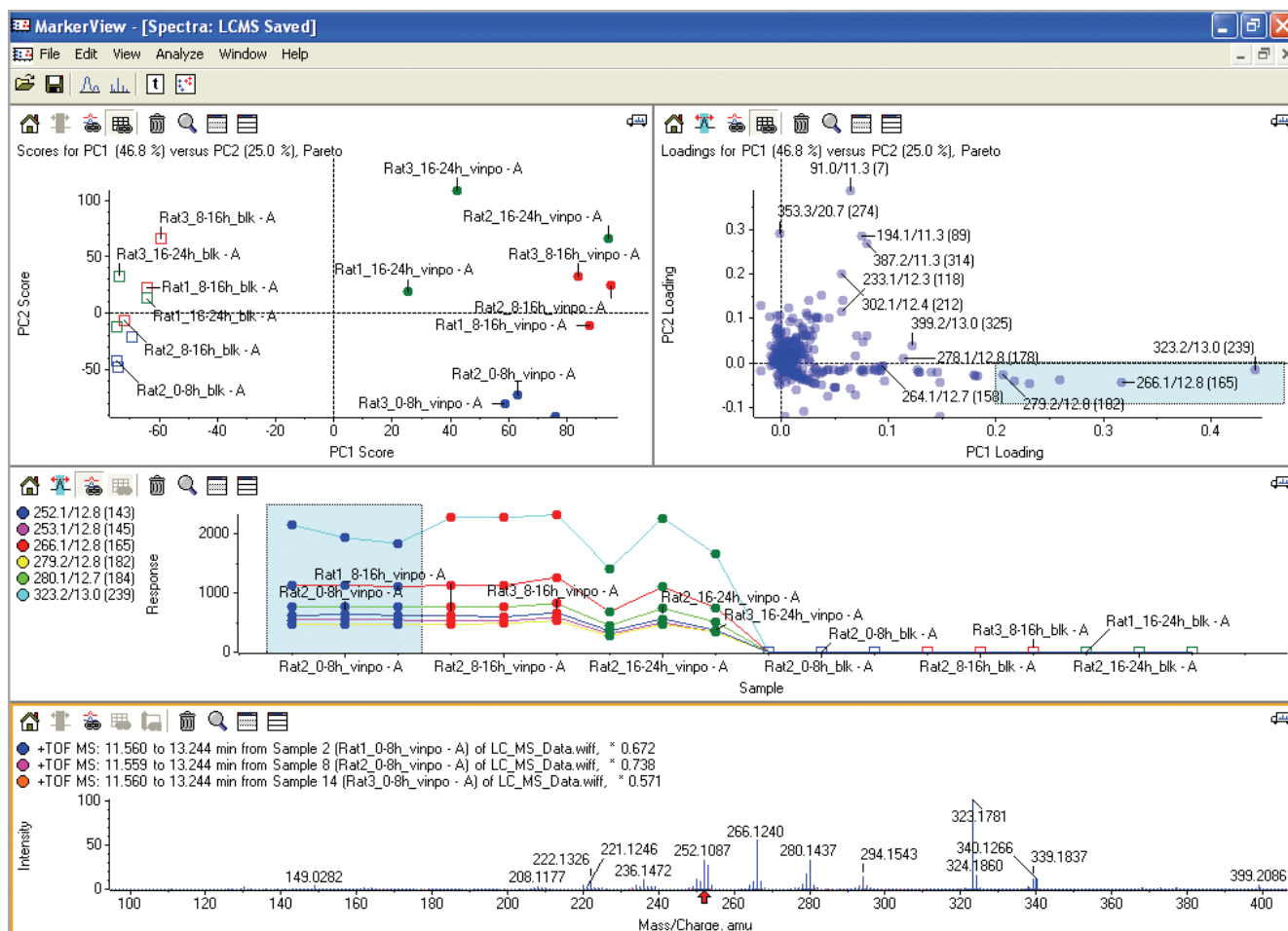


Figure 4. The Profile plot shown below the Scores and Loadings plot confirms that the compounds highlighted in blue in the Loadings plot are present only in drug-dosed animals. The mass spectrum of these compounds is shown below the Profile plot and can be used to assist in identification of these markers.

intensity of selected compounds across multiple samples. This view can highlight patterns resulting from systematic errors as well as assist in the identification of biomarkers.

Create Reports of Potential Biomarkers

During data review, MarkerView™ software allows you to create a list of suspected biomarkers. This list

can be annotated and is used to automatically generate a report in Microsoft® Word containing user-specified information. The reporting tools can easily be customized in terms of both the Word template and layout. Information that can be reported includes the Scores and Loadings plots, Profile plots, Mass Spectra as well as Extracted Ion Chromatograms for all suspected biomarkers.

Summary

Easily go from raw data to results—MarkerView software provides the essential tools to aid in statistical analysis and visualization of large numbers of samples and prevent data overload. Designed for metabolomic and biomarker profiling researchers, the powerful and easy-to-use features of MarkerView software help to accelerate your discovery of new biomarkers.

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Printed in the USA, 06/2005 Publication 114PB13-01