Can “Deconvolution” Improve GC/MS Sensitivity?
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Overview

- In a GC/MS scan analysis, it is always very difficult to identify trace compounds from high matrix background because the matrix ions overwhelm the compound signal. To be certain of the results, spectral averaging and background subtraction are often practiced. It is therefore a very time consuming process to confirm compounds in a complex matrix.
- Deconvolution has been proven to be a powerful data processing tool in finding trace compounds in complex matrices. In this study, results from Deconvolution (AMDIS) is closely looked at and compared to the results from ChemStation. The goal is to determine if Deconvolution can provide better results (sensitivity) than the routine ChemStation data processing.

Deconvolution Process

Deconvolution is a powerful tool that can screen 926 pesticides and endocrine disruptors in a single chromatographic run in just a few minutes.

Here is the Deconvolution process:

Deconvolution finds the components from a complex TIC. Each component is searched against a RTL library in AMDIS format. Besides spectral match, the RT can also be used as a criterion for hits. Depending on the match factor from the search, target compounds in a complex TIC can be identified or flagged.

![Deconvolution Process Diagram](Image)

ChemStation vs. AMDIS (Deconvolution)

40 pesticides at 50 ppb in spinach.
AMDIS finds more compounds (35 out of 40) than ChemStation does.

Conclusions

- AMDIS (Deconvolution) finds more target compounds than ChemStation does with comparable number of false positives. This means Deconvolution improves GC/MS sensitivity.
- In addition, Deconvolution can also find the correct peak and integrate the peak properly, thus, provides more reliable results.

Acknowledgement and Reference

The authors wish to thank Dr. Jon Wong of the US Food and Drug Administration (College Park, MD, USA) for providing numerous standards and food extracts.