

# Accurate Mass Spectral Database: Harnessing the Power of High Performance Mass Spectrometry at Long Last

LORNE FELL<sup>1</sup>; Viatcheslav Artaev<sup>1</sup>; Kevin McNitt<sup>1</sup>; Steve Robles<sup>1</sup>; Albert Lebedev<sup>2</sup> | <sup>1</sup>LECO Corporation, Saint Joseph, MI; <sup>2</sup>Moscow State University, Moscow, Russian Federation

## Introduction

The use of mass spectral databases have been a foundation of identification tools for mass spectrometry. Their use and development has enabled GC/MS to be a dominant and routine technique in many applications of hyphenated MS technologies. Over the past several years the use of high resolution (accurate mass) mass spectrometry and its data expanded into all areas of applications, which could take advantage of spectral databases specifically developed to exploit novel instrumentation capabilities. In this presentation we describe the development and use of an accurate mass-based spectral database, its curation, and application of novel algorithms resulting in similarity searches which are improved by the information obtained by high performance GC/MS.

## Methods

Standard mixtures comprising of alkanes, PAHs, semivolatiles, and pesticides were analyzed using a high resolution time-of-flight (HRTOF) mass spectrometer—Pegasus GC-HRT (LECO Corporation, Saint Joseph, MI)—at 10 spectra-per-second (m/z 40–300) in high resolution mode (25,000 at FWHH). The resulting chromatographic peaks were automatically found, deconvoluted, and curated into an Accurate Mass Library (AML). Typical mass accuracies were <1 ppm. In order to take advantage of this high mass accuracy data, a novel matching algorithm (AML Rank) was developed to improve the identification process. The AML and its ranking algorithm was compared to standard nominal mass libraries for a number of environmental and food samples. Many MS vendors have begun to develop accurate mass libraries (some of them being called databases) in many different forms. In fact, even the highly influential NIST has modified its programs to incorporate aspects of accurate mass in its search engine, but most uses of this high performance data are done solely with formulae assigned to the structure. Formula use is helpful and correct for all cases of non-targeted screening, however, accurate mass data can also be used when the chemical formula is unknown, by answering the question, “How close to the accurate mass is the candidate ion?”. Herein we describe the use of a novel algorithm which ranks deconvoluted accurate mass spectra against a library of curated accurate spectra. The complex samples used in this study were not always allowed to reach sufficient separation to exclude any possible ion interferences from the coeluted analytes. Such interferences could significantly reduce similarity scores of the analytes of interest and put them outside of the top hits in the library search results if applying a standard NIST algorithm. High performance data compared to low performance libraries will not yield the best results. However, this accurate mass algorithm, using a ranking system to sort the hit list, dramatically improved the results and filtered the correct hits to the top of the search results even in the presence of heavily interfering ions. Examples of the results with various forms of interferences are presented.

## AML Ranking

Accurate mass library rank is a measure of how close the masses align between two spectra. The spectral masses are paired if they have overlapping mass confidence intervals which are based on the acquisition resolution. Each pair is scored by the mass difference relative to a mass tolerance value. The final score for the spectra is the sum of the scores for each pair, weighted by the sum of the abundance of both masses in the pair. The score is not affected by the difference in abundance between the matching masses.

The NIST similarity score is based on the relative abundances of the matched pairs of masses, and weighs them based on MW and the abundance ratios of adjacent matching peaks. There is no comparison of accurate masses because the masses are nominal. Therefore AML rank and NIST similarity are independent metrics, each scoring based on different spectral characteristics.

## Results

### MegaMix

New AML was applied to several standard mixture solutions for validating. In case of volatile compounds (8260B MegaMix Calibration Mix, Restek, USA) 46 compounds of the mixture were in the library at the time of the analysis. Among them 27 had 1<sup>st</sup> position (hit 1–59%), in the hit list, 6 in the 2<sup>nd</sup> position (hit 2–13%), and 3 in the 3<sup>rd</sup> position (hit 3–6%). In total, 78% were in the top 3 hits. Ten compounds were in top 10 hits of the library search hit list (see Table 1).

For the semivolatiles the results were comparable, while some results were extraordinary. For benz[a]anthracene the score using AML reached 1000 points, which is quite extraordinary for any library in general (Table 2). Very good identification results were obtained for isomeric compounds. Table 3 shows an example of identification of isomeric anthracene and phenanthrene.

Table 1. Library search results of MegaMix using AML.

Peak #	Name	R.T. (s)	position	Base Mass
1	2,2-dichloropropane	133.528	1	77.0179
2	2-Propenoic acid, methyl ester	134.368	absent	55.0179
3	Methane, bromochloro-	135.04	absent	129.9
6	tetrahydrofuran	152.848	1	86.9606
7	Ethane, 1,1,1-trichloro-	152.848	1	86.9606
8	Ethane, 1,2-dichloro-	155.62	1	81.9918
9	1-Propene, 1,1-dichloro-	160.492	absent	74.9996
12	Carbon Tetrachloride	165.196	1	116.906
22	Propane, 1,2-dichloro-	200.896	1	82.9997
23	Trichloroethylene	201.484	1	129.9138
24	Methane, dibromo-	204.172	1	173.8496
26	Methane, bromodichloro-	210.388	absent	82.945
28	Methyl methacrylate	220.048	2	69.0336
30	1-Propene, 1,3-dichloro-, (Z)-	261.208	absent	74.9997
31	Toluene	310.516	3	91.0542
32	1-Propene, 1,3-dichloro-, (E)-	311.44	3	74.9996
33	Ethane, 1,1,2-trichloro-	322.024	1	96.9697
35	Propane, 1,3-dichloro-	348.148	absent	76.0074
38	Methane, dibromochloro-	355.99	absent	96.9336
39	Ethane, 1,2-dibromo-	363.26	1	106.9491
41	Tetrachloroethylene	389.476	2	165.8719
44	Benzene, chloro-	450.828	5(1)	112.0074
46	Ethane, 1,1,1,2-tetrachloro-	456.844	1	130.9216
48	Ethylbenzene	472.572	1	91.0542
53	p-Xylene	483.22	absent	91.0542
54	Methane, tribromo-	500.692	2	172.8418
57	Styrene	508.42	2	104.0621
58	p-Xylene	510.436	absent	91.0542
61	2-Butene, 1,4-dichloro-, (Z)-	524.632	1	83.0387
63	Ethane, 1,1,2,2-tetrachloro-	531.856	1	82.9449
66	Propane, 1,2,3-trichloro-	538.66	1	74.9996
68	Benzene, (1-methylethyl)-	543.112	1	105.0698
71	2-Butene, 1,4-dichloro-, (E)-	547.144	1	74.9996
73	Benzene, bromo-	548.068	1	77.0388
75	Benzene, 1-chloro-2-methyl-	566.8	1	91.0542
78	Benzene, propyl-	569.068	1	91.0542
79	Benzene, 1-chloro-4-methyl-	571.588	2(1)	91.0542
82	Mesitylene	581.06	1	105.0699
83	Ethane, pentachloro-	586.708	1	106.8796
84	Benzene, (1-methylethyl)-	590.32	1	105.0701
85	Benzene, tert-butyl-	599.512	1	119.0854
88	Benzene, 1,2,3-trimethyl-	600.494	1	105.0699
89	Benzene, 1,2-dichloro-	609.196	10	145.9883
92	Benzene, (1-methylpropyl)-	612.832	1	105.0698
94	Benzene, 1,4-dichloro-	619.924	10	145.9884
96	p-Cymene	622.24	1	119.0855
97	Benzene, 1,2-dichloro-	629.716	10	145.9883
98	Benzene, butyl-	642.736	2	91.0542
100	Ethane, hexachloro-	654.916	1	165.8721
101	Propane, 1,2-dibromo-3-chloro-	660.124	3	156.9235
103	Benzene, nitro-	662.728	1	77.0387
104	Benzene, 1,2,3-trichloro-	712.624	9(9)	179.9294
107	Naphthalene	716.992	8	128.0619
108	1,3-Butadiene, 1,1,2,3,4,4-hexachloro-	720.016	1	224.8406
124	Benzene, 1,2,3-trichloro-	731.02	2	179.9294
125	1,3-Butadiene, 1,1,2,3,4,4-hexachloro-	731.776	3	224.8407

Table 2. Library search results for benz[a]anthracene using AML.

Hit	Name	Similarity	Mass	Reverse	Probability	CAS	Library	Id
21*	Benz[a]anthracene	1000	1000	0.0156-55.3	Lebedev-HRT-Library	170		
2	Chrysene	931	937	0.0218-61.9	Lebedev-HRT-Library	171		
3	Benz[a]anthracene	901	903	41.3156-53	mainlib	59998		
4	Benz[a]anthracene	886	887	30.9156-53	replib	30277		
5	Triphenylene	884	885	25.5217-59.4	mainlib	59999		
6	Triphenylene	884	884	28.5217-59.4	replib	30272		
7	Triphenylene	884	886	26.5217-59.4	replib	30271		
8	Naphthalene	879	882	23.0192-24.0	replib	20206		
9	Triphenylene	878	880	28.5217-59.4	replib	30270		
10	Naphthalene	873	873	15.4192-24.0	mainlib	19921		

Table 3. Library search results for anthracene using AML.

Hit	Name	Similarity	Mass	Reverse	Probability	CAS	Library	Id
21*	Anthracene	988	988	0.0120-12.7	Lebedev-HRT-Library	161		
2	Phenanthrene	931	937	0.0185-61.8	Lebedev-HRT-Library	166		
3	Phenanthrene	939	942	57.2185-61.8	mainlib	65969		
4	Anthracene	935	938	48.6120-12.7	replib	26780		
5	Phenanthrene	917	918	25.1185-61.8	replib	26768		
6	Anthracene	915	920	48.6120-12.7	replib	26794		
7	Phenanthrene	914	915	25.1185-61.8	replib	26756		
8	9H-Fluorene, 9-methylene-	906	958	17.24425-82.5	replib	26765		
9	Anthracene	904	906	48.6120-12.7	replib	26795		
10	Anthracene	902	903	13.9120-12.7	mainlib	66037		

Surprisingly good results were obtained for aliphatic compounds identified in complex environmental samples. Usually, a search using standard mass spectra of aliphatic compounds results in a hit list including homologous compounds (aldehydes, alkanes, naphthenes, alcohols), where the correct compound may have rather low ranking. AML library search often provides the correct analyte as the best hit. For example, the AML library search results of hexadecane and tetradecanol-1 show those compounds as #1 hits (Table 4,5).

Table 4. Library search results for hexadecane using AML (water sample).

Hit	Name	Expected Ion m/z	Similarity	Reverse	CAS	Library	Formula
1	Hexadecane	228.2855	935	945	544-76-3	Lebedev-HRT-Library	C16H34
2	Hexadecane	228.2855	919	921	544-76-3	replib	C16H34
3	Hexadecane	228.2855	911	911	544-76-3	replib	C16H34
4	Heptadecane	240.2812	909	912	629-78-7	replib	C17H36
5	Hexadecane	228.2855	908	910	544-76-3	replib	C16H34
6	Pentadecane	212.2499	901	904	629-62-9	replib	C15H32
7	Tetradecane	198.2342	899	908	629-59-4	replib	C14H30
8	Hexadecane	228.2855	896	896	544-76-3	mainlib	C16H34
9	Tetradecane	198.2342	896	900	629-59-4	replib	C14H30
10	Nonadecane	268.3125	895	901	629-92-5	replib	C19H40

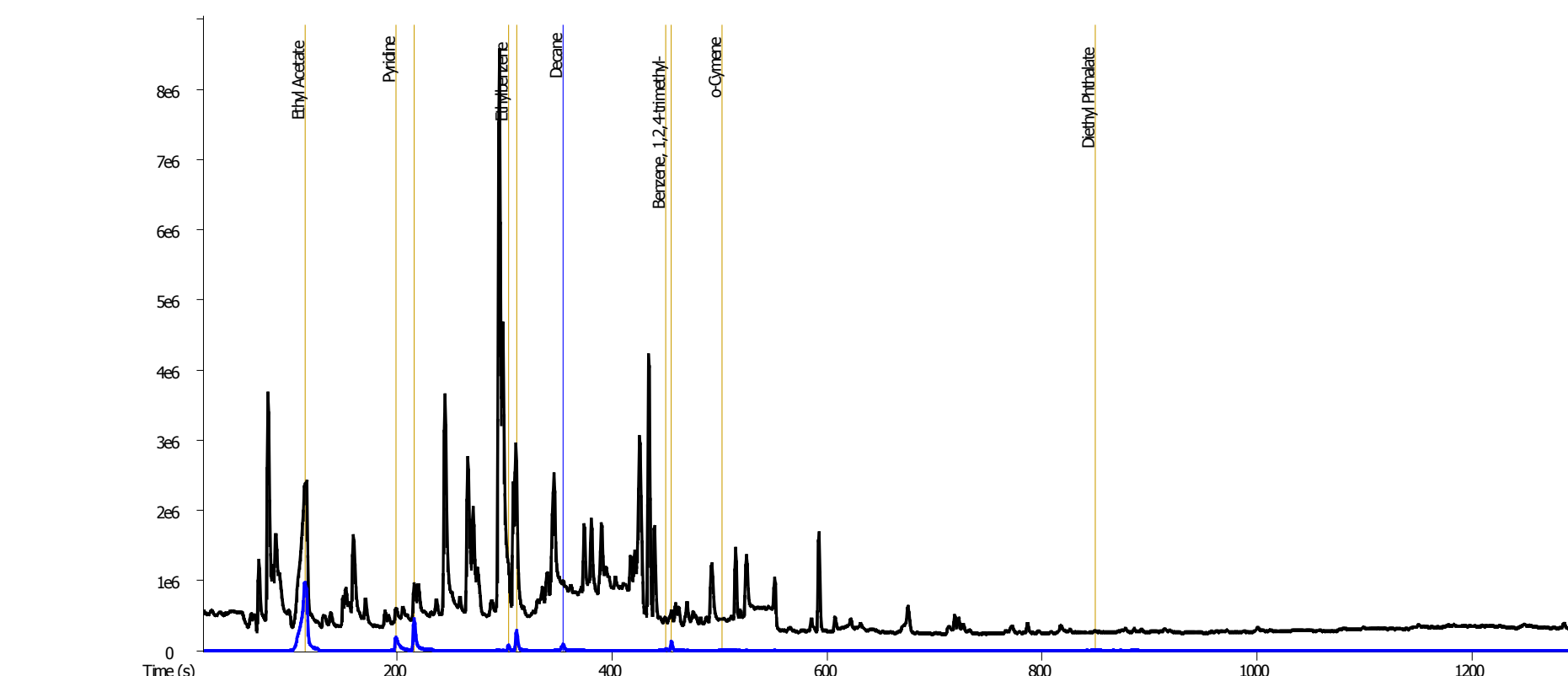
Table 5. Library search results for tetradecanol-1 using AML (water sample).

Hit	Name	Expected Ion m/z	Similarity	Reverse	Library	CAS	Formula
1	1-Tetradecanol	214.2291	897	920	Lebedev-HRT-Library	112-72-1	C14H30O
2	1-Dodecanol	186.1978	890	927	replib	112-53-8	C12H26O
3	1-Hexadecanol	242.2604	888	914	mainlib	36653-82-4	C16H34O
4	1-Tetradecanol	214.2291	888	929	replib	112-72-1	C14H30O
5	1-Tetradecanol	214.2291	877	889	replib	112-72-1	C14H30O
6	1-Hexadecanol	242.2604	876	910	replib	36653-82-4	C16H34O
7	1-Tetradecanol	214.2291	876	886	replib	112-72-1	C14H30O
8	Cyclotetradecane	196.2186	875	913	replib	295-17-0	C14H28
9	1-Dodecanol	186.1978	871	879	replib	112-53-8	C12H26O
10	1-Undecanol	172.1822	870	913	mainlib	112-42-5	C11H24O

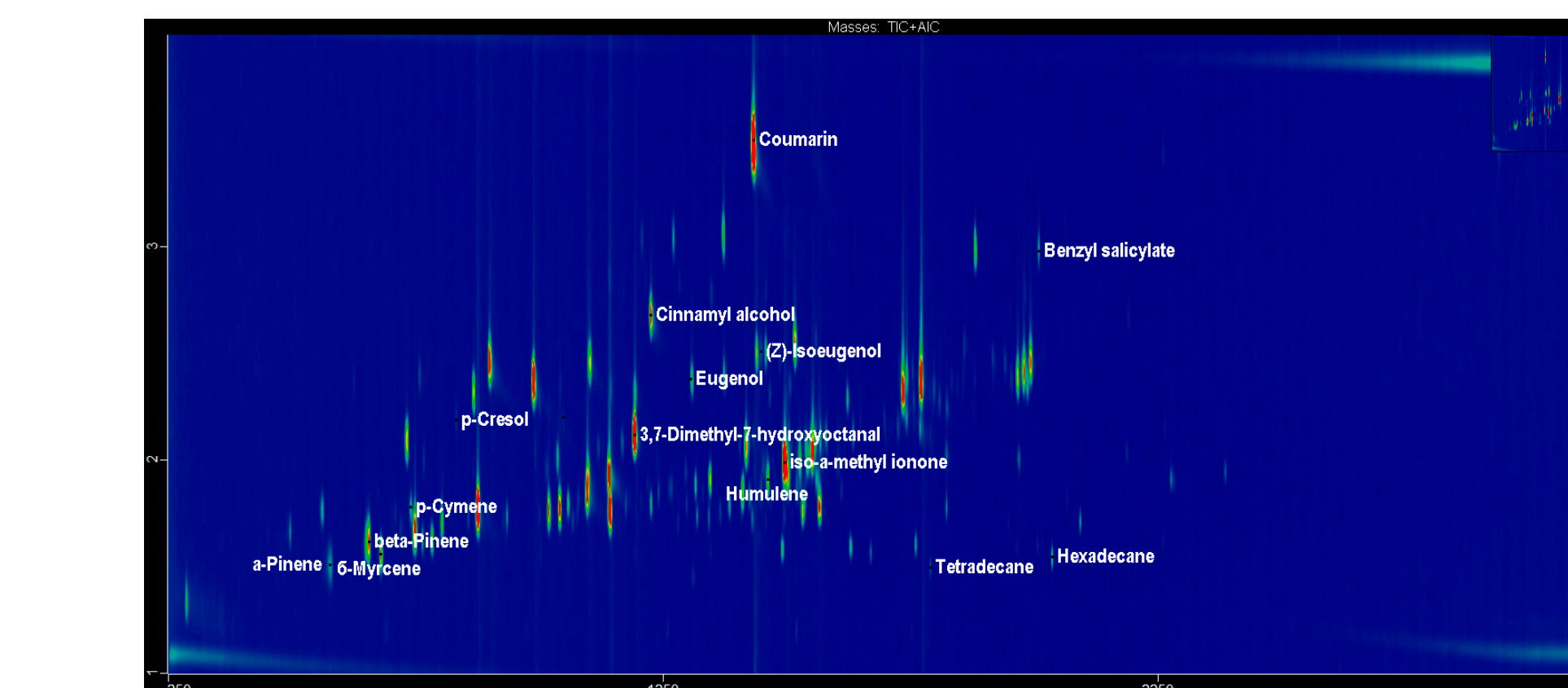
## Food and Fragrance Analysis

The AML search was successfully implemented to the food and fragrance samples obtained using GC-HRT and GCxGC-HRT.

- Extra Virgin Olive Oil GC-HRT – Shown for only those species that match for AML library.



- Perfume Sample GCxGC HRT – Shown only for those species that match for AML



## Conclusions

An Accurate Mass Library was created and used with an AML ranking algorithm to search data obtained with high resolution GC-MS and GCxGC-MS instrumentation.

