

Discovery-based analysis for chromatographic trends using alteration analysis (ALA) and two-dimensional correlation analysis (2DCOR)

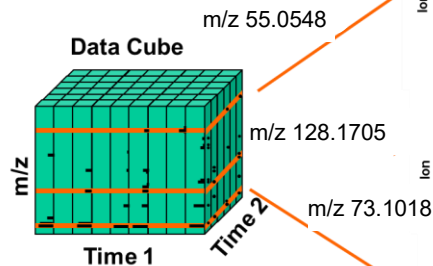
Chris E. Freye and Matthew J. Herman
High Explosives Science and Technology (Q-5)

1/13/2026
MDCW 2026

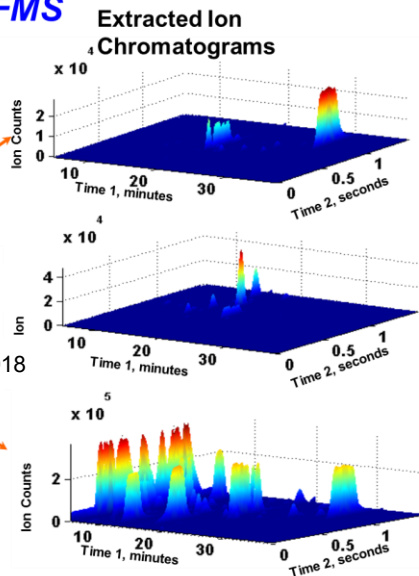
Approaching Complex Samples

3rd Order Data...with TOFMS

- column 1 retention time
- column 2 retention time
- full mass spectrum at each point



We analyze the RAW data!
~40 GB / sample
4.0 **BILLION** data points



Two major regimes of data analysis we want to avoid:

1. Visual comparison of chromatograms
2. Manual combination and analysis of peak tables

The alternative:

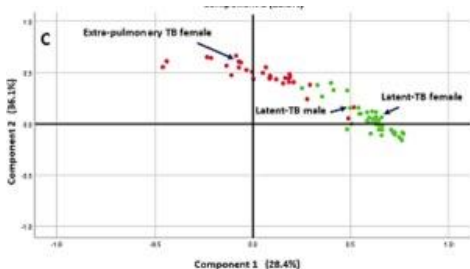
- Statistical methods for data reduction and/or feature selection
- Only spend time working up **important** analytes



Discovery-Based Chemometric Techniques

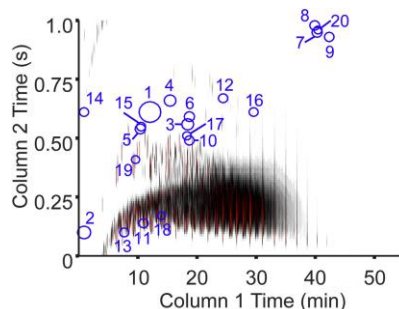
Classification

- PCA
- PLS-DA
- Random forest
- HCA



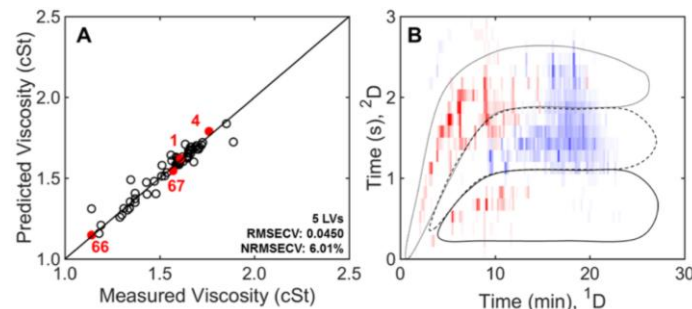
Feature Selection

- Fisher ratio
- Pairwise (Fold-Change)
- Support vector machine (SVM)



Property Prediction


- PLS-R

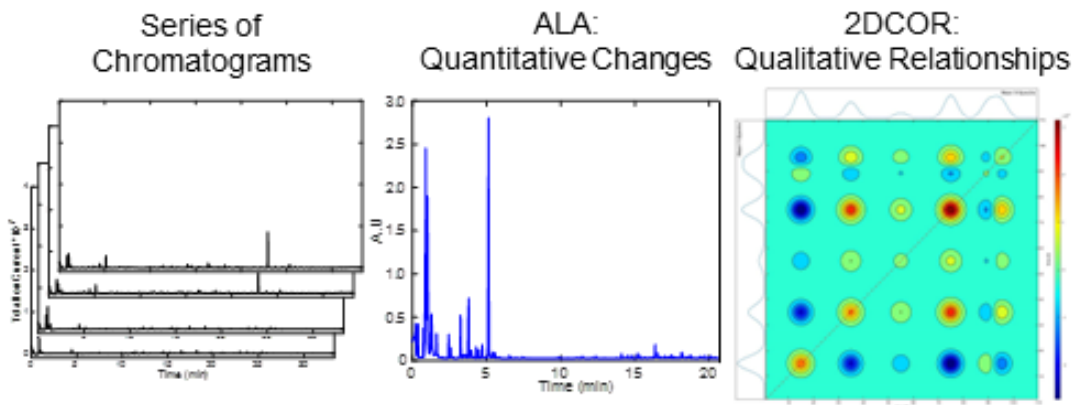


Current chemometric techniques are not suitable or sensitive enough to find trends across a series of samples

Chemometric Techniques for Uncovering Trends

Alteration Analysis (ALA) 2D Correlation Analysis (2DCOR)

- Quantitative understanding of how individual datapoints vary across samples
 - Qualitatively determines relationships between data features and how these features change in respect to one another due to an applied external variable
- Pinpoint chemical trends for a series of experiments  – Understand how chemical trends are related



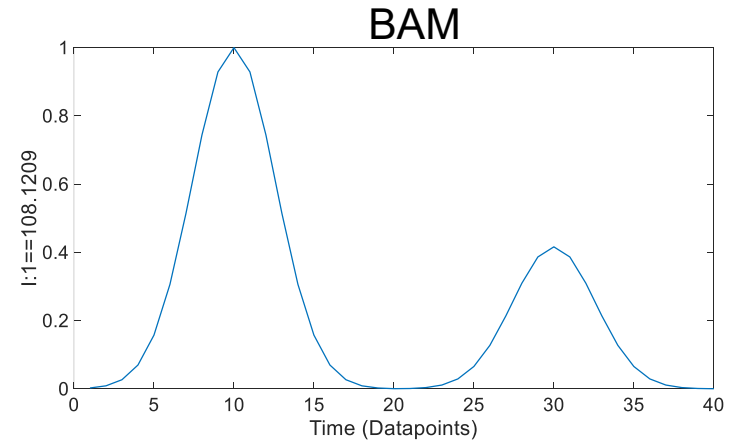
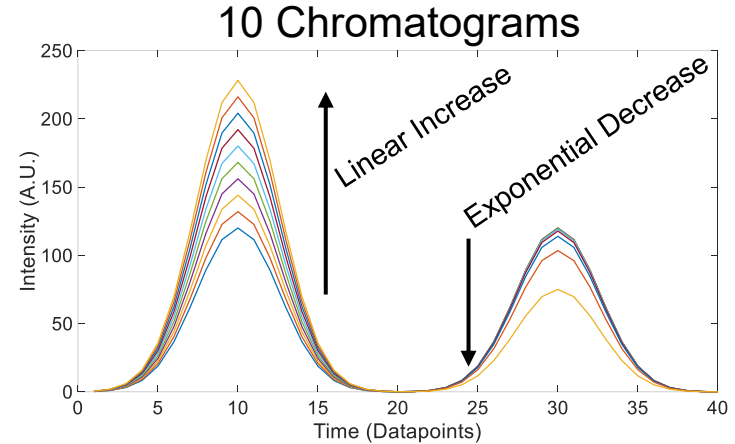
ALA

Series of data (chromatograms)

$$X = (x_{ij}) \quad \begin{array}{l} i = 1, 2, \dots, n \\ j = 1, 2, \dots, m \end{array}$$

Basic Alteration Map (BAM):
Overall change

$$b = (b_j) \quad b_j = \max(x_j) - \min(x_j) \quad j = 1, 2, \dots, m$$



ALA

Difference matrix

$$D = (d_{ij}) \quad d_{ij} = x_{i+1j} - x_{ij} \quad \begin{matrix} i = 1, 2, \dots, n-1 \\ j = 1, 2, \dots, m \end{matrix}$$

Synchronous Alteration Map (SAM):

Linear change

$$s' = (s'_j) \quad s'_j = \frac{b_j \bar{d}_j}{\sigma_{d_j} + 1} \quad j = 1, 2, \dots, m$$

$$s = (s_j) \quad s_j = \frac{s'_j}{\max(|s'|)} \quad j = 1, 2, \dots, m$$

Asynchronous Alteration Map (AAM):

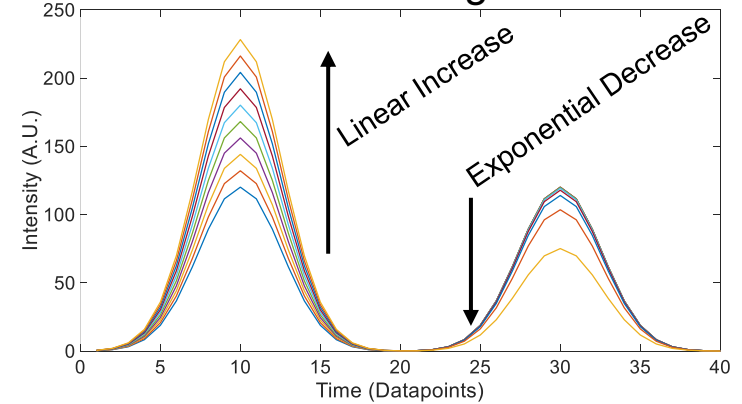
Non-linear change

$$\mathbf{a}' = (a'_j) \quad j = 1, 2, \dots, m$$

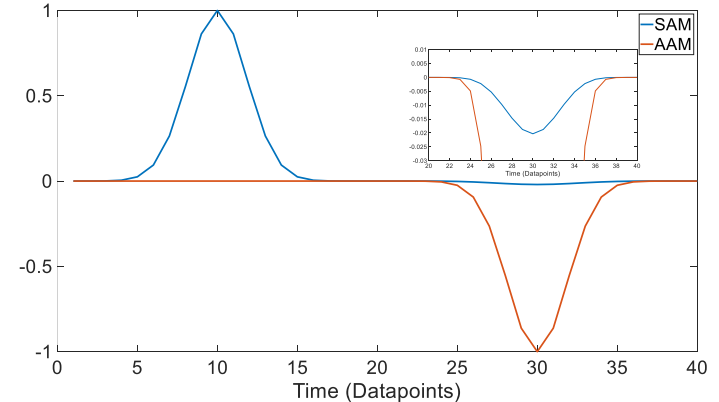
$$a'_j = \left(b_j - \left| \sum_{i=1}^{n-1} d_{ij} \right| \right) \sigma_{d_j} (\max(x_j) + \min(x_j) - 2\bar{x}_j)$$

$$\mathbf{a} = (a_j) \quad a_j = \frac{a'_j}{\max(|a'|)} \quad j = 1, 2, \dots, m$$

10 Chromatograms

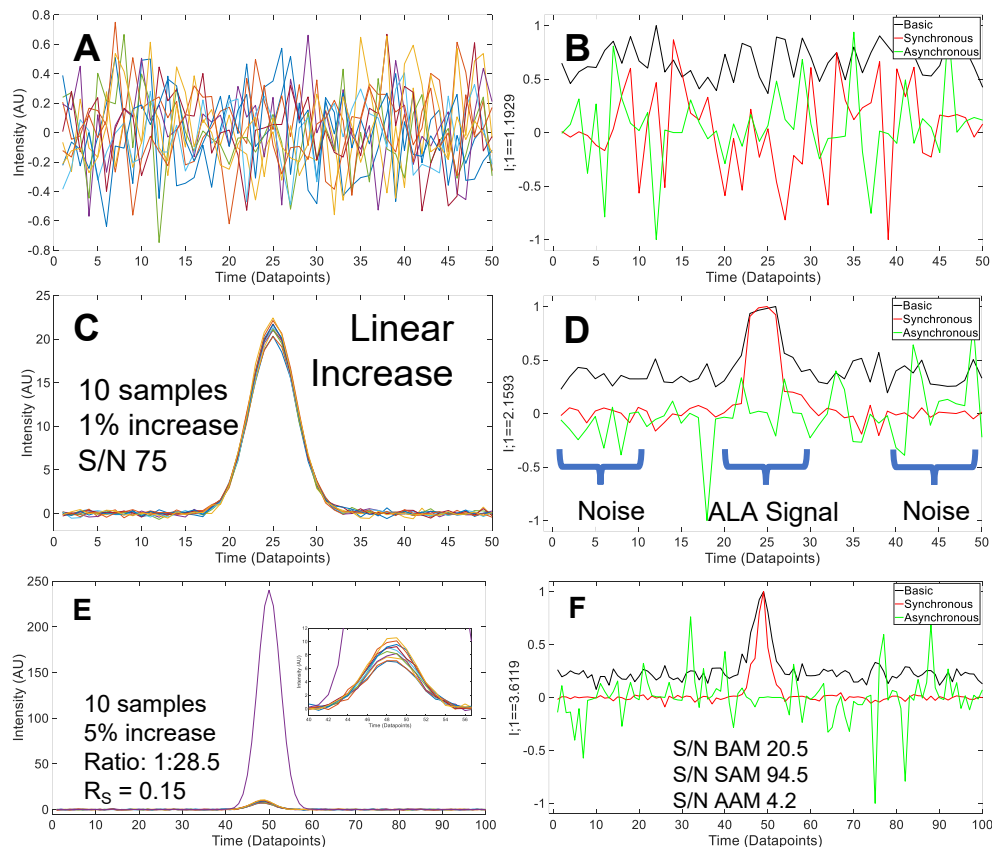


SAM and AAM



Defining Success for ALA

- To evaluate quantitative performance of ALA, simulated noise, different amounts and types of change (linear, exponential, etc.)
- ALA was determined to be successful if a combination of BAM and one of the other two outputs from the ALA calculations had S/Ns greater than 10
- ALA works for peaks that are severely overlapped!



2DCOR

$$\mathbf{Y} = \begin{cases} \mathbf{I}(\mathbf{v}, \mathbf{T}) - \bar{\mathbf{I}}(\mathbf{v}) & \text{for } T_{min} \leq T \leq T_{max} \\ 0, & \text{otherwise} \end{cases}$$

Where \mathbf{Y} is your final dynamic spectra matrix, $\bar{\mathbf{I}}(\mathbf{v})$ is the reference spectrum, and \mathbf{T} is your external perturbation.

Synchronous correlation map ($\Phi(\mathbf{v}_1, \mathbf{v}_2)$)

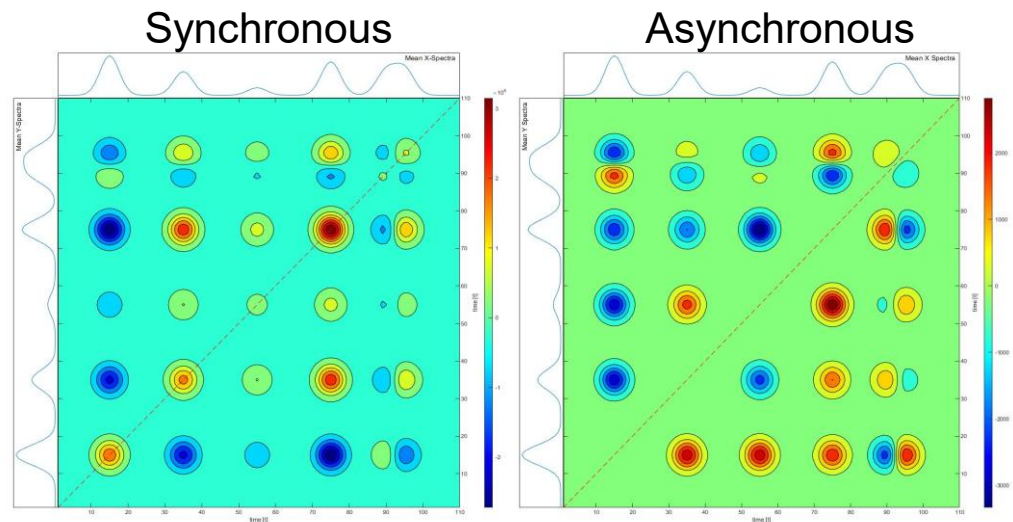
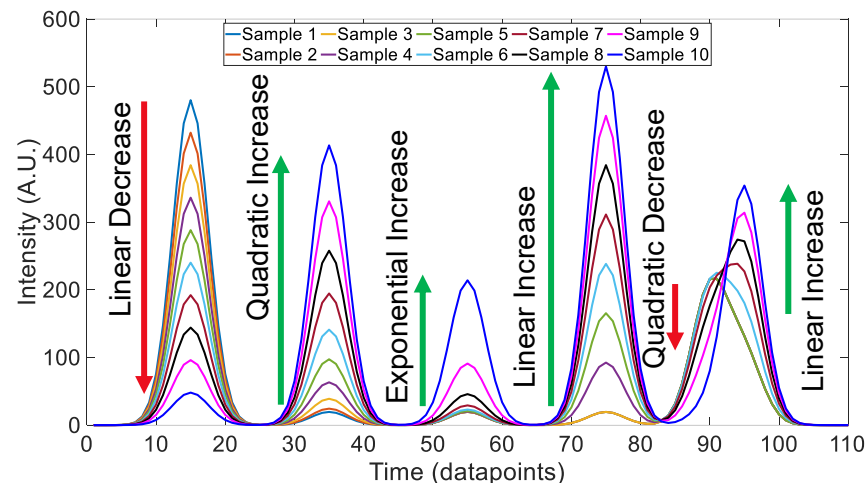
$$\Phi(\mathbf{v}_1, \mathbf{v}_2) = \frac{1}{n-1} \mathbf{Y}^T \mathbf{Y}$$

Asynchronous correlation map ($\psi(\mathbf{v}_1, \mathbf{v}_2)$)

$$\psi(\mathbf{v}_1, \mathbf{v}_2) = \frac{1}{n-1} \mathbf{Y}^T \mathbf{N} \mathbf{Y}$$

$$N_{i,j} = \begin{cases} 0, & \text{if } i = j \\ \frac{1}{\pi} (j - i), & \text{otherwise} \end{cases}$$

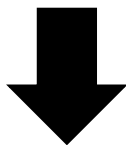
Application of 2DCOR



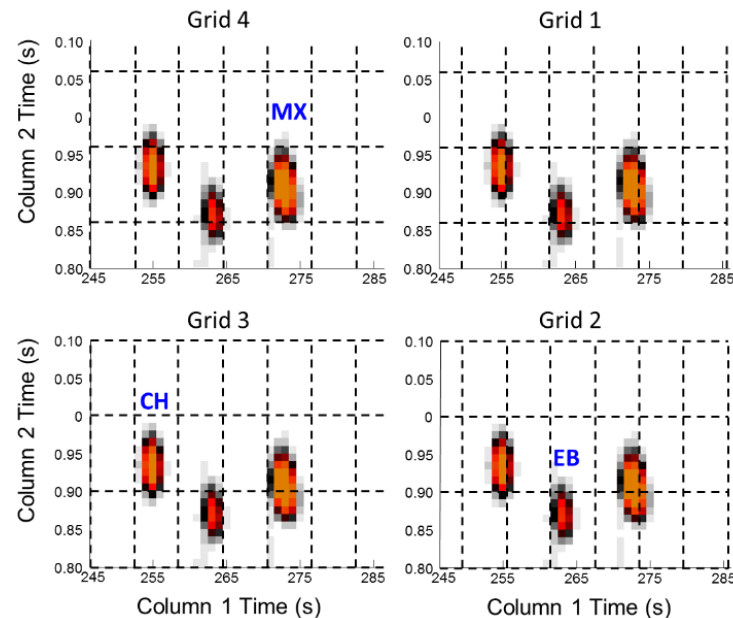
- Synchronous map provides information regarding the relative direction of coincidental change observed in the data set
- Asynchronous map characterizes the degree of coherence between signals measured at two different instances which are separated by a correlation time
- Using Noda's rule we can determine order of changes
 - 15 → 35 → 75 → 55 → 95 → 90

Expansion of ALA and 2DCOR to GC×GC

- Chromatographic misalignment will reduce ability of ALA to discover chemical trends
 - Could be solved with alignment software, but this can be time consuming
- However, 2DCOR squares data size, even with pseudo-TIC chromatograms, the data size will be enormous (~70 billion datapoints)



Only Option is to Tile Dataset



Reproduced from B.A. Parsons, L.C. Marney, W.C. Siegler, J.C. Hoggard, B.W. Wright, R.E. Synovec, Anal. Chem. 2015, 87, 7, 3812–3819

Previous ALA GC×GC Procedure

ALA Preprocessing and Computations

1. Normalization to internal standard
2. Tiling
3. Calculate ALA Parameters
4. Apply ALA S/N Threshold (S/N of 10)
5. Scale BAM, SAM, AAM to 1
6. Enforce requirement 2 of 3 ALA values (BAM, SAM, AAM)



Redundant Hit Removal

1. Pin hits by finding largest BAM within tile
2. Find top BAM, SAM, AAM m/z per tile
3. Remove redundant hits if within clustering window and share BAM, SAM or AAM m/z



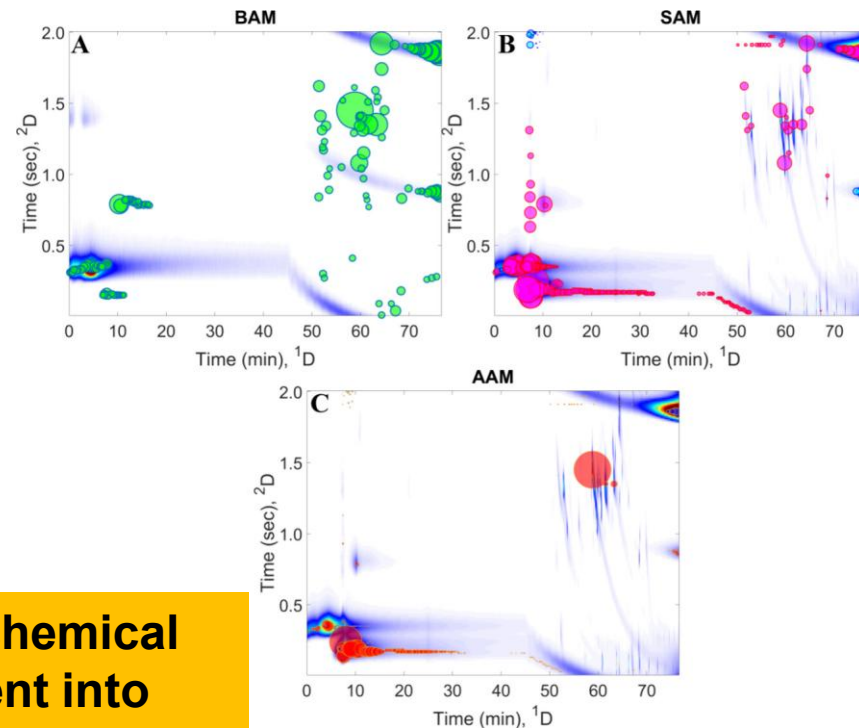
ALA Algorithm Output

- Hit list ranked by BAM values (or SAM or AAM)
- BAM, SAM, AAM Spectra
- Top m/z per hit

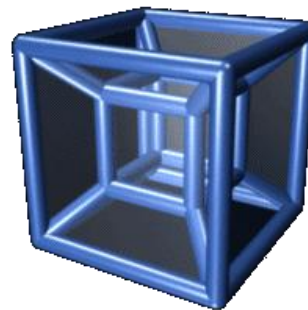
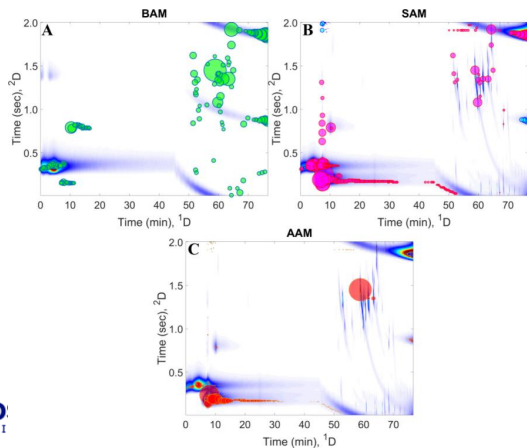
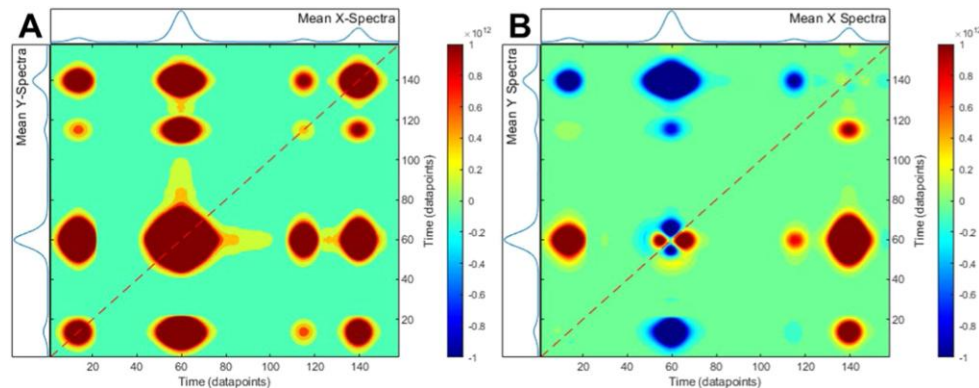
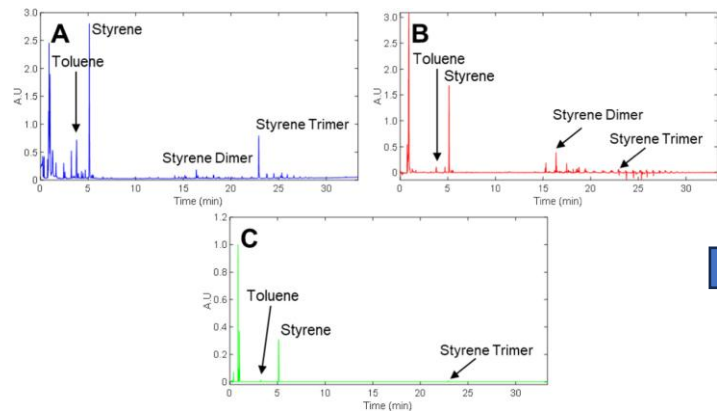
Recent Application of ALA to High Explosives

- Understand aging (chemical changes) of high explosives is critically important to our work
- F-ratio only partially worked since numerous intermediate decomposition products were formed
- Application of ALA discovered 250+ chemical changes but allowed insight into type of change

While ALA was essential to discovering chemical trends, a *significant* amount of effort went into understanding the relationship of the changes



Problem with GC×GC and 2DCOR

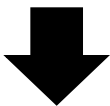


Need to make our GC×GC data 1D

Refined ALA and 2DCOR Procedure for GC×GC

Initial ALA Algorithm Output

- Hit list ranked by BAM values (or SAM or AAM)
- BAM, SAM, AAM Spectra
- Top m/z per hit



Re-calculate ALA

- Re-center tile on pin location (peak maxima)
- Calculate BAM, SAM, AAM for new tile scheme
- Generate new hit list ranked by BAM values (or SAM or AAM)
- New BAM, SAM, AAM mass spectra
- Top m/z per hit



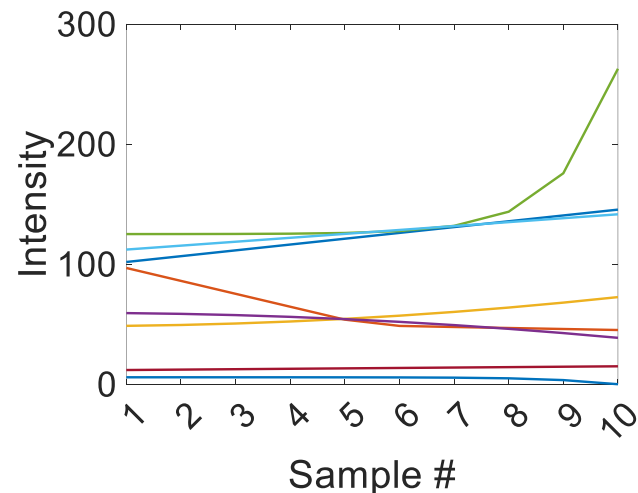
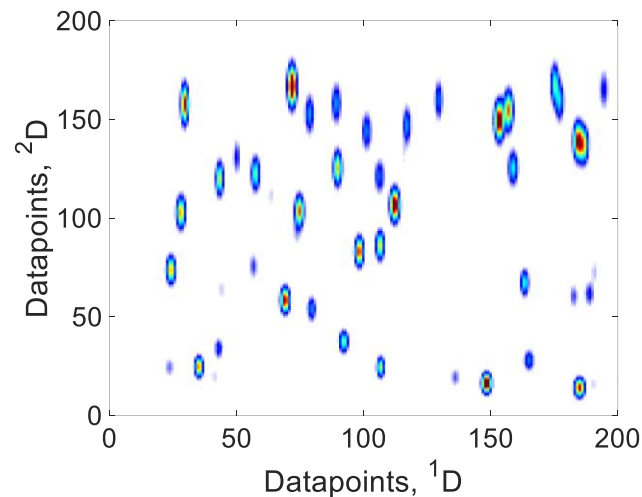
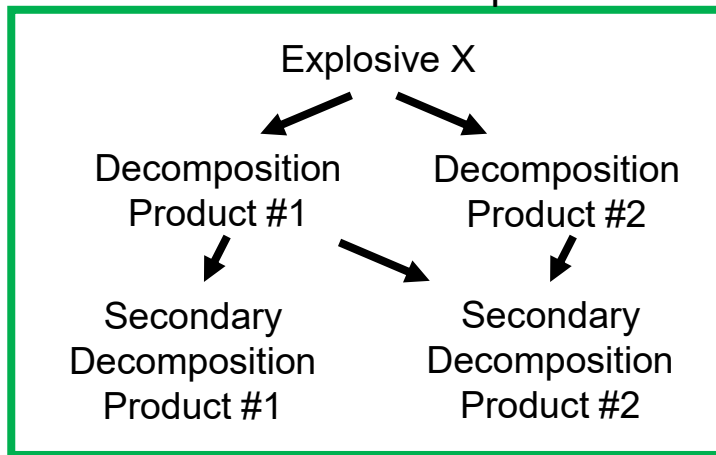
2DCOR

- Using raw data, sum intensities on both dimension for all m/z that have BAM value >0
- Calculate synchronous and asynchronous maps
- Determine order of changes

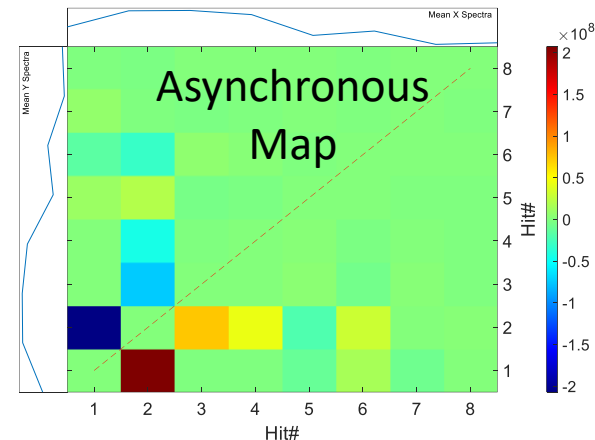
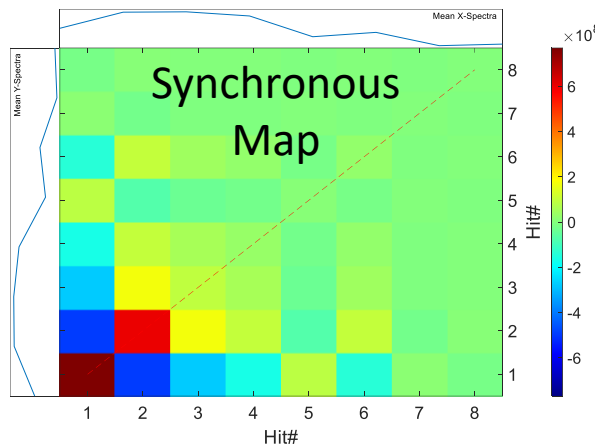
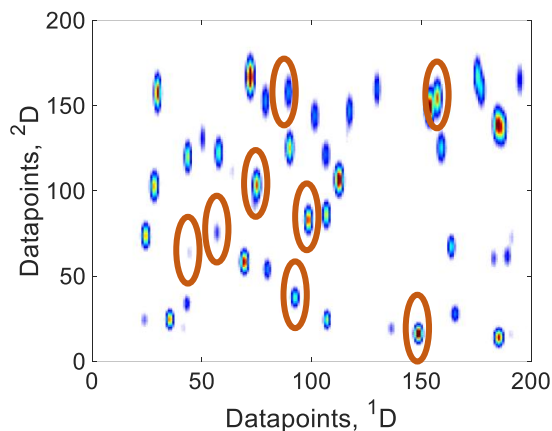
Let's see ALA and 2DCOR in Action

- Use in-silico dataset in order to simplify interpretation
 - Chromatogram with 50 peaks of which 8 peaks are changing at different rates
 - 10 chromatograms for the “experiment”

“Real-World” Example



Let's see ALA and 2DCOR in Action

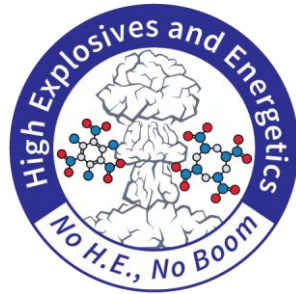


ALA Hit #	$2t_R$	$1t_R$	BAM	SAM	AAM	Top BAM m/z	Top SAM m/z	Top AAM m/z	Norm Sync Magnitude	Rank Order
1	155	157	1.0	0	0.003	113	113	221	1.0	7
2	17	148	0.82	0.06	1.0	187	187	88	0.79	2
3	104	75	0.37	1.0	0.001	7	7	55	0.12	6
4	83	98	0.24	0.42	0.001	12	12	30	0.04	5
5	152	79	0.21	0	0.001	136	3	136	0.01	8
6	38	92	0.16	0.05	0.001	247	247	248	0.03	1
7	62	44	0.05	0	0.001	245	1	245	0.001	3
8	75	57	0.03	0.005	0.001	58	58	15	0.001	4

ALA + 2DCOR informs of the significance of the change, how those changes are related, and the order of the changes

Acknowledgements

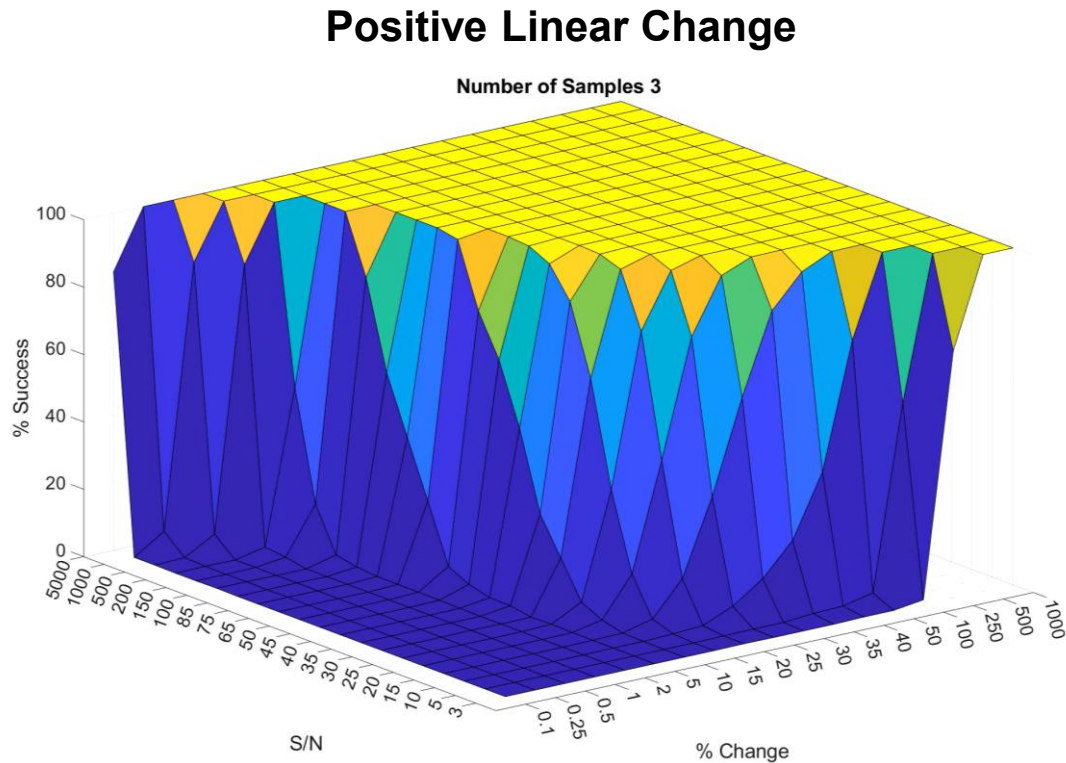
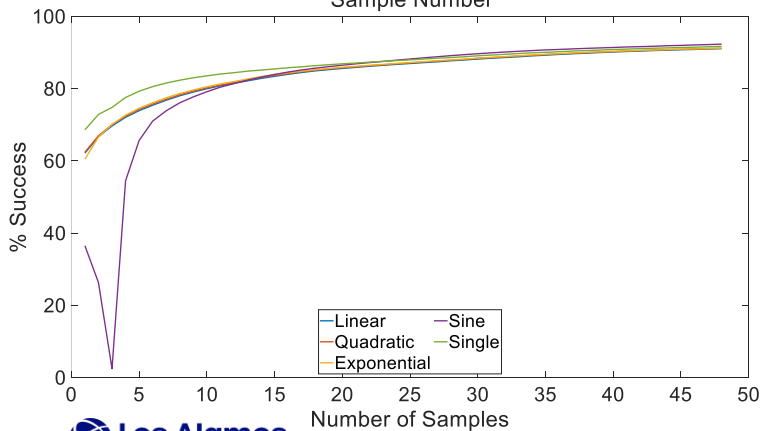
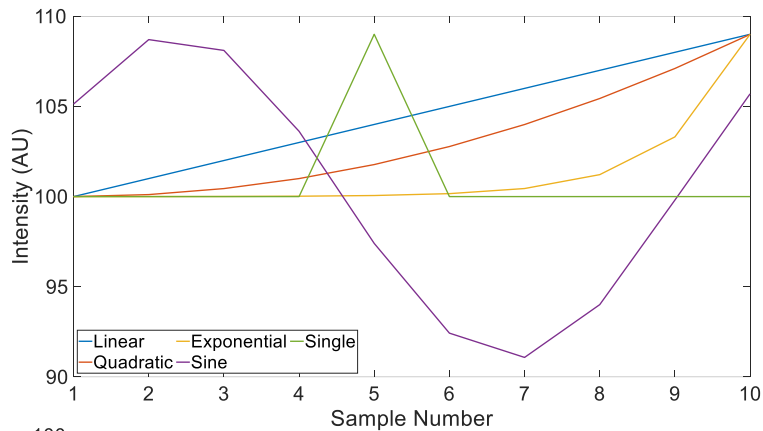
- ***Aging and Lifetimes Program***
 - Mark Boggs
- ***High Explosives and Energetics Program***
 - Cameron Moore
- ***LANL High Explosives Science and Technology (Q-5)***
 - Colleen Ray and Michelle Corbally



Questions?

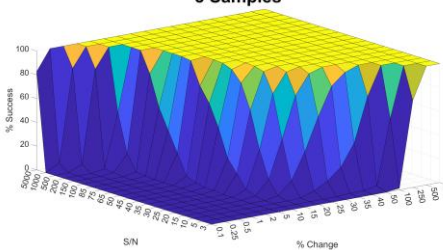
M.J. Herman, C.E. Freye, “Expansion of Alteration Analysis and Two-Dimensional Correlation Analysis to Two-Dimensional Chromatographic Datasets” *in preparation*

Assessing ALA Success for Different Types of Changes

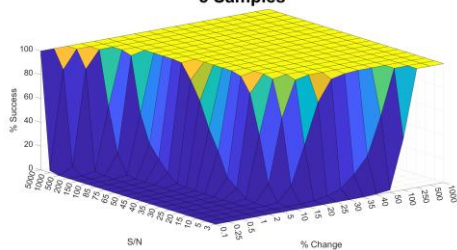


Linear Change (+)

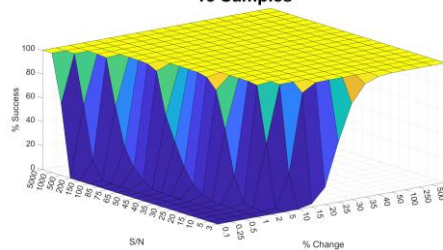
3 Samples



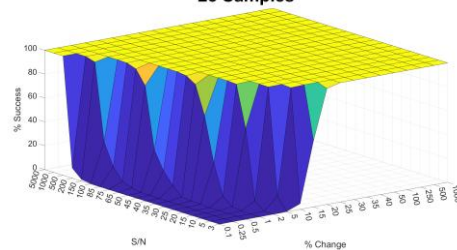
5 Samples



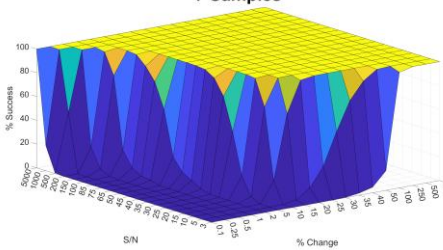
15 Samples



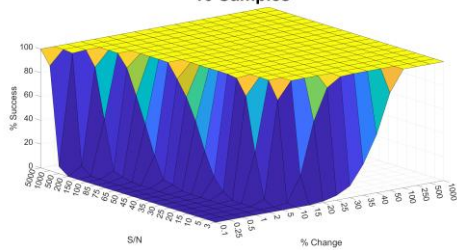
25 Samples



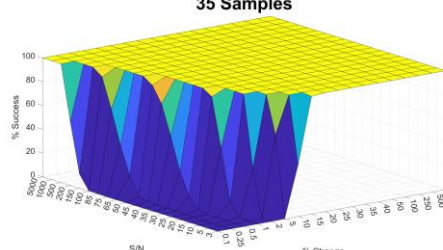
7 Samples



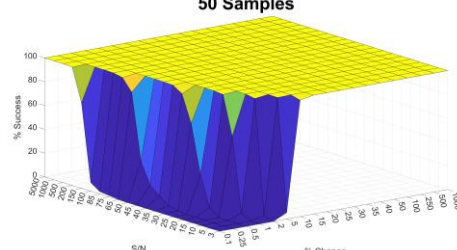
10 Samples



35 Samples

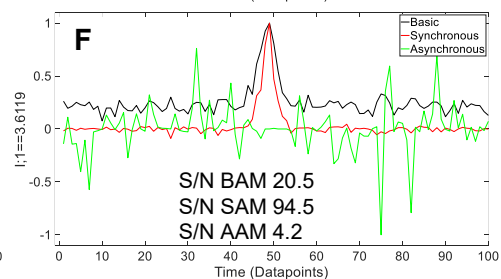
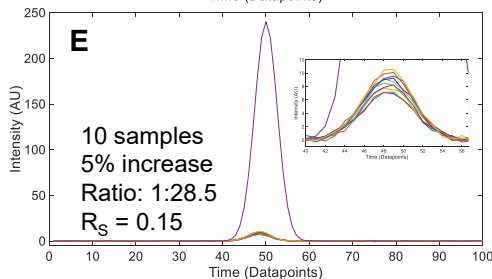
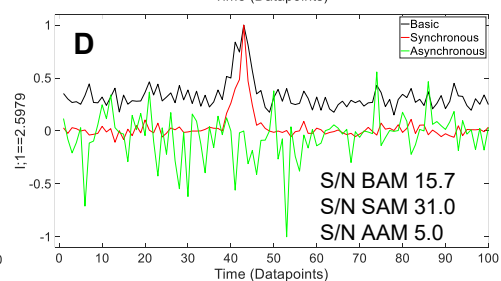
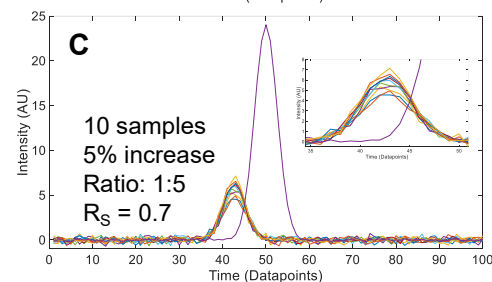
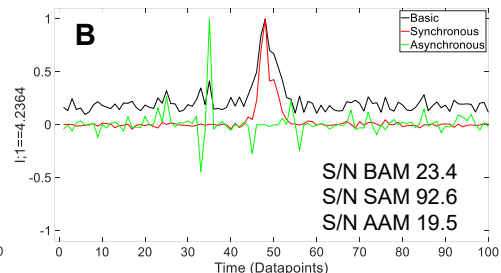
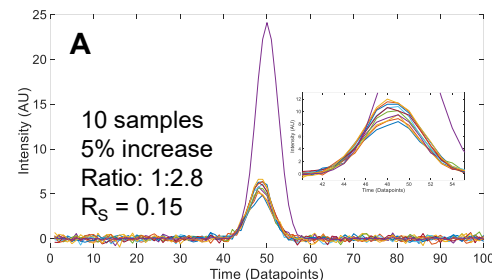


50 Samples



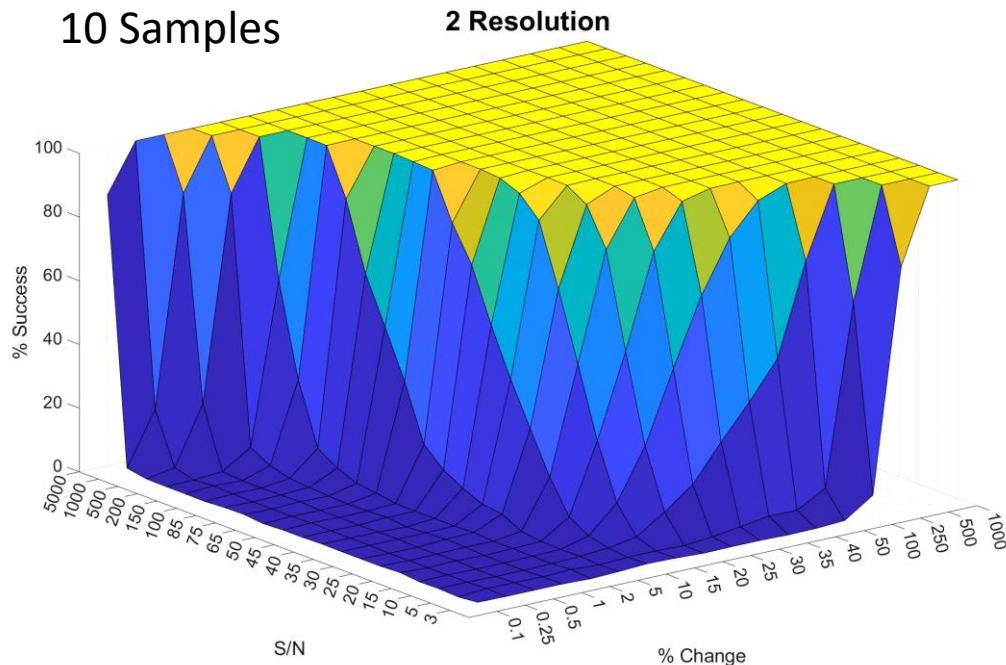
Evaluating ALA for Unresolved Peaks

- For ALA to be applicable to GC / GC×GC datasets it must be able to discover overlapped compounds
- As resolution increases and initial S/N increases, ALA probability of success increases
- Large interferences had less than expected impact on ALA success



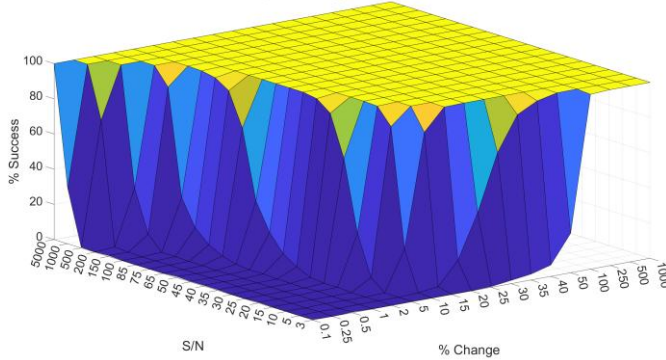
Evaluating ALA for Unresolved Peaks

- ALA success is similar to a single peak down to a R_s of ~ 0.3
- ALA is successful all way down to R_s of 0.01
- As one would expect, as R_s decreases, the initial chromatographic S/N and the amount of change must increase

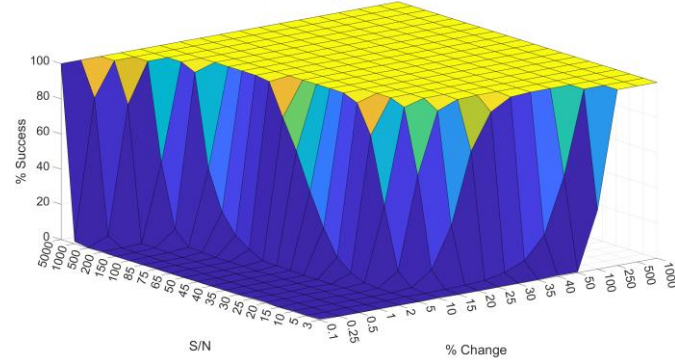


ALA Success at Different Resolutions for 10 Samples

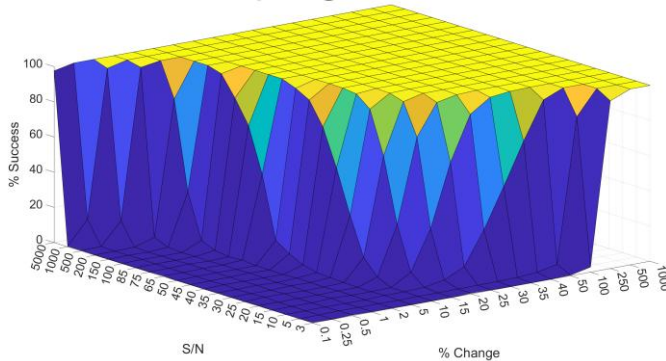
10 Samples @ Resolution 0.3



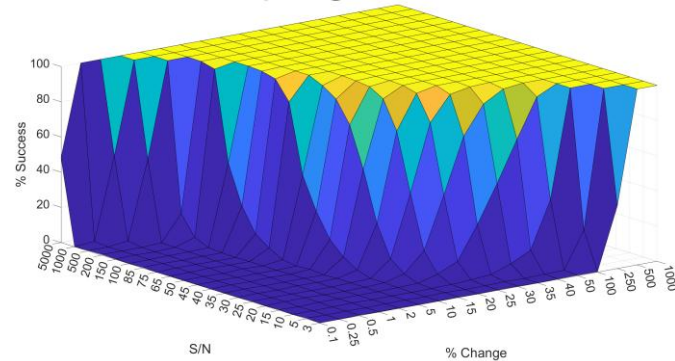
10 Samples @ Resolution 0.15



10 Samples @ Resolution 0.07



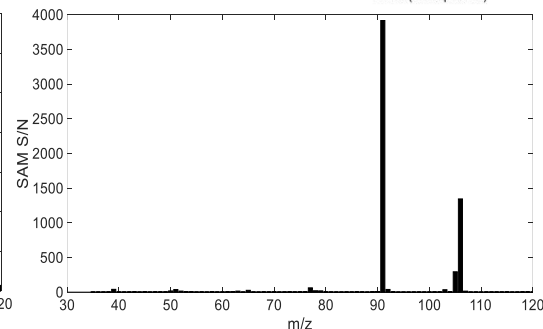
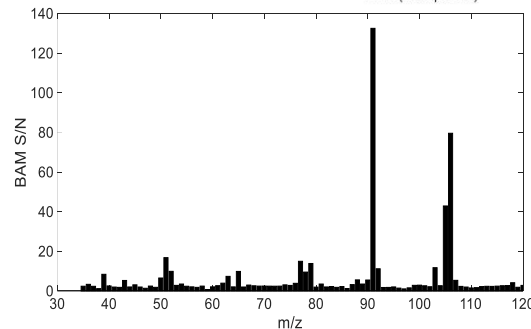
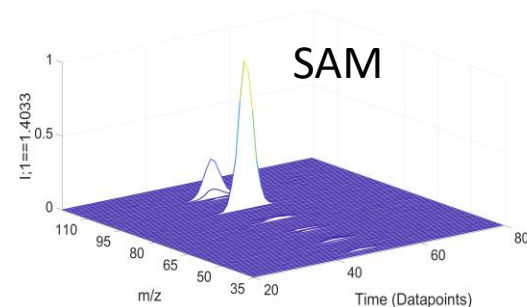
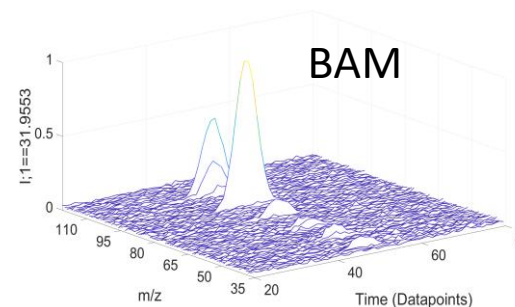
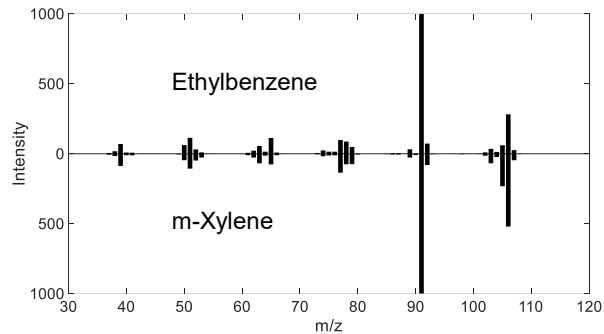
10 Samples @ Resolution 0.01



Expanding ALA to GC-TOFMS

- Evaluation of ALA on multivariate data was successful on highly overlapped, mass spectrally similar compounds
- Defining success if a single m/z passes the ALA S/N requirements

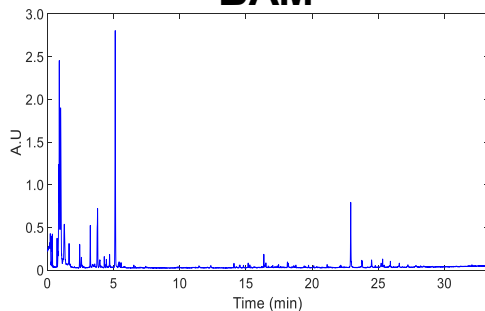
M.J. Herman, C.E. Freye, *Anal. Chem.* 2025, 97, 3, 1528–1538 <https://doi.org/10.1021/acs.analchem.4c03660>



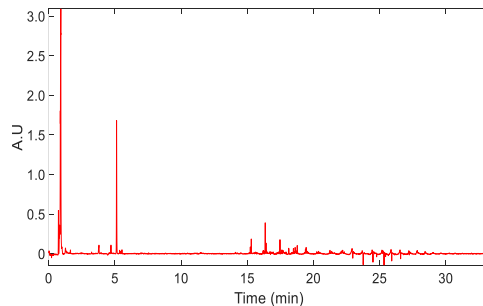
8 m/z had S/N >10 for BAM and 15 m/z had S/N >10 for SAM

ALA and 2DCOR: Application to pyGC-TOFMS

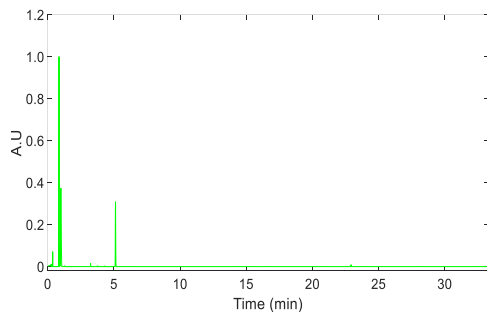
BAM



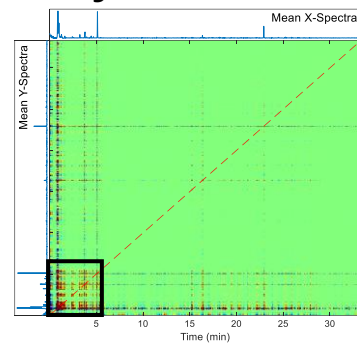
SAM



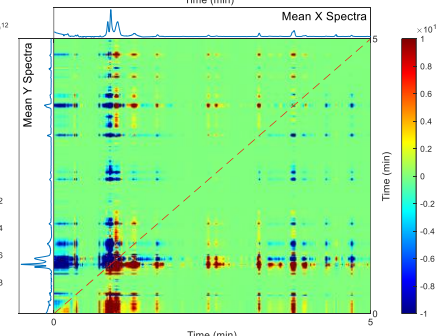
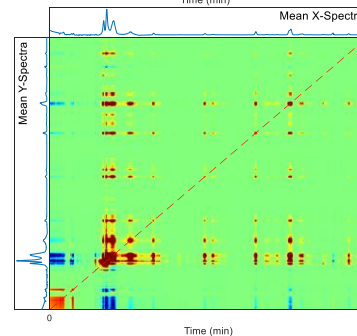
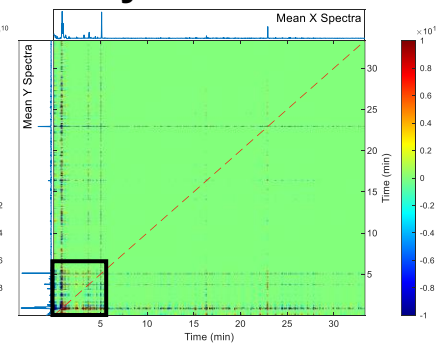
AAM



Synchronous



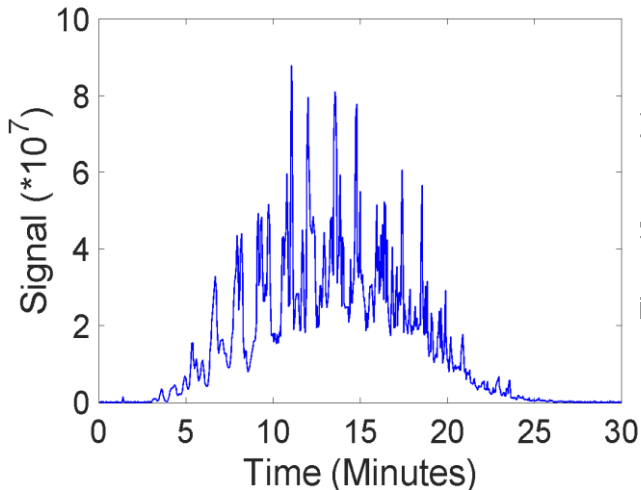
Asynchronous



ALA and 2DCOR works on “real” GC-MS data

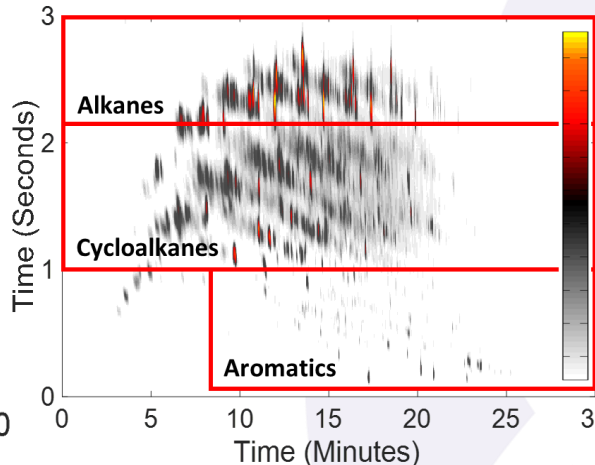
Disadvantages of 2-D Chromatography & High Resolution Mass Spectrometry

GC-TOFMS



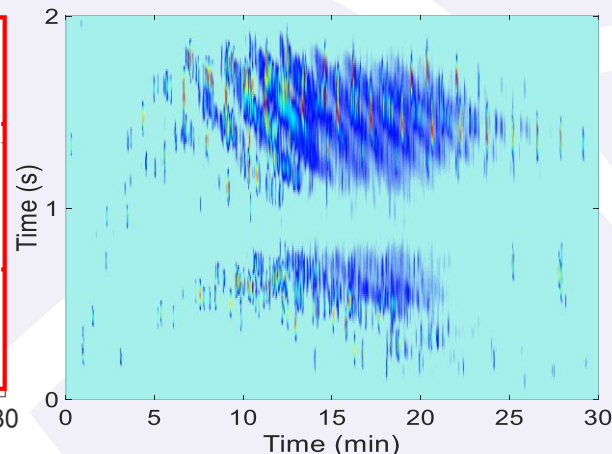
2,700,000 numbers

GC×GC-TOFMS



54,000,000 numbers

GC×GC-HRMS



4,000,000,000 numbers

GC-TOFMS datasets are ~54,000,000 datapoints
GC×GC-HRMS datasets are ~80,000,000,000 datapoints