

Hotelling Trace Criterion as a Figure of Merit for the Optimization of Chromatogram Alignment

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- 1 Introduction to Chromatography
- 2 Theory and Techniques
- 3 Experimental Data
- 4 Results and Future Work
- 5 Acknowledgements

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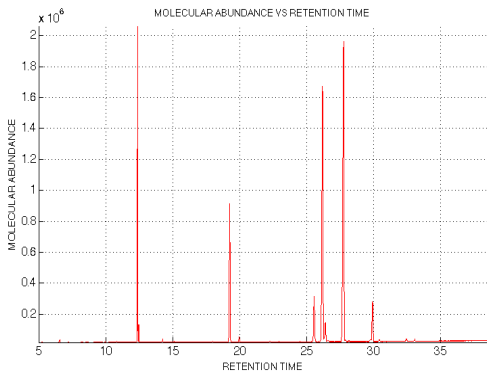
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Gas Chromatography & Mass Spectrometry

- The **gas chromatograph** (GC) and **mass spectrometer** (MS) are two independent instruments which, when combined, create a powerful analytic technique for separating and identifying the components of complex mixtures.

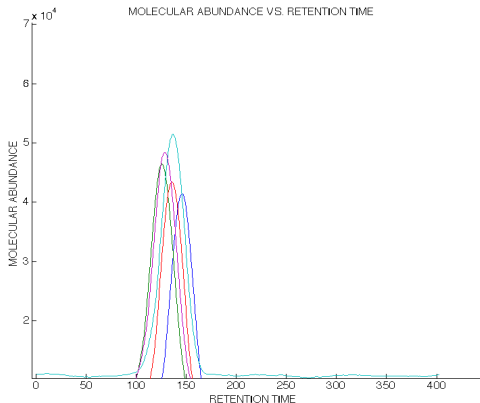
Gas Chromatography & Mass Spectrometry

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- GC + MS produces **chromatograms**:



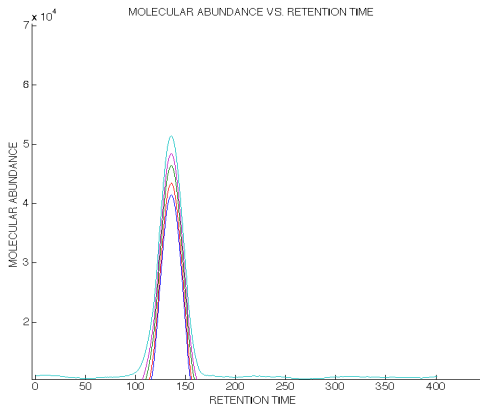
Chromatogram Alignment

- When dealing with multiple samples, fluctuations in peak height and peak location occur.



Chromatogram Alignment

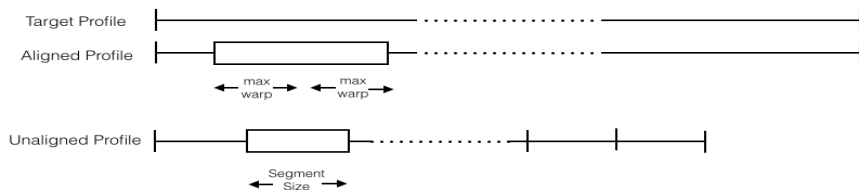
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- Without peak location alignment, trends determined by chemometric methods will be skewed or meaningless.

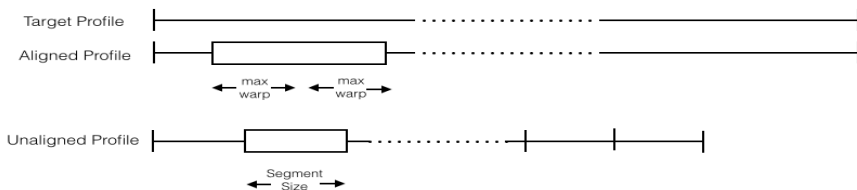
Alignment Techniques

Correlation Optimized Warping (COW): Given two parameters **segment size** and **max warp**, a chromatogram P is aligned to a target chromatogram T .



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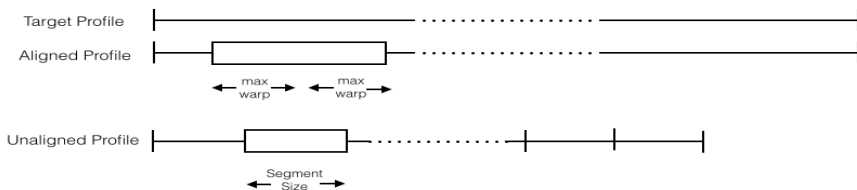


Developed our own..

- Faster version of COW.
- Only Align on Peaks
- Includes a Peak Detection Feature

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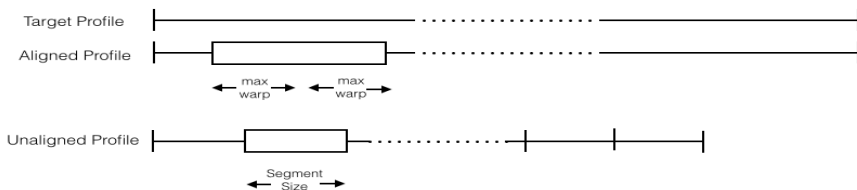


Naturally named, **MOO-COW**:

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What is the optimal choice of COW parameters?

Alignment Metrics

Warping Effect = Simplicity + Peak Factor

- **Simplicity:** *How close is data to rank 1 matrix*

$$\text{simplicity} = \sum_{r=1}^R \left(\text{SVD} \left(\mathbf{x} / \sqrt{\sum_{k=1}^K \sum_{n=1}^{N_k} \sum_{m=1}^M x_{knm}^2} \right) \right)^4$$

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- **Peak Factor:** *How much the shape and peak area of chromatograms have been changed by warping*

$$\text{peak factor} = \frac{1}{N} \sum_{k=1}^K \sum_{n=1}^{N_k} (1 - \min(c_{kn}, 1))^2$$

Alignment Metrics (con't)

Hotelling Trace Criterion

- Incorporates both **within class** and **between class** variation in the data set.

$$HTC = \text{trace}(S_2^{-1}S_1)$$

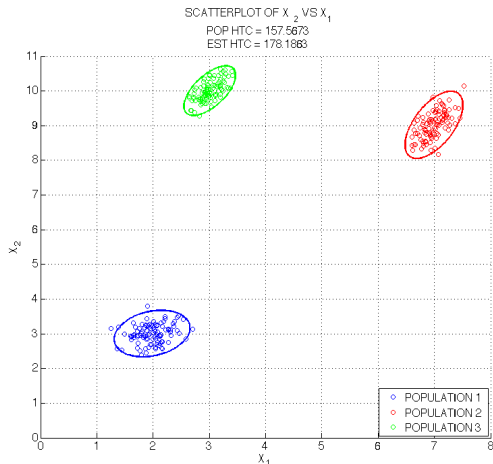
S_1 = Between Class Covariance Matrix

S_2 = Within Class Covariance Matrix

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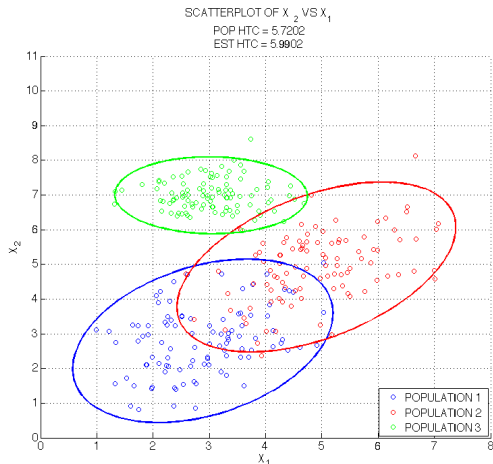


↑ HTC

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- Each sample tested 3 different runs

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- 45 Total Chromatograms

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Data Preprocessing:

Baseline Corrected

Aligned (COW)

Normalized

PC Transformed

Computed Metric

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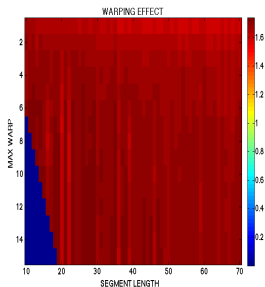
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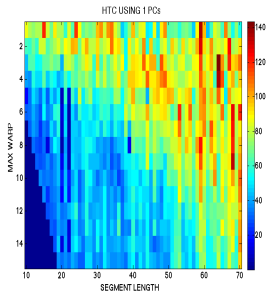
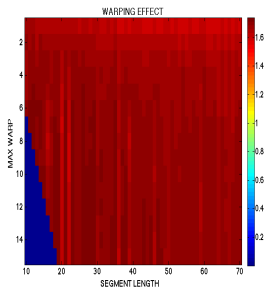
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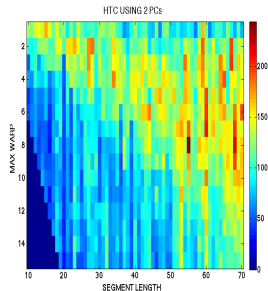
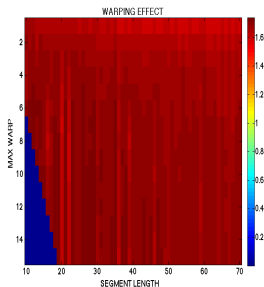
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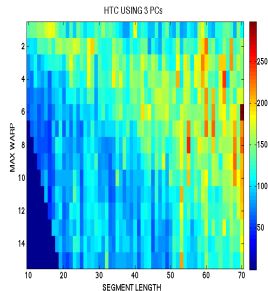
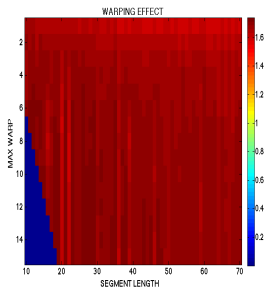
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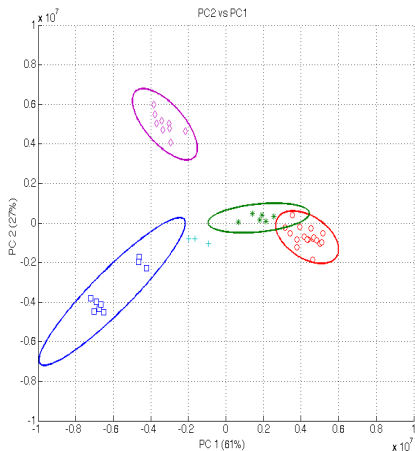
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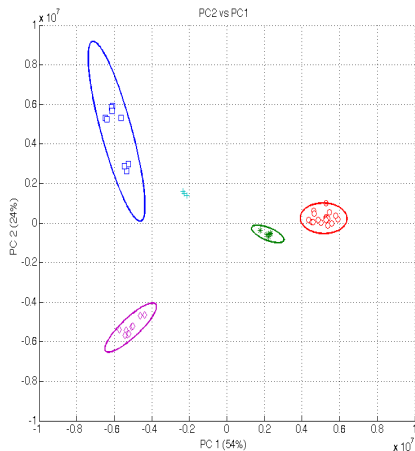


Sample Results

Max Warp Effect



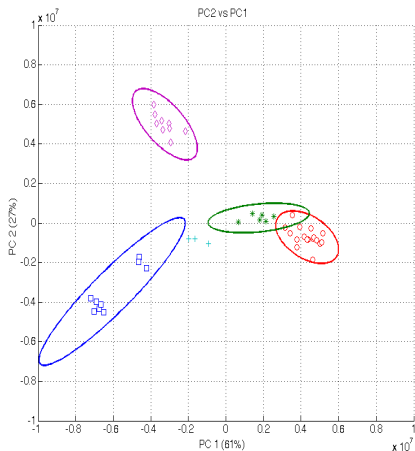
Max HTC (1 PC)



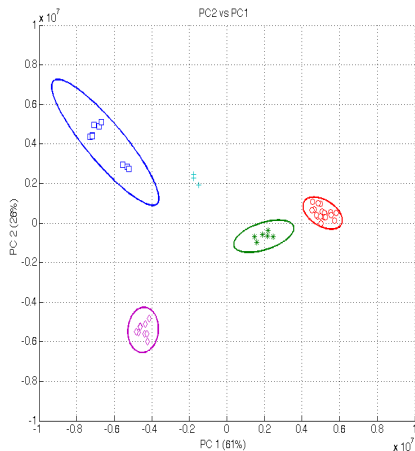
soy (\circ), canola (\diamond), tallow (\square), waste grease ($*$), hybrid ($+$).

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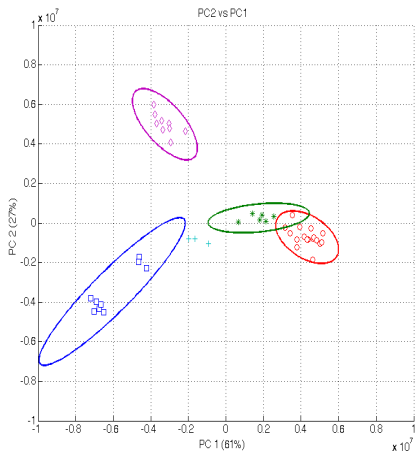
Max HTC (2 PC)



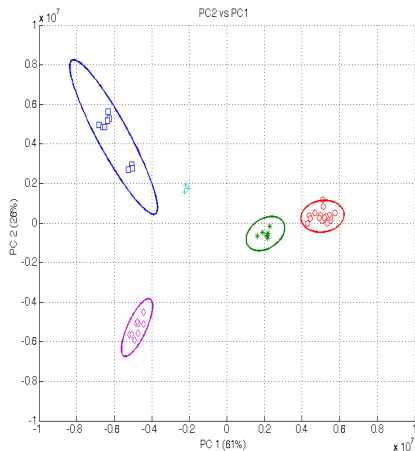
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Max HTC (3 PC)



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Future Work:

- Improve upon COW and other alignment algorithms.
- Build classification scheme for unknown biofuels with similar chemical makeup as a given training set by using HTC as a figure of merit.

Acknowledgements

- *Journal of Chemometrics*

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- Keystone Biofuels,
- TMT Biofuels,
- Texas Green Manufacturing
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