## Retention-Time Based Peak Clustering in Comprehensive Two-Dimensional Gas Chromatography

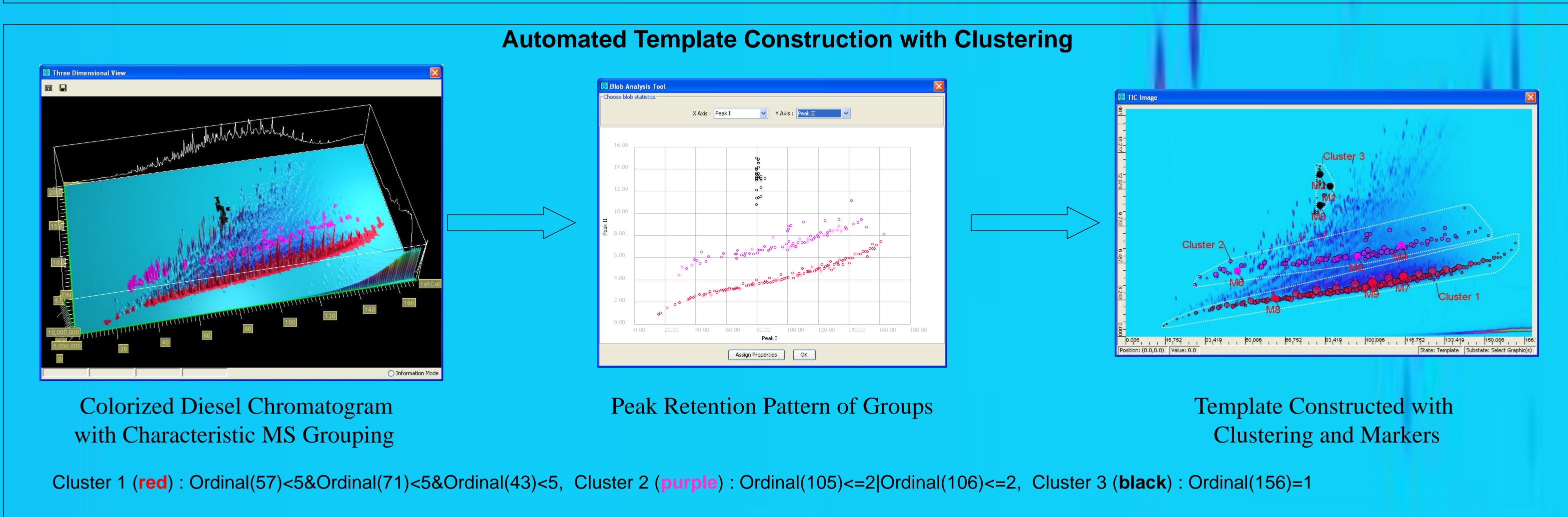
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- Goal: Sample identification and chemical group analysis
  - -GCxGC analyses utilize the inherent relationship between chemical structure and peak position on the retention-time plane.
  - -A template that captures the pattern of peaks in the retention-time plane can be used for registering GCxGC analyses in order to identify chemicals in a sample or to identify similarities and differences between samples.
- Method: Automate construction of templates with retention-time based peak clustering.
  - -Find natural clusters in GCxGC data with the Complete Linkage with PCA algorithm.
  - -Adjust clustering with the Primary Column Weight.
  - -Identify markers for chemical groups.



## **Complete Linkage with Principle Component Analysis**

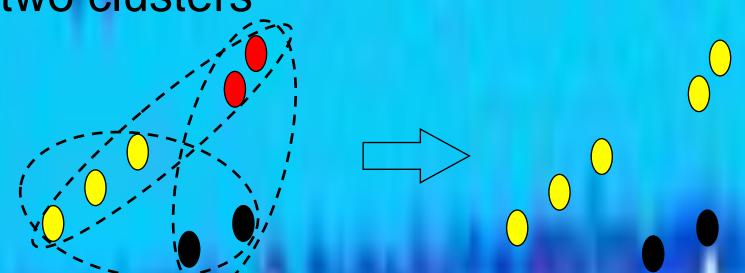
- The objective is to group chemical peaks into "clusters" based on retention times
- Natural clusters of GCxGC data commonly appear as striated bands.
- Complete linkage with PCA is a hierarchical clustering algorithm that uses the "retention-time area", calculated by the PCA of two clusters as the proximity measure.
- The algorithm computes the covariance matrix of the peaks in PC space. The area is equal to the square root of the determinant of the covariance matrix
- The algorithm finds natural clusters in GCxGC data.

## Algorithm:

• Initially, each cluster contains one peak with Gaussian variance.



- Choose the pair of the clusters which, when merged, has the least area.
- Merge these two clusters



• Repeat Steps (2) and (3) until the desired number of clusters are found.

## Comparison on Clustering Algorithms on GCxGC K-means Single Linkage Hierarchical Clustering Complete Linkage with PCA



