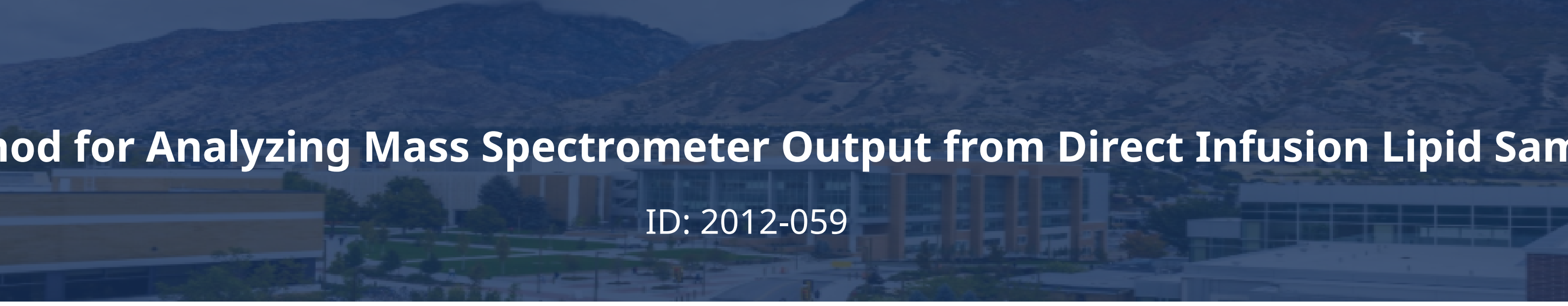

hod for Analyzing Mass Spectrometer Output from Direct Infusion Lipid Sam

ID: 2012-059

Executive Statement:

A novel method to isolate individual isotopic peaks in mass spectrometry data, enhancing accuracy and reliability.

Technology Overview:

This technology presents an innovative approach for analyzing mass spectrometer outputs, specifically targeting the analysis of direct infusion lipid samples. By treating the data as a two-dimensional vector of mass-to-charge (m/z) and intensity pairs, and implementing a unique binning and statistical testing process, this method effectively isolates individual isotopic peaks. This addresses the inherent noise and inconsistency issues found in mass spectrometer outputs, offering a more reliable analysis.

Key Advantages:

- Enhanced accuracy in isolating isotopic peaks
- Improved reliability and consistency between scans
- Outperforms existing commercial software, including proprietary solutions
- Addresses the noisy nature of mass spectrometry data effectively

Problems Addressed:

- Inconsistency and noise in mass spectrometer outputs
- Lack of reliable methods to isolate individual isotopic peaks
- Inefficiency of existing commercial and proprietary software solutions

Market Applications:

- Integration into commercial mass spectrometer software
- Tool for mass spectrometer manufacturers and software providers
- Enhancement for research and development processes in biochemical and pharmaceutical industries