B30 The Development of a Multivariate Mass Spectral Algorithm for the Identification of Seized Drugs

Alexandra Adeoye, BS, West Virginia University, Morgantown, WV 26505; Samantha A. Mehnert, Purdue University, Lafayette, IN 47905; J. Tyler Davidson, PhD, Sam Houston State University, Huntsville, TX 77340; Glen P. Jackson, PhD, West Virginia University, Morgantown, WV 26506-6121*

Learning Overview: After attending this presentation, attendees will understand how correlated relationships between mass spectral ion abundances can be used to discriminate between compounds with seemingly indistinguishable electron ionization mass spectra.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by describing a flexible statistical model that can minimize the risk of false positive and false negative drug classifications in seized drug analyses that use Electron Ionization/Mass Spectrometry (EI/MS) as a basis for identification.

The central hypothesis is that a multivariate algorithm that takes advantage of the innate correlations between ion abundances of replicate spectra can make more accurate predictions than existing compound identification algorithms.

Most search algorithms for EI/MS data make use of a "static" exemplar approach when making unknown identifications. Although different vendors' algorithms vary in their approach, they all compare unknown spectra to discrete, fixed spectra of standards in a library. However, the inter-day or inter-laboratory variance in the abundance of each fragment in a spectrum is known to vary by ±20%, so compounds with somewhat similar EI-mass spectra, like many fentanyl analogs, can be difficult to be confidently distinguished using only the EI spectral comparison. The multivariate algorithm discussed in this presentation takes a more informed approach. It uses an algorithm to effectively interpolate between replicate spectra and provide a continuously variable model of ion abundances for each compound in the database. The model explains most of the variance in replicate mass spectra and enables very confident mass spectral identifications.

A library of spectra for fentanyl analogs was extracted from Gas Chromatography/Electron Ionization/Mass Spectrometer (GC/EI/MS) data by extracting every mass spectrum across the eluting chromatographic peaks of interest. Each chromatogram, therefore, provides seven to ten replicate spectra of various intensities. The 15 most abundant ions were extracted, and the abbreviated spectra were randomly divided into calibration and validation sets. Fifteen General Linear Regression Models (GLMs) were built for each compound by sequentially using each ion's abundance as the dependent variable and the abundance of the remaining 14 ions as the independent variables. In each model, variables were added stepwise until there were no significant improvements in the predictions, which resulted in each model containing four to eight variables. The 15 GLM models for each compound were then used to predict 15 ion abundances in a variety of known positives and known negatives. The predicted abundances were compared to the measured abundances using a variety of similarity and dissimilarity metrics like the Pearson Product-Moment Correlation (PPMC). Each method of similarity scoring was used as a binary classifier to determine True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) rates over a range of threshold values. These classifications were then used to plot Receiver Operating Characteristic (ROC) curves.

PPMC values between measured and predicted spectra of known positives in the fentanyl models exceeded 0.9939 and 0.9977 for the calibration and validation sets, respectively. Known negatives in the validation set typically had PPMC values smaller than the smallest PPMCs for known positives, which resulted in Areas Under the Curve (AUC) of 1 in the ROC plots for binary classification. The residuals in predictions were typically improved by a factor of three or more using the dynamic model relative to the traditional, static approach.

General Linear Model, Mass Spectrometry, Fentanyl Analogs

*Presenting Author