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Automating Data Review for Mass Spectrometry

By Bridgit O. Crews, PhD, DABCC (CC, TC)

Mass spectrometry is an indispensable tool for clinical and forensic toxicology laboratories, but the data generated by these types of assays is complex and relies on manual review by highly trained laboratory professionals. Particularly in toxicology laboratories, liquid chromatography–tandem mass spectrometry (LC-MS/MS) assays often include dozens of analytes, each producing multiple data elements and adding up to tens of thousands of data elements. Highly trained scientists review most of these data elements manually, but this is time-consuming and has potential for human error. There are many potential benefits of automated data review (ADR) for mass spectrometry assays, including improved efficiency, reduction of manual errors, and standardization of data processing.

ADR involves automated rules, calculations, or algorithms that evaluate LC-MS/MS results for acceptability. Many laboratories performing LC-MS/MS are already venturing into ADR in some form, commonly employing mass spectrometry (MS) vendor software to flag specific metrics when they fall outside of preset acceptance criteria. For example, rather than manually check every single ion ratio for every analyte manually during data analysis, it is possible to flag an ion ratio if it deviates too far from the expected value. This saves time and helps to bring focus and attention to problematic specimens. The limitations of this approach are that it still requires the reviewer to manually identify all of the flags (which is prone to error), and there are many steps in the data review process for which it is difficult to develop automated flagging using just MS vendor software.

Breaking Down the Steps of Data Processing and Review

Although the details of a data analysis protocol and review process may vary among different laboratories, the basic steps are universal. The first step that must occur is extraction of the data from the raw MS data file. This raw data file includes mass spectra (for all time points), sample identification information, and other method information recorded during analysis. Clinical and toxicology laboratories do not routinely review the raw data files but rather import these raw data files into other software programs for processing. The most commonly utilized programs are the MS vendor-specific analysis programs, but third-party applications are also available (1, 2). In order to import these raw data files into a third-party program, it is sometimes necessary to convert the MS vendor-specific data files into a format that is compatible with the third-party program (3). Some MS vendor software can convert file formats, and there are open-source external file converters.

Peak Processing and Integration

Once raw data is imported into a processing program (vendor-specific or third-party), it is processed to produce extracted ion chromatograms (EIC), where each multiple-reaction monitoring transition produces one EIC. After this, a peak-finding algorithm identifies "peaks" in the EIC, and the data is often smoothed or processed to reduce noise, which can affect peak shape and peak identification. After peak identification occurs, integration of the identified peaks produces many numerical data elements: peak height, peak width, peak area, signal to

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noise, retention time, etc. These data elements create additional calculated data elements: calibration curves, analyte concentrations, ion ratios, internal standard recoveries, relative retention times, etc.

Peak identification and peak integration are not at all straightforward, and most mass spectrometry vendors have multiple peak integration algorithms because none of them work perfectly on all data. Users can also define peak integration parameters, which is often necessary to achieve the best results, and the resulting quality of all the other downstream data elements relies on the accuracy of peak finding and integration. Peaks that are chromatographically well resolved and relatively symmetric may be easier to identify, but peaks that are noisy and not well resolved from nearby coeluting peaks or the baseline may be more difficult to find and integrate accurately. The performance of peak-finding algorithms depends on method-specific parameters, such as the number points across a chromatographic peak (Clinical Laboratory Standards Institute recommends an absolute minimum of 10 points) (4), the age of a chromatographic column, the performance of the mass spectrometer (whether dirty or clean), and sample-specific interferences. In summary, the parameters for optimal peak integration depend on a variety of assay- and sample-specific input variables that can change over time and even run-to-run or sample-to-sample (5). It is important to stress that good automated peak-finding depends largely on good chromatography and mass spectrometry acquisition methods.

Peak-integration algorithms have improved over time, but this remains one of the main reasons that mass spectrometry data requires so much manual review: visual inspection ensures proper integration and that the auto–peak-integration algorithm did not fail to identify a significant peak. Algorithmic parameters affecting peak detection and integration are complex and a greater description of mathematical underpinnings of peak detection may be found in a review by Lytle et al. (6). Laboratories optimize peak integration settings during method development, but since analytical performance can vary over time, laboratories must continuously monitor the performance of the auto–peak-finding and -integration processes. There is a balance between excluding noise and detecting true peaks, and this may even vary between samples. Unfortunately, there is little guidance for clinical laboratories related to validation of peak-finding algorithms, or even requirements for the review of chromatographic peaks, but laboratories should have an appropriate protocol to ensure the integrity of peak identification and integration, and this typically involves manually reviewing all chromatographic traces (7).

However, in a recent study, Vicente et al. (8) compared a chromatographic review by exception approach utilizing a commercial third-party software (ASCENT, Indigo BioAutomation) to a manual review approach utilizing MS vendor software (TargetLynx, Waters). In the manual review approach, technologists manually reviewed each chromatogram and all the data in the MS vendor software. In the review by exception approach, ASCENT software automatically processed the raw data files after acquisition was completed, including calibration, quality control, and patient samples, and only flagged metrics that violated quality rules (e.g., concentration, ion ratio, fit quality). They validated the ADR approach by correlating manual processing to ASCENT results in 19 batches collected over a span of 7 months using 2 separate LC-MS/MS systems and comparing 1531 patient results with measurable 25-hydroxy vitamin D3 and 249 results with measurable 25-hydroxy vitamin D2. The authors verified all quality flags generated by ASCENT, and tested data flow and integrity across all systems from order to result. Since peak integration can affect calibration accuracy, the authors also analyzed bias in donor serum from the CDC Vitamin D Standardization Certification Program. The authors compared the peak manipulations made by data reviewers in each approach and found 4 times as many manipulations performed by the manual approach compared with the automated approach. They also calculated the median review time for a full batch (96-well plate) dropped from approximately 2 hours with manual review to 14 minutes with automated review.

In another recent study, Yu et al. (9) demonstrated the performance of a machine-learning algorithm to automate data analysis for a gas chromatography mass spectrometry assay for 11-nor-delta-9-carboxy-THC (THC-COOH). The actual data was presmoothed data generated by Mass Hunter (Agilent), which generated 10 quality-related characteristics including peak width, symmetry, and height-to-area ratio, as well as ion ratios and retention times for analyte and internal standards. The initial data set included routine data but excluded results for quality control samples, calibrators, and patient samples with THC-COOH below the analytical measurement range. The final model showed 100% positive percent agreement and 81% negative percent agreement in detecting the results flagged by manual review (in a test data set of 419 results).

It is important to note that in these two examples, automated data review only included analysis of analytes that were always detected (or always measurable). Toxicology applications are particularly challenging areas for automated chromatographic review, because toxicology assays are often multiplex assays containing many analytes, and samples are often negative for many of these analytes. This makes it difficult if not impossible to set up a flagging system to identify

"missed" chromatographic peaks. The high probability for saturated peaks (which are commonly missed by peak integration algorithms) and chromatographic interferences also complicate automated peak detection for some toxicology assays.

Metadata Analysis

Metadata provides information about collected data but does not include the full content of that data. For example, metadata produced by an LC-MS/MS assay might include information on the shape of a chromatographic peak (e.g., peak height, area, peak width, retention time, etc.), but not the actual graph of the chromatographic peak itself. Typical metadata derived from mass spectrometry analyses include concentrations, retention times, basic peak parameters, and also data that can be used to compare different peaks and specimens, including relative retention times, ion ratios, internal standard recovery, analyte concentration, etc. (10, 11). The purpose of metadata analysis is to leverage all of these available elements to systematically carry out multiple quality checks through a systematic and automated (or semiautomated) process.

Most current MS vendor software has the capability to set up flagging rules to compare and flag many different data elements, although some may require user customization. Most MS vendor software can calculate an expected internal standard peak area from one or more calibrators and flag any analyte in an individual batch that has an internal standard recovery outside of this calculated range. This is certainly more efficient (and less error-prone) than manually comparing each internal standard peak area to an expected range, but still requires an element of manual review, and technologists do miss flagged samples occasionally. It is also challenging (and in many cases not possible) to set up flagging criteria that can be compared across analytes and across samples. For example, if a particular analyte exceeds a carryover limit, most software can flag that high sample, but a technologist must still manually check the subsequent samples for potential carryover. If overlooked, there is a risk for false positive results. Additional quality assurance processes include extraction, hydrolysis, or dilution controls; checks for cross-contamination;

Box 1.

Alec Saitman, PhD, DABCC (CC, TC), technical director of chemistry and special chemistry at Providence Health Services in Portland, Oregon, has spent the last few years planning and developing ADR for MS in his laboratory. His lab currently automates data review for THC-COOH confirmations, with more assays in development. He volunteered to share some details of their workflow and challenges.

What is your current workflow?

Our current process includes exporting mass spectrometry data (MultiQuant, Sciex) to a middleware program [Data Innovations, (DI)] via an original driver developed by DI in collaboration with Sciex, and our laboratory. DI receives 27 data elements from MultiQuant (e.g., retention time, peak height, peak width at 50%, asymmetry factor, tailing factor, etc.) and performs calculations and flagging based on rules that our laboratory technologist helped design, write, and test with support from DI and our information technology department.

What challenges did you encounter?

We did receive a large amount of support from our middleware vendor, DI. They took the time to send out DI representatives to our laboratory to review mass spectrometry–based data alongside the toxicologists. The single largest challenge was having the mass spectrometry vendor work with our middleware vendor to build some of the back-end system (namely a driver). There are many data elements available as fields in the mass spectrometry application, but to transmit these to our middleware we needed a unique driver. Although the middleware vendor developed this, it also required collaboration from the mass spectrometry vendor, and our laboratory drove that almost entirely to keep forward traction.

What are the major improvements?

Time-saving and standardization. The review time decreased by around 75% per week (5–15 technologist hours) for this single assay. In addition, every sample goes through identical flagging criteria. There is less subjectivity, which can be significant if many different technologists perform manual review. The validation phase did reveal errors in the manual process. Most were small and clinically insignificant, but it highlighted the fact that manual review fatigue is a potential quality gap that an automated data review approach can help to mitigate.

Is there anything you would do differently?

Setting more realistic expectations about how quickly we could get the project developed and how willing our vendors would be to assist with the build. We expected the project to take 6 months from start to go-live, but it took well over 24 months.

Are you planning to expand the ADR program in your lab?

We developed a road map to validate additional urine drug confirmation assays. Each assay is unique, but some existing rules apply across assays, so each subsequent implementation is more streamlined.

positional control (designed to ensure sample worklist order); and other quality rules such as delta checks or comparison of immunoassay screening or prescription lists to confirmatory results (12). These quality checks are most often reliant on manual review processes or metadata review in programs outside of MS vendor software. ADR for these more complex scenarios is possible using third-party applications, middleware applications, and/or laboratory information systems (LIS). Depending on the complexity of the scenario and the information that is required to determine acceptability, one or more approaches may be suitable.

In order to incorporate additional ADR programs outside of the MS vendor software, those programs need to have access to the metadata produced by the MS vendor software, which requires interfacing. There are different ways to interface mass spectrometry data, but it is typically done through a direct interface, through a middleware, or through a flat-file interface (13). This can require a driver, which enables communication between a device and a program, for example enabling transfer of data from the mass spectrometer to a middleware program, or an LIS. Most interface drivers only deal with a few necessary data elements: sample identifier, test name, and concentration (or value); therefore, getting additional data elements from the MS vendor software into another program can be a challenge, and may require the development of a unique driver. This requires collaboration between the MS vendor and the LIS or middleware, which can be time-consuming and generally involves a fee.

There are other ways to approach the more complex steps of data review using third-applications that do not necessarily require a driver, but these approaches do require access to individuals with more advanced knowledge in software engineering. In one example, Dickerson et al. (14) designed and implemented automated quality control and data analysis for a complex LC-MS/MS assay for urine opioids. The process included a cursory review of the autointegration of chromatographic peaks in the MS vendor software (TargetLynx, Waters), followed by an export of XML files to a server, where they were processed by a script implemented through Python (run at the command line, an environment that is not unfamiliar to laboratory personnel since it is similar to some LIS systems). The authors estimated that the automated quality control process saved around 4 hours per run (in data analysis time) and identified at least one manual error caught by the software (in a set of 13 runs).

Although the process to achieve automated data review is challenging, it is not without benefits, and persistence is a requisite. Laboratories should evaluate what types of review steps they can already semiautomate with their current tools (likely MS vendor specific software) and develop a systematic approach for data review as a starting point. Laboratories with sufficient volume and/or technical expertise may benefit from more advanced third-party applications and should explore these options.

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Gabapentin Misuse in the Context of the Opioid Epidemic

By Sarah S. Shugarts, PhD, DABCC, TC

The landscape of drug use and misuse is constantly evolving, requiring providers and laboratory personnel to reevaluate testing practices and methodologies to ensure appropriate patient care. This applies as much to prescription drugs as to illicit drugs. We've all become all too familiar with the evolution of the opioid epidemic, as the drug of choice shifted from prescription painkillers such as oxycodone, to heroin, to fentanyl and its analogs. Alongside this progression, another drug has quietly come along for the ride.

For a variety of possible reasons, gabapentin use has increased dramatically over the last 10 years. Pauly et al. (1) reported that the prevalence of gabapentin prescriptions approximately doubled from 2009 to 2016 in a privately insured population, with increases seen in every state of the United States. A 2019 Drug Enforcement Administration (DEA) report (2) supported the results of Pauly et al. when looking at gabapentin prescriptions dispensed from 2011 to 2017. In 2011, 33.4 million gabapentin prescriptions were dispensed. This nearly doubled to 64.8 million prescriptions in 2017. As more gabapentin circulates in the licit drug supply, illicit use and supply have also increased. The National Forensic Laboratory Information System, which collects drug analysis information from a variety of federal forensic laboratories across the United States, reported a 9-fold increase in gabapentin reports from 2007 to 2018. The Researched Abuse, Diversion, and Addiction-Related Surveillance system, which monitors diversion and misuse/abuse of prescription drugs, reported that there were 0.027 cases per 100,000 population of gabapentin diversion in 2015. In 2002, there were no cases (2).

Since the mid-2010s, several studies have been done to characterize the nature of gabapentin misuse and abuse with respect to the general population, susceptible populations, and potential drivers of misuse/abuse. Evoy et al. (3) published a systematic review in 2017 of studies performed since 2010 addressing gabapentinoid misuse/abuse. Their research indicated that prevalence of gabapentinoid abuse in the general population was less than 2%, while in those with a history of opioid abuse the prevalence ranged from 3% to 68%. A 2016 study by Bastiaens et al. (4) included interviews with former inmates now living in a correctional community center and found that 26% of respondents with opioid use disorder reported gabapentin abuse. By contrast, only 4% of respondents without an opioid use disorder reported nonmedical gabapentin use. Peckham et al. (5) assessed gabapentin misuse in a commercially insured United States population and also found evidence supporting higher gabapentin abuse in patients taking concomitant opioids vs those without. Overuse of gabapentin in non-opioid–treated patients was 2.0%, while in opioid-treated patients, 11.7% met criteria for sustained overuse of gabapentin. Postmortem toxicology evidence also shows significant presence of gabapentin in opioid overdose deaths. In 2015, 26% of decedents positive for opioids were also positive for gabapentin in cases from the southeastern United States (6).

There are numerous reasons why gabapentin use and abuse has become so prevalent. While its specific mechanism of action is unclear, gabapentin is considered to have an excellent safety profile with low abuse potential. It was originally approved by the US Food and Drug Administration (FDA) in 1993 for adjunctive treatment of partial seizures and was later approved for use in children for the same indication, for treatment of postherpetic neuralgia, and for restless leg syndrome (7, 8). Doses up to 3600 mg/day have been reported to be well-tolerated. Gabapentin has low protein binding (3%), is not metabolized, and shows no inhibition of cytochrome P450 (CYP) isoforms except for low-to-moderate inhibition of CYP2A6 (14% to 30% at 1mM concentration) (9), giving it a nearly ideal pharmacokinetic profile from safety and tolerability aspects.

Bonnet et al. (10) published a review article in 2022 summarizing the evidence regarding the addictive potential of gabapentin. To date, very little evidence exists indicating that gabapentin has substantial addictive potential. Animal studies indicate no rewarding properties and no reports were found regarding patients seeking treatment for gabapentin dependence when no prior history of substance abuse was present.

Gabapentin has a multitude of off-label uses, including for anxiety and mood stabilization, insomnia, nonneuropathic pain, and recreational drug withdrawal symptoms (10). Wide use in these vulnerable populations due to its perceived safety has likely facilitated gabapentin make the transition to a drug of misuse/abuse.

Misuse/abuse of gabapentin generally follows one of two patterns: patients who have a prescription who take higher than recommended doses to achieve a psychoacitve effect and patients without a prescription taking gabapentin to achieve a psychoactive effect or pain relief or self-treat drug withdrawal. Buttram et al. (11) conducted a study in patients entering a treatment/detox facility to gain insight into why patients misused gabapentin. The predominant reason was to achieve a high after taking supratherapeutic doses. Patients also reported using gabapentin to alleviate withdrawal symptoms such as anxiety and insomnia. Other motivations included that gabapentin would not show up on a general drug screen and "freelapsing," in which patients justify getting an attenuated high while not adversely affecting their sobriety. Smith et al. (12) studied a group of people actively abusing diverted prescription opioids (not in treatment) in Appalachian Kentucky and determined that 15% were using gabapentin to achieve a euphoric effect. They reported that physicians were the source of 52% of the gabapentin while drug dealers accounted for 36%.

Gabapentin is not currently classified by the US DEA as a controlled substance, however several state pharmacy boards, including Alabama, Kentucky, Michigan, North Dakota, Tennessee, Virginia, and West Virginia, have made it a Schedule V drug. Additionally, Connecticut, Washington DC, Indiana, Kansas, Massachusetts, Minnesota, Nebraska, New Jersey, Ohio, Oregon, Utah, and Wyoming mandate reporting of gabapentin in their respective prescription drug monitoring programs (13). These actions should help with future research on prevalence of gabapentin use and in determining what effect scheduling has on diversion and misuse/abuse.

Another tool for managing inappropriate use of gabapentin is urine drug monitoring. Currently, few laboratories routinely incorporate gabapentin in urine drug screens. A study from Riley et al. (14) demonstrates why that may need to change. In their study at the SSM Health Saint Louis University Hospital, 100 urine samples from the emergency department were screened by immunoassay (amphetamine/methamphetamine, barbiturates, methadone, phencyclidine, opiates, cannabinoids, cocaine, and benzodiazepines) and by liquid chromatography with tandem mass spectrometry. The results were remarkable for gabapentin being detected by LC-MS/MS in 28% of samples. Of those, 95% were positive for one or more opioids, with 33% of those having fentanyl. This data supports the epidemiological studies that have found significant misuse/abuse of gabapentin in patients taking opioids, both prescription and nonprescription. Given that the FDA in 2019 issued a warning that gabapentin can contribute to serious breathing problems in patients with respiratory risk factors including use of opioid pain medications, gabapentin and gabapentinoid screening may be an important analytical service to offer.

Gabapentin can be a challenging drug to analyze and would benefit from a screen-to-confirmation workflow. Gabapentin doses, especially in misuse/abuse situations, are generally at the higher end of daily recommended doses, with case reports of doses as high as 12,000 mg of gabapentin (7). Additionally, rather than being spread out over time, they are often taken at once to achieve the psychoactive effects. Gabapentin is excreted unchanged in urine, so it is possible to see levels >40 g/L in random urine samples. These high levels can cause poor chromatography due to massive overloading of the analytical column in high performance liquid chromatography. Screening to get preliminary levels would guide dilutions needed for confirmation testing to avoid inaccurate results and possible carryover contamination into subsequent samples (15).

In summary, gabapentin has emerged as a drug of abuse primarily in opioid-dependent populations. It has been implicated in respiratory difficulties, making its use in opioid abusers especially concerning. Efforts to mitigate harm from its abuse include rescheduling it as a Schedule V compound and instituting screening for it in emergency medicine settings. The evolution of gabapentin use from initially being prescribed for only a few approved indications to now being used off label for a wide array of conditions and making its way into the illicit drug supply demonstrates why continued monitoring of drug use trends, even for those drugs with seemingly ideal safety profiles, is extremely important in the quest to best care for patients.

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Update from the International Association of Therapeutic Drug Monitoring and Clinical Toxicology 2022

By Christine Snozek, PhD

The 20th congress of the International Association of Therapeutic Drug Monitoring and Clinical Toxicology (IATDM-CT) was held September 18–21, 2022. Attendance continued to decrease compared to pre-COVID years, but participants from around the world traveled to Prague, Czech Republic, under the theme of "Bridging the Troubled Waters."

The congress was preceded by a symposium on model-informed precision dosing, incorporating didactic and hands-on sessions on pharmacometrics. The conference program kicked off with a plenary talk from current IATDM-CT president, Dr. Dario Cattaneo. Dr. Cattaneo spoke on his 15+ years' experience with therapeutic drug monitoring (TDM) for antiinfective drugs in special populations, particularly patients at the extremes of age and pregnant mothers. Later symposia and oral presentations expanded upon this, with discussions ranging from infections in implanted devices to pharmacokinetic models for antibiotics.

Monday's plenary from Professor Emeritus Hans Maurer highlighted recent progress in mass spectrometry for toxicology and TDM, which set the stage for a strong focus on advances in test methodologies during the rest of the conference. Subsequent speakers emphasized the versatility of high-resolution mass spectrometry and its power for applications such as metabolite discovery, especially when coupled with additional technologies such as molecular networking.

Keeping with the theme of advances in testing, the final plenary speaker Dr. Christophe Stove provided an overview of microsampling for TDM and chaired a symposium on the same topic. Capillary sampling, dried blood spot analysis, and drug biosensors were highlighted for their potential roles in facilitating precision medicine while reducing blood loss and patient discomfort. Other hot topics of the congress included biologics; novel and classic drugs of abuse; and the complementary roles of TDM, pharmacometrics, and pharmacogenetics.

During the congress, the C.E. Pippenger award for outstanding contributions to therapeutic drug monitoring was awarded to Teun van Gelder from Leiden University in the Netherlands. Professor van Gelder was recognized for his work bridging internal medicine, nephrology, and clinical laboratory testing, particularly in the realm of transplant immunosuppression.

Congress social events included a welcome cocktail after the opening plenary and a banquet held at the century-old Municipal House in historic Old Town Prague. Conference attendees were treated to excellent scientific presentations in a highly interactive format, in the setting of one of the most beautiful cities in Europe. Consider joining the 21st IATDM-CT congress, which will be held September 24–27, 2023, in Oslo, Norway!

Christine Snozek, PhD, is director of central processing and support services and codirector of chemistry and point-of-care testing at Mayo Clinic in Arizona. She was previously associate director of the toxicology and drug monitoring laboratory at Mayo Clinic Rochester. She is a member of the Clinical and Forensic Toxicology News *editorial advisory board. Email: Snozek.Christine@mayo.edu.*

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Society of Forensic Toxicologists (SOFT) Annual Meeting Recap

By Jennifer Collins, PhD

The annual meeting of the Society of Forensic Toxicologists (SOFT) was held in Cleveland, Ohio, from October 30 to November 4, 2022. Headquartered at the Huntington Convention Center, over 800

individuals from both within and outside the United States attended. There was no virtual option this year; all sessions and events were live and on-site. A mobile app for the meeting was available to assist with scheduling and navigating the event.

Starting with the National Laboratory Certification Program Inspector/Lab Director workshop on Sunday, October 30, the week included many opportunities for learning, networking, and socializing. There were 10 workshop offerings on Monday and Tuesday that covered a wide range of topics including process improvement and automation, fentanyl and other novel psychoactive substances, analytical methodologies and optimization, drugs and behavior, postmortem alcohol interpretation, expert testimony, and knowledge transfer between forensic and public health labs. The official meeting kicked off with the welcome reception in the exhibit area on Tuesday evening followed by the plenary session on Wednesday morning delivered by Jolene DeFiore-Hyrmer, MPH, of the Ohio Department of Health. Her presentation, *Unintentional Drug Overdose in Ohio: Using Population-Based Data Sources and Surveillance with Toxicology Data to Drive Public Health Action*, reiterated the importance of laboratory-provided toxicology data in public health programs.

The scientific sessions began on Wednesday and continued through Friday's closing ceremony. The sessions were organized by topic and included presentations such as Alternative Matrices and Drug Facilitated Crimes, Postmortem Toxicology, Drugs and Driving, Human Performance Toxicology, Novel Psychoactive Substances and Clinical Toxicology, and Analytical Toxicology. The Thursday afternoon session featured presentations by Educational Research Award and Young Scientist Meeting Award recipients for 2022. In addition, 120 posters over 2 sessions provided the opportunity to interact with presenters up close. Meals and breaks in the Exhibit Hall as well as a variety of lunch-and-learn sessions fostered interactions with vendors and sponsors over the course of the meeting.

SOFT has developed several programs to promote the field and encourage development of young scientists working in toxicology. The Young Forensic Toxicologists (YFT) committee plans events for attendees 40 years old or younger, and the meeting included a YFT Symposium and Professional Development Fair on Sunday, October 30, as well as a Student Enrichment Program on October 31. The symposium keynote speaker, Dr. Teri Stockham, presented information about the business side of being an expert witness.

A SOFT meeting tradition, the Elmer Gordon Open Forum was held on Tuesday, November 1. This evening session is moderated as an informal discussion of problems, experiences, and trends among colleagues working in forensic toxicology laboratories. Always a popular event, the forum is named for Elmer L. Gordon, who was a toxicologist with the Monroe County, New York, medical examiner and a member of the Tuskegee Airmen in World War II.

The off-site event this year was held at the Rock and Roll Hall of Fame and Museum, located on the shore of Lake Erie within walking distance of the convention center and hotels. Designed by the renowned architect I.M. Pei, the museum features 7 levels of exhibits documenting the history of rock music and the artists and other notable figures who have influenced its development. SOFT attendees enjoyed food, beverages, and a cover band at the evening event.

The meeting ended with the closing ceremony on Friday, November 4, 2022. Next year's meeting is scheduled for October 29 to November 3, 2023, in Denver, Colorado. SOFT is a professional organization comprised of practicing forensic toxicologists and those interested in the discipline for the purpose of promoting and developing the field. For additional information, go to www.soft-tox.org.

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