

# Research Newsletter

Supported by:

Laboratories and Educators Alliance Program (LEAP) of The American Society of Crime Lab Directors (ASCLD)



## *This semester at COFSE*

- At the 2020 72<sup>st</sup> Annual American Academy of Forensic Science (AAFS) in Anaheim, California, COFSE members discussed and showcased advancements in various disciplines of forensic science. COFSE held a workshop titled “High-Impact Practices in Forensic Science Education” at the AAFS meeting. If you are conducting research in pedagogical techniques for forensic science education consider contributing to COFSE sessions at the 2021 AAFS meeting.
- COFSE collected and disseminated online educational resources during the COVID-19 transition to online teaching mode. If there are practices that worked well for you, especially in teaching in upper level laboratory based classes, please share them to with the COFSE community.

## Public Repository of Evaluation and Validation Tracking Provided by ASCLD

**Objective:** Provide a centralized location to share information that may be useful to the broader community of forensic practitioners. This will include timely evaluations of new tools or technology that labs are curious about, as well as recent validations of new tools or technology that can serve as a blueprint to help labs avoid reinventing an entire experimental design.

**Status:** The website collector is now live! [ASCLD Validation Evaluation Repository](#)

Please submit your new and exciting evaluations and validations!  
ASCLD- Forensic Research Committee (FRC) STRATEGY: This cultivated repository is designed to catalog the outstanding work of experts in the field and share these results with the forensic science community. ASCLD is excited about creating an environment to foster communication and reduce unnecessary repetition of validations which will benefit the practitioners working in the laboratory and the field. If you find a validation or research project that you would like more information about, simply use the contact information provided to request a copy or chat with the experts who did the work.

**Goal:** To have at least 20 evaluations or validations of new technology available on the website by the end of 2020.

## Spring 2020

To feature your research projects please visit [COFSE Research Committee](#) page and submit the Research information form

For more LEAP information or for additional information about the ASCLD Forensic Research Committee or to sign up as a forensic laboratory or an educator, please visit: [ASCLD FRC](#) or [COFSE LEAP Link](#)

*LEAP- Where Forensic Laboratories and Collegiate Academic Programs can work together to strengthen forensic science.*

[www.asclد.org/forensic-research-committee](http://www.asclد.org/forensic-research-committee)

## Research in the Community

**A fully continuous machine learning approach to predict the number of contributors in sequence-based DNA profiles.**

*PI: Michael Marciano, Ph.D.*

*Co-PIs: Jonathan Adelman and NicheVision Forensics Syracuse University, NY*

*DNA/Biochemistry*

We present NIJ grant 2018-DU-BX-0202 (“A fully continuous machine learning approach to predict the number of contributors in sequence-based DNA profiles” - M. Marciano, J. Adelman, and NicheVision Forensics) as an example of current research that depends on - and leverages - a large, multi-source dataset to explore forensic problems in ways that would not be otherwise achievable. Over the past decade, the field of forensic DNA analysis has experienced significant technological advancements including new methods to increase the sensitivity of detection, the development of software to assess the contributors in mixtures, and probabilistic genotyping. Despite this advancement, mixture interpretation remains a key hurdle for forensic scientists. This challenge is independent of the laboratory method and instrument, existing both in currently validated techniques such as fragment analyses using capillary electrophoresis and in emerging technologies such as massively parallel sequencing. Mixture interpretation has thus far received a paucity of attention in emerging and soon-to-be-validated next generation DNA sequencing (massively parallel sequencing). Within the larger challenge of mixture interpretation lies a singular critical component, the assessment of the number of contributors (NOC). The assumption of the NOC provides the underlying support for the vast majority of subsequent assumptions such as the presence of allelic dropout and the pairing of sister alleles. The primary objective of our research is to develop a fully continuous probabilistic machine learning-based tool to predict the number of contributors in sequence-based data sets. The project’s use of machine learning, which is ideally suited for complex, high-dimensional classification problems, complements the impending transition to NGS. By proactively developing software tools and solutions specifically tailored to NGS-based mixture interpretation, the forensic science community will be given the proper time and resources to scrutinize, optimize, and potentially implement the methods proposed in this project.

**The Aging Process of Latent Fingerprints by 2-D and 3-D Imaging Techniques**

*PI: Josep De Alcaraz-Fossoul, Ph.D*

*University of New Haven, CT*

*Latent Prints/Fingerprints*

Current fingerprint methodologies can successfully identify individuals by the morphological patterns of ridges (i.e. minutiae) in a semi-automatic process. However, the absence of methods and mathematical models to effectively and objectively date a latent (invisible) fingerprint remains an unsolved challenge with valuable practical implications in crime scene investigations and the criminal justice system. While scientific research has focused on effectively visualizing latent fingerprints and reliably matching them to their rightful donor, few studies have been conducted to develop methods to estimate the “age” or the time of deposition at the scene. The factor “time” becomes especially relevant in crime cases where suspects are erroneously released and innocent people wrongly implicated because fingerprint evidence cannot be substantiated in court by the time of placement or by contradicting statements from witnesses or victims. Previous research by De Alcaraz-Fossoul et al. has successfully demonstrated and modeled the relationship between visual changes in topography and the aging process of latents in 2D. The morphometric analyses of fingerprint images have shown this methodology to be less sensitive to environmental fluctuations than the alternative chemical analyses and, thus, more robust as metrics to date fingerprints. These may include changes in ridge width, color contrast between ridges and furrows, number of minutiae, presence of ridge discontinuities and level of visual quality. One of the most significant steps forward in dating latent fingerprints by visual analysis is by shifting research from a 2D train of thought into a 3D approach. The ability to visualize and analyze fingerprints in 3D gives researchers new features and metrics (such as height and volume) to examine minute topographical variations during the aging process. At the University of New Haven - Forensic Science Department, this research approach is being developed with the use of the latest technology in 3D imaging. This novel method to fingerprint age estimations supports the goal of formulating a predictive, spatio-temporal mathematical model that can potentially be used to date a fingerprint as a function of its topography. This requires answering basic questions on how and why a fingerprint visually changes over time when exposed to different environmental conditions.

## Interlaboratory Studies

Currently, there are two interlaboratory studies available in the community. Each survey is designed to gauge interest of the discipline and how often these analyses are conducted in operational forensic laboratories. For additional information and timeline of activities contact Candice Bridge, Ph.D., University of Central Florida, FL. [cbridge@ucf.edu](mailto:cbridge@ucf.edu)

### Organic Gunshot Residue Analysis

The NIST OSAC GSR community is developing a new guide that can be implemented to analysis OGSR. This group is looking for participants for an interlaboratory. For more information we encourage you to complete this [Survey](#) and information will be sent to you about the interlaboratory study.

### Forensic Lubricant Analysis

This is a new group that is developing information and protocols for conducting lubricant analysis in forensic laboratories. They want to gauge how much interest there is in the community. For more information, we encourage you to complete this [Survey](#).

## Community Bulletin

### Big Data and a Paradigm Shift in Forensic Science-A Commentary in the Field of DNA

*Michael A. Marciano, Ph.D. and Jonathan D. Adelman, Ph.D.  
Syracuse University, NY*

We start by posing a question: How can we improve the science in the forensic sciences? Perhaps an obvious answer is focusing on improving the scientific processes and methodologies that we use in the laboratory, such as increasing instrument sensitivity or analyte yield. However, we contend that greater improvements can be realized, in the short term, by focusing on innovation in the methods used for data interpretation. We encourage forensic scientists to look at their counterparts in other scientific disciplines, where “big data” analysis has been leveraged to increase the depth and breadth of data analyses, permitting more information to be gleaned from large, complex data sets. The use of these analysis tools has helped foster changes in how we work (via factory automation), buy (via targeted advertising), invest (via stock market micro-transactions), travel (via driverless vehicles), and manage our health (via computer-assisted diagnoses). These endeavors have included breakthroughs in how accurately patterns and processes can be analyzed and predicted, but all have been made possible only through acquisition of big data, and subsequent analysis of patterns within those data. Forensic data can similarly be used to ask and answer key challenge problems that more traditional analyses cannot as rigorously address, but the key ingredient to leveraging those data is the requirement of having a massive dataset to begin with. We have used machine learning to aid in the interpretation of many DNA-based challenges problems such as the detection of allele dropout, baseline noise, mixture deconvolution, and most notably the classification of the number of contributors in a sample. To develop such a system, a diverse and substantially large data set that represent a multitude of different empirical observations is required. Our success would not have been achievable without data sharing; many forensic laboratories were generous in sharing their validation data sets with us and it was further helped, and by the publicly-available Rutgers University PROVEDIT (1) database has been another key source of electronic samples.

We present NIJ grant 2018-DU-BX-0202 (“A fully continuous machine learning approach to predict the number of contributors in sequence-based DNA profiles” - M. Marciano, J. Adelman, and NicheVision Forensics) as an example of current research that depends on - and leverages - a large, multi-source dataset to explore forensic problems in ways that would not be otherwise achievable. Over the past decade, the field of forensic DNA analysis has experienced significant technological advancements including new methods to increase the sensitivity of detection, the development of software to assess the contributors in mixtures, and probabilistic genotyping. Despite this advancement, mixture interpretation remains a key hurdle for forensic scientists. This challenge is independent of the laboratory method and instrument, existing both in currently validated techniques such as fragment analyses using capillary electrophoresis and in emerging technologies such as massively parallel sequencing. Mixture interpretation has thus far received a paucity of attention in emerging and soon-to-be-validated next generation DNA sequencing (massively parallel sequencing). Within the larger challenge of mixture interpretation lies a singular critical

component, the assessment of the number of contributors (NOC). The assumption of the NOC provides the underlying support for the vast majority of subsequent assumptions such as the presence of allelic dropout and the pairing of sister alleles. The primary objective of our research is to develop a fully continuous probabilistic machine learning-based tool to predict the number of contributors in sequence-based data sets. The project's use of machine learning, which is ideally suited for complex, high-dimensional classification problems, complements the impending transition to NGS. By proactively developing software tools and solutions specifically tailored to NGS-based mixture interpretation, the forensic science community will be given the proper time and resources to scrutinize, optimize, and potentially implement the methods proposed in this project.

We know that innovation is slow in forensics, and rightfully so: processes need to be well-characterized, validated and accepted in the court system. However, we are also entering an era in which big data analysis affords the opportunity to achieve new levels in predictive accuracy, and data - the fuel for this transformation - is also arguably its biggest bottleneck in the forensic sciences. We write this, then, as an appeal to the community to be open to data-sharing with academics, and to industry to help usher in transformative and positive improvements to an already robust scientific discipline. And similarly, we hope that funding agencies will be open to prioritizing the need for data availability, and funding expanded publicly available databases.

#### References:

1. Alfonse LE, Garrett AD, Lun DS, Duffy KR, Grgicak CM. A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt. *Forensic Sci. Int. Genet.* 2018; 32:62-70. doi: 10.1016/j.fsigen.2017.10.006.