National Institute of Justice

Forensic Science Research and Development Symposium

American Academy of Forensic Sciences' 70th Annual Scientific Meeting

Tuesday, February 20, 2018
Seattle, Washington

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Forensic Technology
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STRENGTHEN SCIENCE. ADVANCE JUSTICE.

NIJ is the federal government's lead agency for forensic science research and development as well as the administration of programs that facilitates training, improves laboratory efficiency and reduces backlogs. The mission of NIJ's Office of Investigative and Forensic Sciences is to improve the quality and practice of forensic science through innovative solutions that support research and development, testing and evaluation, technology, information exchange, and the development of training resources for the criminal justice community.

Through the research, development, testing, and evaluation process, we provide direct support to crime laboratories and law enforcement agencies to increase their capacity to process high-volume cases and provide needed training in new technologies. With highly qualified personnel and strong ties to the community, NIJ's Office of Investigative and Forensic Sciences plays a leadership role in directing efforts to address the needs of our nation's forensic science community.

Forensic Technology
CENTER OF EXCELLENCE

A program of the National Institute of Justice

RTI International and its academic- and community-based consortium of partnerships work to meet all tasks and objectives for the Forensic Technology Center of Excellence (FTCoE), put forward under the National Institute of Justice (NIJ) Cooperative Agreement No. 2016-MU-BX-K110.

RTI INTERNATIONAL

The FTCoE is led by RTI International, a global research institute dedicated to improving the human condition by turning knowledge into practice. With a staff of more than 5,000 providing research and technical services to governments and businesses in more than 75 countries, RTI brings a global perspective. The FTCoE builds on RTI's expertise in forensic science, innovation, technology application, economics, DNA analytics, statistics, program evaluation, public health, and information science.

This forum is funded through a cooperative agreement from the National Institute of Justice (2016-MU-BX-K110), Office of Justice Programs, U.S. Department of Justice. Neither the U.S. Department of Justice nor any of its components operate, control, are responsible for, or necessarily endorse, this forum. The opinions, findings, and conclusions or recommendations expressed in this forum are those of the presenter(s) and do not necessarily reflect those of the Department of Justice. Any products and manufacturers discussed are presented for informational purposes only and do not constitute product approval or endorsement by the U.S. Department of Justice.

Greetings,

The National Institute of Justice (NIJ) and its Forensic Technology Center of Excellence at RTI International want to welcome you to the 2018 NIJ Forensic Science Research and Development (R&D) Symposium. This event is held in conjunction with the American Academy of Forensic Sciences' 70th Annual Scientific Meeting in Seattle, Washington. On February 20, hundreds of attendees will join us in person and online to learn about NIJ research awards given to several talented researchers spanning the forensic disciplines.

For more than a decade, NIJ has hosted an annual R&D symposium to showcase great scientific innovations and promote the transition of research into practice. The NIJ supports research to advance efficiency, quality, reliability, and capacity in the criminal justice and forensic science communities; this research focuses on developing new technologies, providing proof for evidence-based practices, and evaluating findings for case investigations and legal proceedings.

This year, members of the NIJ R&D team—including program managers Gregory Dutton, Danielle McLeod-Henning, Minh Nyugen, and Frances Scott—worked to bring you a phenomenal research agenda. The full-day program includes 18 presenters and their researcher partners representing 16 NIJ awards; these awards were received during a 4-year period (2013–2016). The two morning sessions comprise Forensic Anthropology, and Controlled Substances and Toxicology; the afternoon sessions cover Trace Microbiome and Forensic Biology/DNA.

We are pleased to have you—both national and international stakeholders of the criminal justice system—join us for this event; we are confident that you will learn valuable information to help guide your research endeavors and impending cases. The research shared with you at this event will help to efficiently identify, gather, and process evidence related to crime and death scene investigations in the future. Thank you and enjoy this program of research and developments in forensic sciences.

Respectfully,

Jeri D. Ropero-Miller, PhD, F-ABFT
Director
Forensic Technology Center of Excellence
Center for Forensic Sciences, RTI International

Gerry LaPorte, MSFS
Director
Office of Investigative and Forensic Sciences
National Institute of Justice

Directors

Jeri D. Ropero-Miller

Dr. Jeri Ropero-Miller is a Principal Investigator and Director for RTI International's Center for Forensic Sciences. She is a Board-certified Forensic Toxicologist with Fellow status in the American Board of Forensic Toxicology (F-ABFT). Dr. Ropero-Miller has more than 20 years of experience conducting research in forensic toxicology, drug surveillance, and hair drug-testing studies. She has led projects that focus on professional development and training, laboratory efficiency, technology transition, technology evaluation, databases, and program monitoring and evaluation. Prior to her tenure with RTI, she served as the Deputy Chief Toxicologist at North Carolina's Office of the Chief Medical Examiner. She is currently on the Board of Directors for the ABFT and the American Academy of Forensic Sciences (Secretary). She is a member of the Society of Forensic Toxicologists, the International Association of Forensic Toxicologists, the American Society of Crime Laboratory Directors, the International Association of Chiefs of Police, and the Toxicology Subcommittee of the National Institute of Standards and Technology (NIST) Organization of Scientific Area Committees (OSAC). She has served in leadership roles for the Scientific Working Group for Forensic Toxicology, the NIST OSAC, the Chemistry/Instrumental Analysis Scientific Area Committee, and as a Laboratory Inspector for ABFT and for the National Laboratory Certification Program.

Gerry LaPorte

Mr. Gerald (Gerry) LaPorte serves as the Director in the Office of Investigative and Forensic Sciences at the National Institute of Justice (NIJ), whose mission is to improve the quality and practice of forensic science through innovative solutions that support research, development, technology, evaluation, and information exchange for the criminal justice community. His primary duties are to oversee the management of over $400 million in grants and provide expert analysis and advice on agency-wide programs and issues of national impact relating to forensic science. Mr. LaPorte has been employed in various capacities in the forensic sciences since 1993, and prior to joining NIJ, he was the Chief Forensic Chemist at the United States Secret Service. Mr. LaPorte received his Bachelor of Science and Bachelor of Commerce in business administration from the University of Windsor in Canada and his Master of Science in forensic science from the University of Alabama at Birmingham. He is a member of the American Academy of Forensic Sciences, Mid-Atlantic Association of Forensic Scientists, American Society of Questioned Document Examiners, and the American Bar Association – Criminal Justice Section. Mr. LaPorte has conducted over 100 lectures, seminars, and training events in 13 different countries for law enforcement agencies, professional organizations, and technical experts. He has more than 20 publications, including chapters in three textbooks, and his lectures and workshops have related to the analysis of questioned documents and forensic science policy. He is a member of various organizations and served as the co-chair for the Standards Practices and Protocols Interagency Working Group under the Executive Office of the President of the United States and on the National Commission on Forensic Science until its close in 2017.

NIJ Program Managers

Gregory Dutton

Gregory Dutton, PhD, is a Program Manager at the National Institute of Justice (NIJ). His portfolio includes the broad umbrella of trace evidence—microscopic materials, chemicals, or nonhuman biological traces recovered from crime scenes as well as impression and pattern evidence (e.g., latent fingerprints, firearms, and shoeprints). His programs at NIJ seek to bring advances from across the physical sciences into the forensic sciences. Prior to joining NIJ, Dr. Dutton was a Research Fellow at the National Institute of Standards and Technology. Dr. Dutton earned his doctorate in chemistry from the University of Minnesota.

Danielle McLeod-Henning

Danielle McLeod-Henning is a program manager/physical scientist in the Office of Investigative and Forensic Sciences at the National Institute of Justice, US Department of Justice. She is responsible for managing projects in Forensic Science Research and Development, specifically in forensic anthropology, forensic pathology, crime scene examination, and related medicolegal death investigation fields. Ms. McLeod-Henning holds a master's degree in forensic sciences from the George Washington University and a bachelor's degree in anthropology from the Pennsylvania State University.

Minh Nyugen

Minh Nguyen is a Physical Scientist in the National Institute of Justice's Office of Investigative and Forensic Sciences. She currently manages the forensic biology and DNA portfolio of the Research and Development in Forensic Science for Criminal Justice Purposes program. She previously worked at a private forensic DNA laboratory. Prior to her work in forensic science, Ms. Nguyen contributed to the Human Genome Project sequencing and finishing of Chromosome 10. She holds a bachelor's degree in biomedical engineering from The Johns Hopkins University.

Frances Scott

Frances Scott, PhD, is a Physical Scientist at the National Institute of Justice, where she manages the Controlled Substances and Forensic Toxicology research and development portfolios under the General Forensics portfolio and comanages the Paul Coverdell Forensic Science Improvement Grants program and the Research for Publicly Funded Labs program. Dr. Scott received a bachelor's degree in chemistry from the University of California at Davis and a PhD in physical chemistry from the George Washington University.

NATIONAL INSTITUTE OF JUSTICE
GRADUATE FELLOWSHIP
SCIENCE, TECHNOLOGY, ENGINEERING, AND MATHEMATICS

Apply for NIJ's Graduate Research Fellowship in Science, Technology, Engineering, and Mathematics (GRF-STEM). By supporting outstanding graduate research, NIJ is expanding the future pool of young investigators pursuing research with the potential to provide STEM-based solutions to issues that affect crime and the fair and impartial administration of criminal justice in the United States.

To learn more about the GRF-STEM program and see specific examples of research conducted by past and present fellows, visit **www.nij.gov/GRF-STEM**.

Benefits

- $35,000 annually to cover salary and related costs.
- $15,000 annually to cover tuition, fees, and research expenses.
- Up to three years of funding, usable over a five-year period.

Deadline: March 12, 2018

Applications must be submitted via Grants.gov by the academic institution, which must be a fully accredited, doctoral degree-granting institution in the United States or its territories.

Eligibility

Eligible students must be (1) enrolled full time in a STEM discipline doctoral program and (2) propose dissertation research that is relevant to improving criminal justice practice and policy in the United States.

Qualifying disciplines include, among others:

- Anthropology (Physical)
- Biology
- Chemistry
- Cognitive Science
- Computer Science
- Geoscience
- GIS
- Information Sciences
- Materials Science
- Mathematics
- Pathology
- Physics
- Engineering

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NATIONAL INSTITUTE OF JUSTICE
PUBLIC LABS RESEARCH SOLICITATION

Introduction

The Research and Evaluation for the Testing and Interpretation of Physical Evidence in Publicly Funded Forensic Laboratories (Public Labs) program's intent is to fund projects that direct the findings of research and evaluation toward the identification of the most efficient, accurate, reliable, and costC effective methods for the identification, analysis, and interpretation of physical evidence for criminal justice purposes.

With this solicitation, NIJ seeks applications for research and evaluation projects that will:

- Identify and inform the forensic community of best practices through the evaluation of existing laboratory protocols.
- Have a direct and immediate impact on laboratory efficiency and assist in making laboratory policy decisions.

Program Overview

The Public Labs program is specifically targeted toward applicants from publicly funded laboratories and has the following objectives:

- Assessing existing laboratory protocols.
  - Improve understanding of the rationales underpinning existing laboratory processes.
- Evaluating emerging methods
  - Assess the value of emerging laboratory processes.

Eligibility

Applicants are limited to publicly funded forensic science laboratories. For detailed eligibility information, please refer to the solicitation document.

Applying to the NIJ Public Labs Solicitation

FY 2018 solicitation is coming!
In advance of NIJ releasing the FY18 solicitation, we are calling on public laboratories to submit contact information to connect with postgraduate researchers to assist in preparing an application for the forthcoming solicitation.

Are you a postgraduate researcher with an interest in forensics? If so, the National Institute of Justice has a program that can help you gain experience in working forensic labs with real-world applications.

As part of our "Research and Evaluation for the Testing and Interpretation of Physical Evidence in Publicly Funded Forensic Laboratories" program, we encourage applicant laboratories to consider funding a postgraduate (master's or doctorate) fellowship as part of their proposal.

Learn more at https://www.nij.gov/topics/forensics/lab-operations/Pages/public-labs-research-fellowships.asp

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NATIONAL INSTITUTE OF JUSTICE
FORENSIC SCIENCE R&D GRANTS

The National Institute of Justice (NIJ) funds basic and applied research through its **Research and Development in Forensic Science for Criminal Justice Purposes** program. NIJ funded projects are expected to:

- Increase the body of knowledge to guide and inform forensic science policy and practice; or
- Result in the production of useful materials, devices, systems, or methods that have the potential for forensic application.

Goals

Projects address at least one of the following goals:

- **Fundamental/Basic Research Goal:** Improve the understanding of the accuracy, reliability, and measurement validity of forensic science disciplines.
- **Applied Research Goal:** Increase knowledge or understanding necessary to guide criminal justice policy and practice related to the forensic sciences.
- **Development Goal:** Produce new materials, devices, systems, or methods that have the potential for forensic application for criminal justice purposes.

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NIJ is interested in funding innovative research that aligns with administration priorities and attempts to address the needs of the forensic science community.

Priority Areas of Research

Proposals that advance the following national priorities may be given special consideration in award decisions:

- Supporting Innovative Early-Stage Research
- Maximizing Interagency Cooperation
- Developing a Future-Focused Forensic Science Workforce
- Modernizing and Managing Research Infrastructure

Needs of the Community

For more information on what research and technology forensic practitioners would benefit from, see NIJ's Forensic Science Technology Working Group operational requirements at go.usa.gov/xnvJ3.

Funding Opportunity Anticipated for 2018

NIJ typically posts solicitations for grant proposals once annually. Sign up for email alerts when new NIJ funding opportunities are posted at nij.gov/funding. Begin the application process early by registering with Grants.gov.

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AGENDA

Short Agenda

Tuesday, February 20

8:30–8:40	Welcome
8:40–9:55	Morning Session I – Forensic Anthropology
10:35–12:15	Morning Session II – Controlled Substances and Toxicology
1:35–3:15	Afternoon Session I – Trace Microbiome
3:30–5:10	Afternoon Session II – Forensic Biology/DNA
5:10	Adjourn

Full Agenda

Tuesday, February 20: 8:30 a.m.–5:10 p.m.	
8:30–8:40	**Welcome** Gerald LaPorte, Director, Office of Investigative and Forensic Sciences
	Morning Session I: Forensic Anthropology Moderated by NIJ Scientist/Program Manager Danielle McLeod-Henning
8:40–9:05	**The Macromorphoscopic Databank: A New Tool for Forensic Anthropologists** Joseph Hefner, Michigan State University—2015-DN-BX-K012
9:05–9:30	**Analysis of Inter- and Intra-Observer Error Associated with the Use of 3D Laser Scan Data of the Pubic Symphysis** Jieun Kim, Florida State University, and Bridget F.B. Algee-Hewitt, Stanford University—2015-DN-BX-K010
9:30–9:55	**Building a Science of Adult Cranial Fracture** Mariyam Isa and Todd Fenton, Michigan State University—2015-DN-BX-K013
9:55–10:20	**Standardizing a Large-Scale, Whole Body CT Image Database** Heather J.H. Edgar, University of New Mexico—2016-DN-BX-0144
10:20–10:35 — BREAK	
	Morning Session II: Controlled Substances and Toxicology Moderated by NIJ Scientist/Program Manager Frances Scott
10:35–11:00	**Liver "Doesn't DIE," or at Least its Enzymes, and Other Useful Information Discovered While Evaluating the Effect of Sample Preparation Techniques on Matrix Effects and Absolute Recovery of Opiates in Liver Tissue Using UPLC-MS/MS** Carl Wolf, Virginia Commonwealth University—2016-DN-BX-0148

Tuesday, February 20: 8:30 a.m.–5:10 p.m.	
11:00–11:25	**Evaluating Trends in Novel Psychoactive Substances Using a Sentinel Population of Electronic Dance Music Festival Attendees** Alex Krotulski, Center for Forensic Science Research and Education at the Fredric Rieders Family Foundation—2015-IJ-CX-K012
11:25–11:50	**Assessing the Impact of Implementing Portable Mass Spectrometers for On-Site Drug Evidence Processing** Jamie Wieland, Illinois State University—2015-IJ-CX-K011
11:50–12:15	**Rapid Peptide Analysis Utilizing Matrix-Assisted Inlet Ionization and Paper Spray Ionization Mass Spectrometry** Kyle Vircks, Harris County Institute of Forensic Sciences—2013-DN-BX-K020
12:15–1:35 — LUNCH BREAK (on your own)	
	Afternoon Session I: Trace Microbiome Moderated by NIJ Scientist/Program Manager Gregory Dutton
1:35–2:00	**Developing Reliable Methods for Microbial Fingerprinting of Soil Evidence: Collection, Contamination, Storage, and Analysis** David Foran, Michigan State University—2015-DN-BX-K031
2:00–2:25	**Evaluating the Skin Microbiome as Trace Evidence on Common Surface Types** David Carter, Chaminade University of Honolulu—2014-R2-CX-K411
2:25–2:50	**Forensic Geosourcing Potential of the Human Microbiome** Lauren Brinkac Leone, J. Craig Venter Institute—2015-R2-CX-K036
2:50–3:15	**Candidates of Skin Microbiomes for Human Identification** Bruce Budowle, University of North Texas Health Science Center—2015-NE-BX-K006
3:15–3:30 — BREAK	
	Afternoon Session II: Forensic Biology/DNA Moderated by NIJ Scientist/Program Manager Gregory Dutton
3:30–3:55	**Multi-locus Match Probability Dependencies** Bruce Weir, University of Washington—2014-DN-BX-K028
3:55– 4:20	**Record Linkage of CODIS Profiles with SNP Genotypes** Michael D. Edge, University of California, Davis—2014-DN-BX-K015
4:20– 4:45	**Microhaplotypes Analyzed by Massively Parallel Sequencing Are Valuable Forensic Tools** Kenneth Kidd, Yale University—2015-DN-BX-K023
4:45– 5:10	**Production of High-Fidelity Electropherograms Results in Improved and Consistent Match-Statistics: Standardizing Forensic Validation by Coupling Laboratory Specific Experimental Data with an In Silico DNA Pipeline** Catherine Grgicak, Rutgers University, Boston University—2014-DN-BX-K026
5:10 — Adjourn	

SESSION ABSTRACTS

Morning Session I: Forensic Anthropology

8:40 A.M.–9:05 A.M.

The Macromorphoscopic Databank: A New Tool for Forensic Anthropologists

NIJ Award #: 2015-DN-BX-K012

Presenting author: Joseph T. Hefner, PhD, D-ABFA

Description: This presentation introduces the Macromorphoscopic Databank (MaMD), a data repository for macromorphoscopic trait data obtained primarily from recent and well-documented forensic cases or donated skeletal material. The MaMD currently contains macromorphoscopic trait data for over 7,000 individuals from modern American black and white populations to Hispanic populations from throughout Latin America. These data are used to construct classification algorithms, provide method validation, and conduct inter- and intra-observer error tests. Further refinement of the classification algorithms and the user interface provides end users a more objective approach to trait analysis and data collection.

Abstract: The purpose of this research is to address a substantial gap in best practice in forensic anthropology. That is, very little reference data are publicly available for the objective analysis of macromorphoscopic traits in assessing ancestry. Consequently, forensic anthropologists rely on their own experience or outdated methods having very little empirical support to estimate a fundamental component of the biological profile. This approach provides no error rates and is not verifiable because it is not replicable. The result is post hoc trait selection, experience-based justifications, and anecdotal expert judgment with no empirical support.

This presentation addresses this issue by introducing the Macromorphoscopic Databank (MaMD). The purpose of any databank is to serve as a repository of data and to make those data accessible to many end users or practitioners. To that end, the MaMD serves as a repository for macromorphoscopic trait data obtained primarily from recent and well-documented forensic cases or donated skeletal material. To facilitate data sharing and to maximize analytical output, the databank comprises relational databases housing not only macromorphoscopic trait scores, but also demographic data on each decedent. These data include but are not limited to age at death, sex, stature, ancestry, place of birth, occupation, and self-identified ancestry (social race). All data are maintained in these relational databases on a central server, using a database platform to perform the essential managerial and analytical functions necessary for data management.

The MaMD is populated using Macromorphoscopic Traits (v. 1.61), a newly developed data collection program for 17 macromorphoscopic traits. The end user provides provenience information after data are collected, retaining trait scores to a sample-specific database for subsequent submission to the MaMD. The MaMD currently contains macromorphoscopic trait data for 6,670 individuals. Examples of populations for which data are available include samples of modern American black and white, Hispanic, Guatemalan, Colombian, Fijian, Thai, Japanese, Pacific Islander and Peruvian.

The MaMD and a forthcoming analytical program using classification algorithms appropriate for categorical data will be available for wider use following extensive beta testing, method validation, and inter- and intra-observer error tests. Forensic anthropology laboratories (applied and academic) are encouraged to help validate and beta test this research through a data-sharing model similar in scope and function to the Forensic Anthropology Databank1. Further refinement of several classification algorithms and the user interface for the analytical program will be completed within the next year.

9:05 A.M.–9:30 A.M.

Analysis of Inter- and Intra-Observer Error Associated with the Use of 3D Laser Scan Data of the Pubic Symphysis

NIJ Award #: 2015-DN-BX-K010

Presenting author: Jieun Kim, PhD (with grant PI, Bridget Algee-Hewitt, PhD, as co-author), Department of Scientific Computing, Florida State University

Co-authors: Bridget Algee-Hewitt, PhD, Department of Biology, Stanford University; Detelina Stoyanova, PhD, Department of Scientific Computing, Florida State University, Department of Mathematics and Statistics, University of North Carolina at Charlotte

Description: This study evaluates the repeatability of the novel fully computational age estimation methods using 3D laser scans of the pubic symphysis by assessing intra-scan variation, within-/between-observer differences in scan editing, and the impact on age estimation. The test data represent triplicate scans of the Suchey-Brooks' male casts (n=36) edited by four different observers with various experience levels and training backgrounds. The results show high repeatability of the computational methods regardless of the level of observer experience or training background and support using a 3D laser scanner and scanned images to aid in resolving the issue of subjectivity in age estimation.

Abstract: In age-at-death estimation based on visual assessment, objective evaluation and correct diagnosis of age-related skeletal traits are crucial to achieving accurate and reliable age estimates. Nevertheless, the traditional, phase-based methods have been reported to yield inconsistent age estimates both within and between observers.[1,2] The reasons for these discrepancies lie in the fact that accurate macromorphoscopic analysis depends heavily on the interpretation of qualitative trait descriptions, conformity of the bone, and experience of the observer.

Recently, Slice and Algee-Hewitt[3] and Stoyanova et al.[4,5] have introduced three fully computational methods using 3D laser scans of the pubic symphysis that minimize subjectivity in age estimation by reducing both the effects of observer experience in skeletal-trait assessment and methodological bias. However, the reproducibility of these methods has not been fully explored. This is of concern because there is potential for introducing error in the scanning and editing of the raw scans at different times by different observers. In response to this concern, the current study evaluated the repeatability of these novel methods by assessing intra-scan variation, within-/between-observer differences in scan editing, and the impact on age estimation.

The test data represent triplicate scans of the Suchey-Brooks' (SB) male casts, taken using a 3D desktop laser scanner by a single observer (n=36). Four different observers with various experience levels and training backgrounds independently edited the three sets of the raw scans using the scanner's accompanying software. From the edited scans, shape measures were computed via the subarachnoid hemorrhage (SAH)-Score method,[3] the thin plate splines/bending energy (TPS/BE) method,[4] and the ventral curvature (VC) method.[5]

These measures were subjected to various regression models to obtain age estimates for each replicate scan per observer. Finally, a series of the intraclass correlation coefficient was calculated to evaluate observer reliability in scan editing. Extra editing conditions were tested to simulate the situation where the practitioner misidentifies age-related traits because of unfamiliarity with the scan editing protocol. A set of the SB casts was edited with different widths of the margin (2 mm vs. 4 mm vs. 1 cm) left around the symphyseal face and with/without the pubic tubercle, which may affect the VC values as it protrudes ventrally.

Results of this study demonstrate that the raw scans were edited consistently within and between observers and the derived shape measures and age estimates were in excellent agreement among observers. For the test of improper scan editing, simulated with various margin widths, the methods were robust enough to produce consistent and accurate age estimates with an exception of the faces with 1 cm margin. Interestingly, the inclusion of the pubic tubercle for the shape analysis did not necessarily yield inaccurate age estimates for the VC method, while it produced significant differences between the documented chronological age and age estimates of the SAH-Score and TPS/BE methods and the two multivariate regression models. These results show high repeatability of the computational methods regardless of the level of observer experience or training background and support using a 3D laser scanner and scanned images to aid in resolving the issue of subjectivity.

References:

1. Kimmerle, EH, Prince DA, Berg GE. Inter-observer variation in methodologies involving the pubic symphysis, sternal ribs, and teeth. J Forensic Sci. 2008;53(3):594-600.
2. Shirley, NR, Ramirez Montes, PA. Age estimation in forensic anthropology: quantification of observer error in phase versus component-based methods. J Forensic Sci. 2015;60(1):107-111. doi:10.1111/1556-4029.12617.
3. Slice DE, Algee-Hewitt BF. Modeling bone surface morphology: a fully quantitative method for age-at-death estimation using the pubic symphysis. J Forensic Sci. 2015;60(4):835-43.
4. Stoyanova D, Algee-Hewitt BF, Slice DE. An enhanced computational method for age-at-death estimation based on the pubic symphysis using 3D laser scans and thin plate splines. Am J Phys Anthropol. 2015;158(3):431-40.
5. Stoyanova D, Algee-Hewitt BF, Kim J, Slice DE. A fully computational framework for age-at death estimation from the adult skeleton: surface and outline analysis of three-dimensional laser scans of the pubic symphysis. J Forensic Sci. 2017;62(6):1434-4. doi:10.1111/15564029.13439.

9:30 A.M.–9:55 A.M.

Building a Science of Adult Cranial Fracture

NIJ Award #: 2015-DN-BX-K013

Presenting author: Mariyam Isa, Michigan State University

Co-author: Dr. Todd Fenton, PhD, Michigan State University Department of Anthropology

Description: We present key findings in new research on adult cranial fracture and potential implications for analyzing blunt force cranial trauma. This research used adult human cadaver heads in a series of biomechanical impact experiments documenting the

influence of several forensically relevant variables including implement shape, input energy, and number of impacts on cranial fracture initiation and fracture patterning. The results of these cranial impact experiments reveal flaws in currently accepted understanding of cranial fracture initiation that may be misleading practitioners regarding number and location of cranial impacts.

Abstract: We present key findings in new research on adult cranial fracture and potential implications for analyzing forensic cases involving blunt force cranial trauma. The fields of forensic anthropology and pathology currently lack guidelines for making forensically significant assessments about implement type, impact energy, location of impact, and number of impacts based on cranial fracture patterns. In practice, these assessments are often based on practitioners' past case experience and on post hoc applications of biomechanical principles, rather than scientifically informed methods compliant with Daubert standards. In the absence of hypothesis-driven, experimental studies confirming links between injury scenario and fracture pattern, the work of even highly experienced practitioners may be called into question in a court of law.

This research used adult human cadaver heads in a series of biomechanical impact experiments documenting the influence of several forensically relevant impact variables on cranial fracture patterns. Our three primary objectives were to document (1) the influence of implement on the initiation, propagation, sequence, and pattern of cranial fracture; (2) the influence of input energy on these same parameters; and (3) patterns of cranial fracture following sequential blows. The ultimate goal of this project was to provide a body of experimental evidence as a resource for practitioners to make more accurate interpretations of adult cranial fractures.

We performed cranial impact experiments using a pneumatic impact system designed to simulate a blow to the head of an upright individual using three aluminum impactors selected to approximate the shapes of objects commonly implicated in forensic cases: a brick, a baseball bat, and a hammer. The effects of impact energy were investigated in two phases of testing: the first with impacts performed at a base energy level and the second at a high energy level. Each impact experiment was filmed with a high-speed camera that captured fracture initiation and propagation at 10,000 frames per second.

The data set consists of measured and calculated mechanical variables, high-speed video footage of fracture initiation and propagation following impact, photographic and diagrammatic representations of fracture patterns after each impact, and anthropological assessment of ectocranial and endocranial fracture patterns after three sequential impacts.

This research represents a major shift in understanding of cranial fracture initiation and propagation. A key finding of this research is that cranial fractures can initiate in one or more locations peripheral to the point of impact. Additionally, peripherally initiated cranial fractures do not always propagate back to the point of impact, resulting in fractures concentrated remote from the impact site. This finding contradicts recent, widely cited sources in the literature that assert fractures always initiate at the point of impact.

This presentation highlights the implications of these results and this research for forensic trauma analysis. Trauma analyses guided by the flawed assumption that fractures occur only at the point of impact will result in inaccurate assessments regarding the location of impact and may lead to overestimations of number of impacts.

9:55 A.M.–10:20 A.M.

Standardizing a Large-Scale, Whole Body CT Image Database

NIJ Award #: 2016-DN-BX-0144

Presenting author: Heather J.H. Edgar, PhD, University of New Mexico, Albuquerque, NM, Office of the Medical Investigator, Albuquerque, NM

Co-author: Shamsi Daneshvari Berry, PhD, MS, CPHI, University of New Mexico, Albuquerque, NM, University of Mississippi Medical Center, Jackson, MS

Description: In 2016, we received a National Institute of Justice grant to create a free-access Decedent CT Database, which will make 15,250 high-resolution whole-body computed tomography scans (CTs) available to the research public. These scans represent approximately 30% of the deaths in New Mexico from 2010 to 2017. This database will be de-identified, anonymized, and associated with metadata regarding life history and cause- and manner-of-death variables, derived from medical investigator data and next-of-kin interviews. Informatics work toward developing this metadata is challenging and ongoing. The resulting database will be available in late 2018 and will be a valuable research resource in many forensic and nonforensic fields.

Abstract: In 2016, a National Institute of Justice grant was awarded to the Center for Forensic Imaging in the Office of the Medical Investigator (OMI), a statewide, centralized medical examiner's office for New Mexico, to create a free-access Decedent CT Database, which will make 15,250 whole-body computed tomography scans (CTs) available to the research public. Work is currently underway to populate the new database. Populating the database presents numerous challenges in that the majority of fields within the database are free-text fields without any limitations. As a result, even sex can be recorded in multiple ways (e.g., Male, male, M, m), limiting the ability of future researchers to query efficiently. To combat this issue, the CT database being developed will use data standards, terminologies, and classification systems.

A step-by-step process is underway to determine the best standards to implement. First, we are searching Unified Medical Language System to identify all of the standards for a particular concept (e.g., race) that exist. Second, each standard is then identified and compared for usefulness in this particular database. A standard can be implemented as is, modified, or all can be rejected. If all current standards are rejected for use in the database (or none are found), a new standard will be proposed and implemented.

The free-access Decedent CT Database is slated to be available by the end of 2018.

Reference:

1. US Census Bureau. 2010 US Census. 2010 [cited 2011 January 19, 2011]; Available from: http://2010.census.gov/2010census/pdf/2010_Questionnaire_Info.pdf.

Morning Session II: Controlled Substances and Toxicology

10:35 A.M.–11:00 A.M.

Liver "Doesn't DIE" or at Least its Enzymes, and Other Useful Information Discovered While Evaluating the Effect of Sample Preparation Techniques on Matrix Effects and Absolute Recovery of Opiates in Liver Tissue Using UPLC-MS/MS

NIJ Award #: 2016-DN-BX-0148

Presenting author: Carl E. Wolf, PhD, MS, Department of Pathology and Department of Forensic Science, Virginia Commonwealth University

Co-authors: Justin L. Poklis, BS, Department of Pharmacology and Toxicology; Casey M. Spencer, BS, Department of Forensic Science; Jean A. Heneks, BS, Department of Forensic Science; Makinzie D. Mott, MD, Department of Pathology; Hope Richard, MD, Department of Pathology; Charles Clevenger, MD, PhD, Department of Pathology, Virginia Commonwealth University

Description: In forensic toxicology, analysis of the liver with blood is a routine way to circumvent the effects of postmortem redistribution. The liver is a difficult matrix to analyze because of interferences (protein and fatty matrix, potential purification). Thus, effective clean-up or sample preparation before analysis is necessary. Twelve techniques based on solid-phase extraction, liquid-liquid extraction, and filtration were evaluated for effectiveness, using opiates as the model. Sample preparation of the liver is not as simple as preparation of blood or urine. Chemically similar drugs do not always extract similarly, and not all sample preparation techniques are effective or robust for the extraction of opiates from the liver.

Abstract: With the "opioid crisis" currently occurring in the United States, the ability to analyze biological specimens for opiates (i.e., heroin and oxycodone) and opioids is very important. Blood is the most common sample analyzed for drug concentration. In forensic toxicology, blood is collected from a living person for human performance testing cases and analyzed as whole blood. However, in postmortem cases, blood is no longer a true whole blood because bodily processes have stopped. Assumptions are commonly made that all bodily processes have stopped. Blood in the thoracic and abdominal cavity can become contaminated as a result of postmortem redistribution. This contamination can affect the determination of manner and cause of death, which can have dire criminal and/or civil consequences. Analysis of the liver in conjunction with blood is a routine way to circumvent this issue. Disadvantages of analyzing the liver are the interferences by protein and fatty matrices and potential putrification. These disadvantages necessitate effective cleanup or sample preparation before analysis of the liver.

Newer sample preparation techniques are primarily designed for blood or urine analysis, and the use of difficult matrices such as the liver has occurred without the complete understanding of the effects of the liver on the analysis of the drug(s) of interest. The newer sample preparation techniques are predominantly based on traditional techniques with manufacturers' improvements. These improvements include solid-phase extraction, liquid-liquid extraction, and filtration. However, these techniques have limited published data regarding tissue matrices such as the liver. For these techniques to be effectively used for liver analysis, matrix effects and absolute recovery must be evaluated. We evaluated these techniques using opiates (codeine, hydrocodone, hydromorphone, morphine, oxycodone, oxymorphone, and 6-acetylmorphine [6AM], a heroin metabolite) as the model class of drugs. The sample preparation techniques evaluated were performed following manufacturers' guidelines whenever possible or using a laboratory validated liquid-liquid

extraction technique. Prepared liver samples were analyzed using a previously validated ultra-performance liquid chromatography-mass spectrometry (MS)/MS method.

We discovered that liver homogenates fortified with 6AM contained no detectable concentrations of 6AM after a couple of hours. After several attempts and much research, it was determined that while the liver hepatocyte may die in a couple of days, the liver enzymes within the hepatocyte are still active for at least 4 months when stored frozen. While the majority of the sample preparation techniques had a published or recommended protocol for use with tissue samples, the results varied greatly among the methods evaluated. The observed matrix effects varied between −35% and +50%, and recoveries varied between 30% and 122%. These variations were even observed between different opiates analyzed using the same sample preparation technique.

The liver is a difficult matrix to analyze. Sample preparation is not as simple as for blood or urine, and even chemically similar drugs do not always extract similarly. We observed that not all sample preparation techniques are effective or reliable for extracting opiates from liver tissue.

11:00 A.M.–11:25 A.M.

Evaluating Trends in Novel Psychoactive Substances Using a Sentinel Population of Electronic Dance Music Festival Attendees

NIJ Award #: 2015-IJ-CX-K012

Presenting author: Alex J. Krotulski, MSFS, Center for Forensic Science Research and Education at the Fredric Rieders Family Foundation

Co-authors: Amanda L.A. Mohr, MSFS, and Melissa Friscia, MSFS, Center for Forensic Science Research and Education at the Fredric Rieders Family Foundation, PA; Jillian K. Yeakel, MSFS, Lehigh Valley Toxicology, PA; Barry K. Logan, PhD, F-ABFT, Center for Forensic Science Research and Education at the Fredric Rieders Family Foundation, PA, NMS Labs, PA

Description: Novel psychoactive substances (NPSs) continue to cause widespread issues for forensic science communities. During this study, we conducted a 4-year longitudinal study of drug use by attendees at three major electronic dance music festivals in the United States. At each venue, our research team collected survey information about drug use and collected biological specimens for laboratory confirmation of drugs used. Through this study, we have been able to compare reported drug use with actual drug use (e.g., molly/ecstasy vs. NPSs and/or 3,4-methylenedioxymethamphetamin MDMA) and monitor trends of novel drug use from year to year and between geographical locations.

Abstract: Novel psychoactive substances (NPSs), ingested for their euphoric and stimulating effects, have become widely circulated at electronic dance music (EDM) festivals and have had several adverse events associated with their use at festivals in the United States. Many of these products have been found to contain unregulated phenethylamines, cathinones, and synthetic cannabinoids. The range of NPSs currently available on the market has continued to grow because of their widespread availability over the Internet and constant variation in product composition to circumvent changes in legislation.

We conducted a longitudinal study of drug use by attendees at three major EDM festivals in the United States between 2014 and 2017. Each year, our peer recruiters contacted participants outside the venue and solicited survey participation and provision of a biological sample to compare their admitted drug use with actual drug use and to identify novel emerging substances and metabolites of these substances in these fluids.

The evolution of oral fluid as a suitable biological matrix for drug detection coupled with the ease of sample collection provided the ability to collect a larger sample set. Between three sample collections, 1,067 oral fluid samples were collected. Our survey responses suggest as many as 79% of attendees at the events we studied admitted to recent drug or alcohol use. The most common response was alcohol (49%), and the second most common answer was marijuana (31%), followed by "molly" (10%), "MDMA" (methylenedioxymethamphetamine) (3%), and "ecstasy" (2%), the latter three accounting for a total of 15% of responses.

Across all years, the diversity of NPSs confirmed in biological specimens has continued to evolve. NPSs confirmed in 2014, such as alpha-PVP, methylone, and 4-fluoroamphetamine, have decreased in positivity with compounds such as ethylone, dibutylone, butylone, and n-ethyl pentylone positivity increasing along with the resurgence in positivity for MDMA. Positivity rates also generally increase over the days of the festival, with the last day having the highest positivity for NPSs. Related to the survey results, there is a large discrepancy between the users believing they are ingesting the NPSs and the NPSs being confirmed in their biological samples.

These results stress the importance of updating laboratory-based methods for detecting emerging drugs, the ability to distinguish between isomeric NPSs, and the utility of this target population for monitoring trends.

11:25 A.M.–11:50 A.M.

Assessing the Impact of Portable Mass Spectrometers for On-Site Drug Evidence Processing

NIJ Award #: 2015-IJ-CX-K011

Presenting author: Jamie R. Wieland, PhD, Department of Management and Quantitative Methods, Illinois State University

Co-authors: Christopher C. Mulligan, PhD, Department of Chemistry, Illinois State University; and Michael C. Gizzi, PhD, Department of Criminal Justice Sciences, Illinois State University

Description: This presentation highlights cross-disciplinary research to determine the analytical, legal, and fiscal impacts of adopting drug screening protocols using portable mass spectrometers in the field. Of specific interest to this work is determining which usage modes (e.g., patrol officer usage, crime scene investigation usage, precinct-only operation) are the most cost-effective. Results suggest that considerable cost savings are probable under some usage modes. Overall, this research seeks to inform and guide criminal justice decision-makers in adopting portable forensic instrumentation.

Abstract: Forensic evidentiary backlogs are indicative of the growing need for cost-effective, high-throughput instrumental methods. One such emerging technology that shows promise in meeting this need, while also allowing on-site investigation, is portable mass spectrometric (MS) instrumentation, particularly instrumentation that enables the coupling of rapid, ambient ionization methods. Such technology has the potential to assess the probative value of chemical evidence at the crime scene, requiring only pertinent samples to be sent to off-site laboratories for confirmation, which eases the burden of casework and therefore reduces the magnitude of backlogged evidence. Screening of physical evidence at the crime scene also has the capability to rapidly determine whether a criminal investigation is needed and to provide law enforcement personnel with necessary information in a timely manner, which in many cases is crucial.

Through National Institute of Justice funding, a cross-disciplinary team of researchers developed direct-evidence screening methods on a commercially available, portable MS system, culminating in a fieldable instrument that is simplistic in operation, yet robust to the needs of today's forensic and law enforcement practitioners. A rigorous analytical validation using common and emerging illicit chemicals was performed to ensure that reliable and reproducible use by nontechnical operators is feasible and to facilitate future court admissibility of field-collected forensic data. A significant aspect of this project was designed to not only anticipate but also predetermine the legal and economic impacts of adopting this technology for field use to inform and guide forensic science policy and practice. In an effort to ascertain the legal implications of adopting this technology for field use, we examined the current state of US search and seizure law to recommend legal investigation strategies by law enforcement, including the potential legality of using this technology to prompt a "probable cause" search. To assess the financial viability of instrument-based analysis of forensic evidence in the field, we created fiscal impact models to compare this proposed methodology to the current system of off-site evidence processing at publicly funded laboratories in terms of both cost and processing time.

11:50 A.M.–12:15 P.M.

Rapid Peptide Analysis Utilizing Matrix-Assisted Inlet Ionization and Paper Spray Ionization Mass Spectrometry

NIJ Award #: 2013-DN-BX-K020

Presenting author: Kyle E. Vircks, MS, Harris County Institute of Forensic Sciences, TX

Co-authors: Jesse M. Zavala, MS, Harris County Institute of Forensic Sciences, TX; Yibin Wang, PhD, Harris County Institute of Forensic Sciences, TX; Robert B. Cody, PhD, JEOL USA, Inc, MA; Warren C. Samms, PhD, Harris County Institute of Forensic Sciences, TX; and Roger Kahn, PhD, Harris County Institute of Forensic Sciences, TX

Description: This presentation demonstrates a simple method for analyzing peptides and large biomolecules that can be easily implemented in drug identification laboratories, often using preexisting equipment with little to no sample preparation. By using both inlet ionization and paper spray ionization as complementary techniques, the vast majority of peptide samples that would be encountered in a crime laboratory could be readily characterized.

Abstract: This presentation demonstrates a simple method for analyzing peptides and large biomolecules that can be easily implemented in drug identification laboratories, often using preexisting equipment with little to no sample preparation.

The ease with which consumers can purchase performance-enhancing peptides and cosmetic peptides online is astounding. Hidden behind the anonymity of the Internet, online vendors sell peptide products at minimal cost with no questions asked. To avoid legal action, such products are marketed for research purposes only. Unfortunately, consumers purchase these products to inject into the body to promote muscle growth or cosmetic augmentation. Although the sale of peptides may be legal, it is a major concern. Counterfeit peptide sales are known to be fairly common, especially those reportedly containing recombinant human growth hormone. These trends lead to questions regarding the authenticity of the peptides being sold and, more importantly, concerns regarding health and safety.

Many crime laboratories do not have protocols in place for successfully identifying peptides and large biomolecules. The workhorse of forensic drug analysis, gas chromatography-mass

spectrometry, is limited to the analysis of relatively small molecules that are readily vaporized at the inlet. High-resolution mass spectrometers capable of ambient ionization, however, are well suited for analyzing peptides. Moreover, such instrumentation is becoming more prevalent in forensic laboratories as ambient ionization techniques, such as Direct Analysis in Real Time (DART), continue to gain popularity.

Through this project, we developed a protocol to analyze peptide samples using a time-of-flight mass spectrometer that is typically used for DART-MS analysis. In many cases, this technique required no external ion source or additional equipment aside from the mass spectrometer.

Using matrix-assisted inlet ionization mass spectrometry, as well as paper spray ionization, we successfully analyzed various peptide standards and case samples. An array of peptides was also purchased from an online vendor to determine the authenticity of the products using this technique. Direct inlet ionization was accomplished by placing the samples in solution with the matrix compound 3-nitrobenzonitrile and introducing approximately 5 µL directly into the mass spectrometer inlet with a micropipette. In a matter of seconds, electrospray ionization–like spectra were obtained. Molecular masses were calculated using a mass spectral interpretation software package.

To further characterize the peptides, we used a simple enzymatic protein digestion procedure. Matrix-assisted inlet ionization was employed to analyze the resulting peptide fragments. We assigned possible identifications for each peptide by comparing each digested spectrum against an online peptide database. Combined with the molecular mass attained from analyzing the intact peptides, we identified each peptide at a reasonable level of certainty.

Finally, we explored peptide analysis using paper spray ionization. This ionization method was favored for extremely large peptides for which inlet ionization was not feasible. By using both inlet ionization and paper spray ionization as complementary techniques, the vast majority of peptide samples that would be encountered in a crime laboratory could be readily characterized.

Afternoon Session I: Trace Microbiome

1:35 P.M.–2:00 P.M.

Developing Reliable Methods for Microbial Fingerprinting of Soil Evidence: Collection, Contamination, Storage, and Analysis

NIJ Award #: 2015-DN-BX-K031

Presenting author: David Foran, PhD, Michigan State University

Co-authors: Emily Heinz, BS, and Alyssa Badgley, MS, Forensic Science Program at Michigan State University

Description: Soil associated with evidence has the potential to provide valuable information on a victim's or suspect's whereabouts, and establishing evidentiary soil's origin via microbial DNA profiling shows tremendous promise. However, this strategy depends on successfully associating a questioned soil sample with a known, which may fail if the ex situ evidence soil's profile changes temporally. Here, the influence of time and storage conditions on ex situ soils were examined. Further, potential confounders, including the human microbiome or body fluids, were introduced. Overall, ex situ conditions and time strongly influence the microbial makeup of evidence soils, meaning their consideration is essential for forensic purposes.

Abstract: Soil can represent valuable trace evidence, helping link a victim or perpetrator of a crime to a scene. Research has shown that the microbial makeup of soils is variable enough that a soil sample can be linked to a specific location with a high degree of accuracy. However, most studies have examined freshly collected or frozen samples, neither of which mimic a forensic scenario, wherein the evidentiary soil will have aged ex situ for some period of time, potentially allowing temporal or environmental change in its bacterial makeup.

In the current set of studies, we examined the influence that evidence stored at room temperature has on ex situ soil. Soils from different habitats (agricultural field, coniferous forest, dirt road, yard) were placed on evidence items (t-shirts and trowels) and allowed to age. Soil samples were collected weekly and then monthly. Known soil samples were also collected and stored at −80°C, −20°C, 4°C, and room temperature and sampled over time. In a second study, we examined the influence of the human microbiome on soil evidence by having volunteers wear t-shirts for 24 hours, after which we applied soils from different habitats. Samples were again collected over time. Finally, we examined the influence of blood (a good growth medium for some bacteria) on soil evidence by mixing soil with fresh swine blood at 10:1, 1:1, and 1:10 ratios and applying it to t-shirts and trowels. Evidence was either dried or stored wet and sampled over time.

We isolated bacterial DNAs using a MoBio PowerSoil kit, the V3/V4 region of the bacterial 16S rRNA gene was amplified using barcoded universal primers, and sequences were obtained on an Illumina Mi-Seq. We processed sequence data and analyzed the data using bacterial abundance charts (generally at the taxonomical class level), nonmetric multidimensional scaling, and Random Forests.

Bacterial profiles from all evidence changed temporally, showing increases in the bacterial classes Actinobacteria and bacilli and decreases in Sphingobacteria and Acidobacteria. At later time points, the evidence soils were more likely to misclassify with the knowns, unless the knowns were also aged, in which case the evidence samples classified well. The human microbiome had no perceptible influence on soil profiles, with evidence soils always classifying with the correct habitat of origin. Likewise, blood on evidence had no temporal classification effect when the evidence was dried or when the stain was primarily soil (10:1). In contrast, greater ratios of blood (1:1) stored wet misclassified after 1 week, while 1:10 misclassified even on day 0, showing extremely high levels of bacilli and reduced levels of Actinobacteria.

Overall, the results demonstrate that soil bacterial profiling is highly effective for identifying its place of origin, although time and storage conditions must carefully be considered.

2:00 P.M.–2:25 P.M.

Evaluating the Skin Microbiome as Trace Evidence on Common Surface Types

NIJ Award #: 2014-R2-CX-K411

Presenting author: David O. Carter, PhD, Forensic Sciences Unit, Division of Natural Sciences and Mathematics, Chaminade University of Honolulu

Co-authors: Jessica L. Metcalf, PhD, Department of Animal Sciences, Colorado State University; Se Jin Song, PhD, Department of Pediatrics, University of California, San Diego; Zhenjiang Zech Xu, PhD, Department of Pediatrics, University of California, San Diego; Rob Knight, PhD, Department of Pediatrics, Department of Computer Science and Engineering, University of California, San Diego

Description: Recent research has shown that skin microorganisms can be used as spatial and temporal evidence; skin microbial communities can be used to associate individuals with locations and objects. The current presentation demonstrates that plastic and ceramic are the most reliable surfaces in this regard, with microbial signals persisting on these materials for 24 hours before becoming less accurate. Current data also show that postmortem skin microbial communities, which remain stable during morgue storage prior to autopsy, can be used to associate individuals with handheld objects located at the scene of death.

Abstract: Each of our bodies is covered in billions of microbial cells, which we shed on objects that we touch. Recent work on the built environment (human-made structures) has highlighted the ubiquity of human microbiome signatures in these human-dominated ecosystems. Previous work has demonstrated that the transfer of skin microbes to surfaces can associate objects with individual people and that the microbial signatures are generally stable within a person, raising the potential that these microbial fingerprints could provide important physical evidence. However, a knowledge gap exists about whether skin microbes transfer to different material types, whether they persist over timescales relevant to forensic investigations, and whether they are stable on a decedent's skin after death.

To investigate properties of skin microbiome transfer to surfaces, we investigated the antemortem skin microbiome in a set of experiments at University of California, San Diego and the postmortem microbiome in collaboration with the City and County of Honolulu Medical Examiner. At University of California, San Diego, we investigated the effect of surface type (wood, plastic, metal, glass, and ceramic tiles) on the ability of skin microbes to transfer to an object. By applying machine learning methods using a Random Forests classifier, we discovered that plastic and ceramic surfaces were most accurate for classifying the correct participant, followed by glass and metal. We determined that skin microbial signatures persisted on ceramic and plastic surfaces for at least 1 day and became less accurate over time. We found that microbiome trace evidence samples can be tracked back to individuals with high accuracy and can be used to narrow pools of suspects even when multiple people have touched a surface and when the reference microbiome was collected 1 year previously.

Additionally, we investigated the skin microbiomes of recently deceased individuals at 15 death scenes in Honolulu, Hawaii. We discovered that skin microbiomes were fairly stable after death and during morgue storage prior to autopsy. Further, we found that household and personal objects could still be linked with a person after death. We conclude that skin microbes are uniquely positioned to augment friction ridge impressions when sufficient ridge detail is not available to make an identification. Thus, the potential for microorganisms to reveal whether a particular person has touched an object is substantial.

2:25 P.M.–2:50 P.M.

Forensic Geosourcing Potential of the Human Microbiome

NIJ Award #: 2015-R2-CX-K036

Presenting author: Lauren Brinkac Leone, MS, J. Craig Venter Institute, Rockville, MD

Co-authors: Andres Gomez, PhD, J. Craig Venter Institute, Rockville, MD, Department of Animal Science, University of Minnesota-Twin Cities, MN; Harinder Singh, PhD, J. Craig Venter Institute, Rockville, MD; Toby Clarke, MS, J. Craig Venter Institute, Rockville, MD; Chris Greco, MS, J. Craig Venter Institute, Rockville, MD; Manolito G. Torralba, MS, J. Craig Venter Institute, La Jolla, CA; and Karen E. Nelson, PhD, J. Craig Venter Institute, Rockville, MD

Description: The human microbiome harbors biological signals with potential for geosourcing individuals. Subjects from different cities in the same country can be accurately distinguished based on the presence and abundance of specific bacterial taxa across diverse sites in the human body. The Forensic Microbiome Database (FMD) (http://www.fmd.jcvi.org) is a publicly available analysis resource that enables investigators to infer geographical origin of a human microbiome sample.

Abstract: Next generation sequencing technology has advanced our understanding of the human microbiome, enabling researchers to predict various physiological states based on microbial community composition and function across diverse body sites. In addition to overall physiology, the composition of the human microbiome also correlates with geographical location, subsistence, and culture. Here, we evaluated the use of microbiome data from different body sites to predict geographical provenance of subjects, using 16S rRNA data and combining classic multivariate and machine learning techniques. The results indicate that the microbiome of diverse body sites can be used to predict geographical origin of a sample or subject at narrow geographical scales, with high accuracy, sensitivity, and specificity, and linking specific geolocators to particular human groups and body sites. The data also indicate that diverse body sites have varying geolocation accuracy, with specific skin and oral samples showing higher performance than stool. As an outgrowth of the skin, the microbial communities of human hair shafts show significant body site and geographical compositional differences indicating that hair shafts have the potential to be used to predict the source location of the hair. As such, the potential of the human microbiome as a reliable and specific geolocation tool in forensics should be considered, along with efforts to formally implement geosourcing from microbiome data in forensic investigations. The Forensic Microbiome Database (FMD) (http://www.fmd.jcvi.org) is a publicly available analysis resource that correlates 16S rRNA data obtained from multiple human body sites to metadata as it relates to forensics. The goal of the FMD is to be used as a valuable tool to predict the geographical location of subjects using human microbiome data. The FMD is an actively updated database and will be expanded through the inclusion of paired oral and stool microbiome samples from 100 healthy adult women residing in Hong Kong, Barbados, Chile, and two cities in South Africa. The addition of these large-size datasets will strengthen the FMD's geolocation prediction model and incorporate multiple currently underrepresented geographical locations worldwide.

2:50 P.M.–3:15 P.M.

Candidates of Skin Microbiomes for Human Identification

NIJ Award#: 2015-NE-BX-K006

Presenting author: Bruce Budowle, PhD, Center for Human Identification, University of North Texas Health Science Center, Fort Worth, Texas

Co-authors: Sarah E. Schmedes, PhD, and August E. Woerner, PhD, Center for Human Identification, University of North Texas Health Science Center, Fort Worth, Texas

Description: Human microflora on the skin may be a high-copy source of DNA for identifying individuals. This study used supervised learning methods and *Propionibacterium acnes* pangenome presence/absence features and nucleotide diversities of stable clade-specific markers to determine classification accuracies of the microbial source. The hidSkinPlex was developed and evaluated on bacterial control samples and then on eight individuals from three body sites. All samples (n =72) regardless of body site origin (foot, manubrium, and hand) were correctly classified with up to 94% accuracy, and body site origin could be predicted with up to 86% accuracy.

Forensic human DNA typing relies primarily on characterization of short tandem repeat (STR) markers (residing on autosomal and Y chromosomes). The types of evidence presented to the laboratory today often contain mixtures of human DNA from multiple sources and/or contain low amounts, making interpretation of mixed or partial profiles difficult or inconclusive. In these cases, alternative markers, such as sequencing the high-copy mitochondrial genome, or methods to enhance sensitivity of detection sometimes are considered. The human microbiome possibly may be considered another high-copy number genetic marker because microbial cells may be at a ratio of 1:1 to 10:1 to human cells. Indeed, microbes on human skin may be more readily deposited than human cells. Thus, human microbiome flora may be a potential target to complement partial or inconclusive STR profiles to increase resolution for human source attribution. Previous studies have demonstrated the potential to use microbiome profiling for forensic applications; however, a method has yet to identify stable features of skin microbiomes that produce high classification accuracies for samples collected over reasonably long time intervals. A novel approach has been developed to classify skin microbiomes and associate them with their donors.

This study compared two features types: *Propionibacterium acnes* pangenome presence/absence features and nucleotide diversities of stable clade-specific markers. Supervised learning was used to attribute skin microbiomes from 14 skin body sites from 12 healthy individuals sampled at three time points over a more than 2.5-year period with various accuracies for multiple skin body sites. With feature selection, we identified a subset of markers (187 markers from 12 clades) from each body site that are highly individualizing. We compared the classification accuracies in a formal model testing framework, and the results indicate that nucleotide diversity performed better than presence/absence encodings. These selected features provided a preliminary marker panel for developing a robust and reproducible method for skin microbiome profiling for forensic human identification. Likely for forensic applications informative targets will need to be enriched, because they are for current human identification methods. Targeted enrichment and sequencing using a panel of the most informative markers are being sought for microbiome profiling for forensic identification to obtain high coverage at stable informative sites. A multiplex panel has been designed and is being tested empirically for classification accuracy and sensitivity at various sites on the human skin, including the currently low-informative foot region. Performance assessment is underway, and preliminary data indicate that the candidate panel can characterize human-based selected microbes even at initially low-abundant body sites.

Afternoon Session II: Forensic Biology/DNA

3:30 P.M.–3:55 P.M.

Multi-locus Match Probability Dependencies

NIJ Award #: 2014-DN-BX-K028

Presenting author: Bruce Weir, PhD, University of Washington

Description: With the recent increase in the number of Combined DNA Index System (CODIS) core loci from 13 to 20, would more loci provide even higher discriminatory potential? Do match probabilities for different people's profiles continue to decrease at the same rate as the number of loci increases? Dependencies exist among single-locus match probabilities in finite populations, but using the single-locus "theta-corrections" at each locus was believed to compensate for these dependencies. Caveats for this approach are

based on theoretical, simulation, and empirical results for autosomal and Y-chromosome short tandem repeats and autosomal single nucleotide polymorphisms, suggesting consideration of a multi-locus population structure parameter theta as a predictor of match probability for multi-locus profiles.

Abstract: With the recent increase in the number of Combined DNA Index System (CODIS) core loci from 13 to 20, would more loci provide even higher discriminatory potential? Or are we approaching the point of diminishing return?

Donnelly (Heredity 75:26-24, 1995) discussed the question: "after the observation of matches at some loci, it is relatively much more likely that the individuals involved are related (precisely because matches between unrelated individuals are unusual) in which case matches observed at subsequent loci will be less surprising. That is, knowledge of matches at some loci will increase the chances of matches at subsequent loci, in contrast to the independence assumption." Laurie and Weir provided a theoretical prediction of dependencies in match probabilities, focusing on the effects of mutation (Theor. Pop. Biol. 63:207-219, 2003), following an earlier treatment of the effects of population size by Cockerham and Weir (Theor. Pop. Biol. 4:300–330, 1973). Weir provided an empirical demonstration (J. Foren. Sci. 49:1009-1014, 2004): among 15,000 forensic short tandem repeat profiles the ratios of multi-locus match proportions to products of single-locus proportions were 1.000, 1.000, 1.008, 1.034, and 1.041 for two, three, four, five, and six loci, respectively.

The hope has been that using the single-locus "theta-corrections" at each locus would compensate for the between-locus dependencies. Some caveats for this approach will be presented, based on theoretical, simulation, and empirical results for autosomal and Y chromosomes and autosomal single nucleotide polymorphism. This work suggests consideration of a multi-locus population structure parameter theta as a predictor of match probability for multi-locus profiles.

3:55 P.M.–4:20 P.M.

Record Linkage of CODIS Profiles with SNP Genotypes

NIJ Award #: 2014-DN-BX-K015

Presenting author: Michael D. Edge, PhD, University of California, Davis

Co-authors: Bridget F.B. Algee-Hewitt, PhD, Stanford University; Trevor J. Pemberton, PhD, University of Manitoba; Jun Z. Li, PhD, University of Michigan; and Noah A. Rosenberg, PhD, Stanford University

Description: The Combined DNA Index System (CODIS) markers are widely used for forensic identification. Here, we describe a method for assessing whether a set of genotypes at the CODIS microsatellite markers is drawn from the same person as a set of genome-wide single nucleotide polymorphism (SNP) genotypes. The method raises possibilities for some degree of backward compatibility as forensics databases transition to SNP-based datasets, and it also suggests some possible privacy concerns.

Abstract: Forensic-genetic work in the United States relies largely on the Combined DNA Index System (CODIS) markers, a set of 20 (until recently, 13) microsatellite loci in heavy use since the 1990s. One premise that has influenced forensic practice—figuring in discussions of both backward compatibility of single-nucleotide polymorphism (SNP)-based systems with the CODIS database and of genetic privacy—is that the information provided by the CODIS loci is completely distinct from the information provided by larger

sets of SNPs. Although the associations between CODIS markers and specific genetic variants known to influence phenotypes are weak, there may still be a connection between CODIS records and SNP information if pairs of CODIS and SNP genotypes can be identified as coming from the same person—that is, if CODIS and SNP records can be linked. We present a method for assessing whether a particular set of genotypes from the CODIS markers is likely drawn from the same person (or an identical twin) as a set of genome-wide SNP genotypes, extracting a signal arising from linkage disequilibrium between CODIS and SNP markers. In subsets of a dataset of 872 people, 90 to 98% of records of the original 13 CODIS markers can be linked to corresponding SNP records and vice versa. As more short tandem repeat (STR) markers are used, accuracy improves, reaching 99 to 100% when ~30 STRs are used. Our results suggest possibilities and limits for backward compatibility of SNP-based databases with existing forensic-genetic databases, and it also raises privacy concerns associated with maintaining forensic databases containing even small numbers of genetic markers.

4:20 P.M.–4:45 P.M.

Microhaplotypes Analyzed by Massively Parallel Sequencing Are Valuable Forensic Tools

NIJ Award #: 2016-DN-BX-0162

Presenting author: Kenneth Kidd, PhD, Yale University

Description: Microhaplotypes, very short segments of DNA with multiple polymorphisms, are markers of great potential when massively parallel sequencing is used. Microhaplotypes can be very informative in (1) identifying and deconvoluting mixtures of DNA, (2) identifying biological relationships, (3) identifying biogeographic ancestry, and (4) providing very small random match probabilities. Those uses will be demonstrated with various analyses involving over 150 loci and up to 96 population samples (>5,000 individuals). Because large numbers of loci can be multiplexed, the statistical power of microhaplotypes can greatly exceed that of standard forensic markers typed by capillary electrophoresis.

Abstract: With the advent of massively parallel sequencing (MPS), microhaplotypes (microhaps) have become a valuable new type of DNA marker for use in forensics. Microhap loci are small (<300 base pairs, generally <200 bp) regions of DNA with two or more single nucleotide polymorphism (SNPs) defining three or more common haplotypes (alleles) in multiple populations. Microhaps have the potential to be very informative in (1) identifying and deconvoluting mixtures of DNA, (2) identifying biological relationships, (3) identifying biogeographic ancestry, and (4) providing very small random match probabilities. Publications and presentations to date have demonstrated proof of principle, using typing of the individual SNPs and statistical phasing into haplotypes with lengths ranging from 11 bp to about 250 bp. MPS typing by collaborators has confirmed the broadly accepted accuracy of statistical phasing of data for population allele frequencies.

A full analysis of 130 loci evaluated on 83 population samples (>5,000 individuals) was recently published. Analyses of the data demonstrate theoretically the near certainty of detecting a mixture (unambiguous presence of three or more alleles in a sample) using just the 28 loci with the highest global average effective number of alleles. Mixture analyses using MPS have also been performed, demonstrating an enhanced mixture detection capability by detecting the minor contributor at a 40:1 ratio when the mixture is sequenced in a 36-locus multiplex starting with only 250 pg. Both greater sensitivity and absence of stutter interference make microhaps much better than the forensic short tandem repeat

polymorphisms (STRPs) in the interpretation of mixtures. Data on an additional 38 loci are now available for those 83 population samples, and 65 of the loci have been extended to 96 population samples.

Anthropologic analyses of the microhap data on these 96 populations show that up to 10 biogeographic clusters can be defined. Because they are multiallelic and many loci can be multiplexed, microhaps are also excellent at quantifying biologic relationships without worrying about high mutation rates. These MPS analyses allow the unequivocal conclusion that these loci are of great value for forensic questions that cannot be answered using just the CODIS STRP loci. The very large number of microhap loci characterized on at least 83 populations from around the world provides a resource for sets of markers targeted to specific questions and circumstances, such as highly degraded DNA. Definitions and allelic data of the published loci are accessible in ALFRED <https:alfred.med.yale.edu> [supported by NIJ 2016-DN-BX-0162] under the keyword microhap; the newly characterized data are being added to the database.

4:45 P.M.–5:10 P.M.

Production of High-Fidelity Electropherograms Results in Improved and Consistent Match-Statistics: Standardizing Forensic Validation by Coupling Laboratory Data with an In Silico DNA Pipeline

NIJ Award #: 2014-DN-BX-K026

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Description: We parameterized an in silico DNA laboratory using the laboratory's experimental data, resulting in fast prediction of optimal settings. Distributions of noise and signal were used to assess signal-to-noise resolution and signal detection error rates, which can determine optimal analytical thresholds. We established that metrics of signal quality can be consistent between platforms and that a high-fidelity signal improves downstream probabilistic interpretation. We show that a high-fidelity signal results in statistics that are similar across platforms, demonstrating that variation in continuous measures of evidence strength can be minimized. This is potentially the first step toward standardizing the analytical and validation DNA pipelines across laboratories.

Abstract: Samples containing low-copy or complex DNA mixtures are routinely encountered in operations. The signals acquired from these sample types are difficult to interpret because they do not always contain all of the genotypic information from each contributor, and the loss of genetic information is associated with sampling and detection effects. This study developed a validation scheme to help mitigate the effects of the loss of genetic information. We developed a process by which high-fidelity electopherograms (EPGs) are produced consistently, improving interpretation by all probabilistic genotyping systems.

We developed a systematic approach to forensic DNA signal optimization and validation. Specifically, we developed ReSOLVIt (Resolving Signal for Objective Laboratory Validation), a simulation-based tool that allows for quick evaluation of multifarious laboratory scenarios, illustrated how the careful evaluation of a single-copy DNA signal from multiple scenarios provides a mechanism by which to choose laboratory conditions that consistently lead to a high-fidelity signal, and demonstrated that optimized conditions lead to improved and consistent likelihood ratios for true contributors and noncontributors.

We devised ReSOLVIt, which generates synthetic EPGs in a laboratory-specific manner, using a large number of single-source profiles of known genotype provided by the laboratory. From these data, we modeled the distribution of the peak heights at noise positions as a function of the starting template amount using a log-normal distribution. We also acquired the electrophoresis sensitivity, which is used to generate the DNA height distribution, from the single-source experimental data procured from the laboratory. Other pertinent laboratory conditions, such as the number of polymerase chain reaction cycles, injection time, and starting template mass, for instance, are input parameters and are easily modified by the user.

Because ReSOLVIt uses a simulation approach based on experimental data acquired from the laboratory, each laboratory can explore multifarious scenarios cost-effectively. Metrics such as signal copy-to-noise resolution and false-positive and false-negative signal detection rates are used to select tenable laboratory conditions that result in a high-fidelity signal in the single-copy regime. We demonstrate that the metrics acquired from simulation are consistent with experimental data obtained from two capillary electrophoresis platforms and various injection parameters. Once good resolution is obtained, analytical thresholds can be determined using detection error trade-off analysis, if necessary.

Decreasing the limit of detection of the forensic process to one copy of DNA is a powerful mechanism by which to increase the information content on alleles from minor components of a mixture, which is particularly important for probabilistic system inference. By using another fully continuous probabilistic system, CEESIt (Computational Evaluation of Evidentiary Signal), we demonstrate that if the forensic pipeline is engineered to produce a high-fidelity EPG signal, then the likelihood ratio (LR) of a true contributor increases and the probability that the LR of a randomly chosen person is greater than one decreases. CEESIt has been developed to not only compute the LR but also the probability that the LR is greater than one for millions of randomly chosen contributors, making it a powerful validation tool. This systematic, in silico, laboratory-specific, computational-based approach to improve allele information content is potentially the first step toward standardizing the bio-analytical pipeline and DNA validation process across operational laboratories.

PRESENTER BIOS

Bridget F.B. Algee-Hewitt

Bridget F.B. Algee-Hewitt, PhD, is a biological anthropologist at Stanford University. She studies human skeletal and genetic trait variation to understand population structure and to develop methods for human identification. She also considers life-history data to uncover how biological, environmental, and social factors interact and together lead to differences in physical expression and contribute to personal or group identity. Much of her published work addresses the statistical challenges of inferring age at death and ancestry from the skeleton, the role of social identifiers like race in forensic anthropology, the evidentiary value of biological profile parameters in medico-legal casework, and the relationship between individual and population identifiability using genetic markers.

Shamsi Daneshvari Berry

Shamsi Daneshvari Berry, PhD, is an assistant professor in the Department of Health Informatics and Information Management, University of New Mexico. She is also a biomedical informatics consultant, standardizing and building databases. She received her PhD in anthropology and completed a postdoctoral fellowship in biomedical informatics. Dr. Daneshvari Berry's dissertation focused on determining body mass from skeletal remains to aid in forensic identification and identify social stratification. Her current research focuses on using data collected from medical examiners to improve the health of the living.

Bruce Budowle

Bruce Budowle, PhD, earned his doctorate in genetics in 1979 from Virginia Polytechnic Institute and State University. From 1979 through 1982, Dr. Budowle was a postdoctoral fellow at the University of Alabama at Birmingham. Working under a National Cancer Institute fellowship, he carried out research predominately on genetic risk factors for such diseases as insulin-dependent diabetes mellitus, melanoma, and acute lymphocytic leukemia.

In 1983, Dr. Budowle joined the research unit at the FBI Laboratory Division to carry out research, development, and validation of methods for forensic biological analyses. Dr. Budowle has contributed to the fundamental sciences as they apply to forensics in analytical development, population genetics, statistical interpretation of evidence, and quality assurance (QA). Dr. Budowle has worked on laying some of the foundations for the current statistical analyses in forensic biology and defining the parameters of relevant population groups. He has published approximately 600 articles,

made more than 720 presentations (many of which were as an invited speaker at national and international meetings), and testified in well over 250 criminal cases in the areas of molecular biology, population genetics, statistics, QA, and forensic biology. In addition, he has authored or coauthored books on molecular biology techniques, electrophoresis, protein detection, and microbial forensics. Dr. Budowle has been directly involved in developing QA standards for the forensic DNA field. He has been a chair and member of the Scientific Working Group on DNA Methods, Chair of the DNA Commission of the International Society of Forensic Genetics, and a member of the DNA Advisory Board. He was one of the architects of the Combined DNA Index System (CODIS) National DNA database, which maintains DNA profiles from convicted felons, from evidence in unsolved cases, and from missing persons.

Some of Dr. Budowle's efforts over the last 15 years also are in counter-terrorism, including identification of victims from mass disasters and in efforts involving microbial forensics and bioterrorism. Dr. Budowle was an advisor to New York State in the effort to identify the victims from the World Trade Center attack. In the area of microbial forensics, Dr. Budowle has been the chair of the Scientific Working Group on Microbial Genetics and Forensics, whose mission was to set QA guidelines, develop criteria for biologic and user databases, set criteria for a National Repository, and develop forensic genomic applications. He also has served on the Steering Committee for the Colloquium on Microbial Forensics sponsored by American Society of Microbiology, as an organizer of four Microbial Forensics Meetings held at The Banbury Center in the Cold Spring Harbor Laboratory, and on steering committees for NAS-sponsored meetings.

In 2009, Dr. Budowle became Executive Director of the Institute of Applied Genetics and Professor at the University of North Texas Health Science Center at Fort Worth, Texas. He currently directs the Center for Human Identification. His research efforts focus on the areas of human forensic identification, microbial forensics, emerging infectious disease, molecular biology technologies, and pharmacogenetics.

David O. Carter

David O. Carter, PhD, is Director and Associate Professor of Forensic Sciences at Chaminade University of Honolulu. He also serves as Principal Investigator of the Laboratory of Forensic Taphonomy. His primary research interest is the decomposition of human remains, particularly in tropical environments. Current research projects focus on the structure and function of antemortem and postmortem microbial communities: using microbiomes as spatial and temporal evidence. He is interested in understanding the relationships between decomposing remains, microbial communities, and the environment. Dr. Carter's ultimate goal is to get quality science and technology in the hands of first responders and investigators.

Dr. Carter is an active member of the forensic science community with a significant interest in undergraduate education. He is a Fellow in the Pathology/Biology Section of the American Academy of Forensic Sciences and recently served as Secretary for the Pathology/Biology Section. Dr. Carter also serves on the Organization of Scientific Area Committees, Medicolegal Death Investigation Subcommittee, a joint endeavor between the US Department of Justice and US Department of Commerce. He incorporates these experiences into undergraduate education where he plays an active role in curriculum development, assessment, academic advising, and recruiting.

Heather J.H. Edgar

Heather J.H. Edgar is an associate professor in the Anthropology and Pathology departments at the University of New Mexico. She is the forensic anthropologist for the Office of the Medical Investigator in Albuquerque, New Mexico. Her training in anthropology was at the University of Nevada, Las Vegas (BA); Arizona State University (MA); and The Ohio State University (PhD). Her research interests include biocultural aspects of human variation, especially as understood through forensic anthropology; bioarchaeology; dental anthropology; human biology; and the interface of biological anthropology and biomedical informatics. The majority of her work has focused on African American, Hispanic American, and Mexican biohistory. Her current projects include the development of a large-scale, free-access, documented database of whole-body decedent CT scans for research and education. Other current work includes the standardization of dental morphological characteristics for forensic estimation of ancestry; the biological consequences of colonization in Mexico; and the relationship among sub-ethnic group variation, health, and wealth in contemporary New Mexicans of Spanish-speaking descent.

Michael D. Edge

Michael "Doc" Edge, PhD, is a postdoctoral researcher at University of California, Davis, where he studies population genetics and quantitative genetics. He is the first author of a recent study on linkage disequilibrium-based genetic record linkage (Edge et al., 2017, PNAS), which he conducted while completing a PhD with Noah Rosenberg at Stanford University.

David Foran

David Foran, PhD, is the Director of the Forensic Science Graduate Program at Michigan State University, the nation's oldest continuous forensic science program, celebrating its 70th anniversary this year. Dr. Foran obtained his PhD in molecular genetics from the University of Michigan and was a postdoctoral fellow at McGill University in Montreal. He became a research associate at the University of California at Santa Cruz and then an assistant professor in the Forensic Science Department at George Washington University in Washington, DC, where he developed the forensic biology track and laboratory. He joined Michigan State 16 years ago, founding its Forensic Biology Laboratory and graduate track, and became Program Director 13 years ago.

Dr. Foran is a Fellow of the American Academy of Forensic Sciences. He has long served on the editorial board of the *Journal of Forensic Sciences* and became its first associate editor for forensic biology last year. He has served on the National Institute of Standards and Technology Organization of Scientific Area Committees since its inception and regularly

assists law enforcement, medical examiners, and attorneys. He is court qualified in nuclear and mitochondrial DNA profiling, forensic serology, and specialized matters such as species identification. Dr. Foran's laboratory at Michigan State University became interested in the forensic identification of soils based on microbial profiling over a decade ago. Since that time, the laboratory has been on the cutting edge of objective and statistically relevant microbial comparisons of soil samples for their forensic identification.

Catherine Grgicak

Catherine Grgicak, PhD, serves as the Henry Rutgers Chair in Chemistry, is an Associate Professor in the Department of Chemistry, and is a member of the Center of Computational and Integrative Biology at Rutgers University in Camden, NJ. Previously she was faculty at Boston University, where she was an Assistant Professor of Biomedical Forensic Sciences. Dr. Grgicak is a member of editorial board of the Journal of Forensic Sciences, OSAC's Biological DNA Interpretation and Reporting subcommittee, the International Society of Forensic Genetics, the American Academy of Forensic Sciences, and the Electrochemical Society. She earned her BSc (physical sciences) and BEd at the University of Windsor; her MSFS at the University of Alabama at Birmingham; and her PhD in chemistry from the University of Ottawa in 2007.

Joseph Hefner

Joseph Hefner, PhD, is an assistant professor specializing in forensic anthropology and quantitative methods. His interests in forensic anthropology include the estimation of ancestry using macromorphoscopic (cranial nonmetric) traits and cranial and postcranial metrics. The focus of Dr. Hefner's research is the standardization and quantification of macromorphoscopic traits with robust and appropriate classification statistics, including data mining techniques and machine learning methods. One aspect of this type of research is the seemingly endless need for more data. To that end, Dr. Hefner is currently establishing the Macromorphoscopic Databank at Michigan State University. Dr. Hefner's professional activities center on forensic anthropological method and theory and statistical approaches to biological anthropology, including biodistance analysis, categorical data analysis, geometric morphometric methods, data excavation, and parametric/nonparametric classification statistics. Dr. Hefner is a board-certified forensic anthropologist (D-ABFA) and a member of the Board of Directors for the American Board of Forensic Anthropology; a Fellow of the American Academy of Forensic Sciences; a member of the Register of Professional Archaeologists, American Association of Anatomists, Sigma Xi; and an Assessor for the American Society of Crime Laboratory Directors, Laboratory Accreditation Board.

Mariyam Isa

Mariyam Isa is a PhD student in the Department of Anthropology at Michigan State University in East Lansing, Michigan. Since 2012, she has assisted her advisor, Dr. Todd Fenton, on several of his skeletal trauma research projects including two funded by the National Institute of Justice.

Ms. Isa is the lead graduate student on the current National Institute of Justice grant Building a Science of Cranial Fracture (Award No. 2015-DN-BX-K013). In 2015, she received a National Science Foundation Graduate Research Fellowship (Grant No. DGE1424871) in support of her dissertation work investigating the effects of various impact variables on the production of cranial and postcranial fractures in blunt force impact experiments. In addition to her work on trauma research, Ms. Isa assists with forensic anthropology casework in the Michigan State University Forensic Anthropology Laboratory (MSUFAL). She served as Laboratory Manager of the MSUFAL from 2016 to 2017.

Kenneth K. Kidd

Kenneth K. Kidd, PhD, Professor Emeritus of Genetics and Senior Research Scientist at Yale University, is a human population geneticist. He has published over 550 scientific papers on a variety of subjects before and during his 44-year career at Yale. His research has included medical genetics, gene mapping, database design, pharmacogenetics, and a variety of molecular methodologies. His long-standing interest in human population genetics has been combined with his laboratory's expertise in molecular technology to examine human genome diversity at the DNA level. In the late 1980s and early 1990s, his expertise in both population and molecular genetics provided helpful expert testimony in getting DNA accepted in the courts. After serving on the advisory panels for DNA identification of victims of the World Trade Center attack and of Hurricane Katrina, he began research in his lab on panels of single nucleotide polymorphisms (SNPs) for various uses in forensics as an extension of his active research on human genetic diversity. His lab is now very active in identifying SNPs useful in forensics and in using bioinformatics to make the data available and useful. His group designed and maintains ALFRED, the large ALlele FREquency Database <alfred.med.yale.edu>, and is actively enhancing FROGkb, the Forensic Reference/Resource on Genetics knowledge base <frog.med.yale.edu>. Since 2013, he has also been recognized for his development of microhaplotypes as a new type of forensic marker suited for the coming transition from capillary electrophoresis to massively parallel sequencing as a common method in forensic practice.

Jieun Kim

Jieun Kim, PhD, is a biological anthropologist whose research foci are centered on modeling age-progressive changes in the adult skeleton using Bayesian statistics. Her doctoral research investigated population variation in skeletal aging for South-East and East Asian samples. Dr. Kim is a postdoctoral research associate working under the supervision of Dr. Bridget Algee-Hewitt at Stanford University and Dr. Dennis Slice at Florida State University.

Alex Krotulski

Alex Krotulski graduated with a bachelor's degree in chemistry from Loyola University New Orleans. He then obtained a master's degree in forensic science from Arcadia University, focusing on forensic toxicology through research involving novel psychoactive substances and drugs of abuse in blood and oral fluid. Mr. Krotulski is currently enrolled at Temple University, seeking his doctorate in analytical chemistry.

Mr. Krotulski serves as a Research Scientist at the Center for Forensic Science Research and Education at the Fredric Rieders Family Foundation. In this role, he is involved in forensic toxicology grant research funded by the National Institute of Justice, focusing on novel psychoactive substances and emerging drugs of abuse. Mr. Krotulski works directly with Waters, Agilent, and Sciex instrumentation, developing methods for drug screening in blood, urine, and oral fluid, as well as emerging drug metabolite identifications using various software and processing programs.

Lauren Brinkac Leone

Lauren Brinkac Leone, MS, is a Staff Scientist at the J. Craig Venter Institute working in the Informatics Department. Ms. Leone's research is focused on genomics and comparative analysis of bacterial virulence and drug resistance as well as the study of the human microbiome in health and disease and as an evidence type for forensic investigations. Ms. Brinkac Leone is a principal investigator on NIJ award, 2015-R2-CX-K036, working to develop a comprehensive data-rich forensic microbiome database, the FMD, consisting of analysis tools and 16S rRNA sequence data and associated metadata used to predict the geographical origin of a human microbiome sample. Prior to working at the J. Craig Venter Institute, Ms. Brinkac Leone was part of a team working at The Bode Technology Group that processed and analyzed convicted offender STR profiles to establish and maintain a criminal DNA database with the state of Virginia. Also, at The Bode Technology Group Ms. Brinkac Leone managed a team working to detect and identify trace botanical, microbial, and human specimens.

David B. Muhlhausen

David B. Muhlhausen, PhD, leads the National Institute of Justice (NIJ)—the research, development, and evaluation agency of the US Department of Justice. He is a former research fellow in empirical policy analysis at the Heritage Foundation and has championed using rigorous, empirical research to formulate and evaluate government policies. He has testified frequently before Congress on the efficiency and effectiveness of various federal programs. He has been called most often by the House and Senate Committees on the Judiciary to discuss how to improve policing strategies, prisoner reentry programs, and other important criminal justice programs.

Dr. Muhlhausen joined Heritage in 1999 after serving on the staff for the Senate Judiciary Committee, where he specialized in crime and juvenile justice policies. Prior to that, he was a manager at a juvenile correctional facility in Baltimore, Maryland.

He holds a doctorate in public policy from the University of Maryland, Baltimore County and a bachelor's degree in political science and justice studies from Frostburg State University. For 11 years, Dr. Muhlhausen taught program evaluation and statistical methods to graduate students at George Mason University Schar School of Policy and Government.

Detelina Stoyanova

Detelina Stoyanova, PhD, is a computational scientist whose specialty lies in shape analysis and visualization. She received a PhD in computational science from Florida State University in 2015. She is currently a postdoctoral associate at the Department of Scientific Computing at Florida State University and a part-time faculty member at the Mathematics and Statistics Department at the University of North Carolina at Charlotte. Dr. Stoyanova is working on developing computational techniques for age-at-death estimation using 3D laser scan data of the human pubic symphysis.

Kyle Vircks

Kyle Vircks received his bachelor's degree in chemistry (emphasis in criminalistics) from the University of Wisconsin–Platteville in 2010 and his master's degree in chemistry from Illinois State University in 2013. His thesis research involved the use of portable instrumentation and ambient mass spectrometry for applications in forensic science. Mr. Vircks joined the Harris County Institute of Forensic Sciences staff in December 2012. Before joining the Institute, he held internships with the Bureau of Forensic Fire and Explosives Analysis in Havana, FL, and Nippon Telegraph and Telephone's Energy and Environment Systems Laboratory in Tokyo, Japan. Mr. Vircks is also a regular member of the American Chemical Society, the Southwestern Association of Forensic Scientists, and the Midwestern Association of Forensic Scientists.

Bruce Weir

Bruce Weir, PhD, is Professor of Biostatistics and Director of the Institute for Public Health Genetics at the University of Washington. He is a Fellow of the American Academy of Forensic Sciences and of the American Statistical Association. He serves as a member of the Biology/DNA Scientific Area Committee of the Organization of Scientific Area Committees (OSAC) and of the Committee on Forensic Statistics of the American Statistical Association. He is an Associate Editor of the *Journal of Forensic Sciences*. He teaches a short course in Forensic Genetics each July as part of the Summer Institute in Statistical Genetics at the University of Washington.

Jamie R. Wieland

Jamie R. Wieland, PhD, is an Assistant Professor in the Department of Management and Quantitative Methods at Illinois State University. Dr. Wieland obtained her PhD in industrial engineering from Purdue University and bachelor's degree in industrial engineering and management science from Northwestern University. Her research interests lie in developing and applying statistical methods and probability models for policy and decision analysis, with an expertise in Monte Carlo simulation. Previous publications have appeared in the *Journal of Business Research, Journal of Service Management*, and *Journal of the American Society for Mass Spectrometry*. Dr. Wieland's current research involves assessing the operational and economic impacts of portable technologies used for on-site analysis of forensic evidence during crime scene investigation processes. This cross-disciplinary project has been funded by the National Institute of Justice (Award Nos. 2015-IJ-CX-K011 and 2017-R2-CX-0022) and was recently featured in the *Chicago Tribune*.

Carl Wolf II

Carl Wolf II, PhD, received his bachelor's degree in chemistry from Gannon University in 1986, where he received the CRC Press' Outstanding Freshman Chemist Award. Dr. Wolf received his MS in criminal justice with a forensic science option from Virginia Commonwealth University in 1994 and received his PhD in pathology with a focus on forensic toxicology from the Medical College of Virginia campus at Virginia Commonwealth University in 2005.

Dr. Wolf has been employed at Medical College of Virginia Hospitals since 1987 in various roles in the Clinical and Forensic Toxicology Laboratories. He regularly consults and/or lectures on toxicology and drug testing issues. Dr. Wolf has given expert testimony in several jurisdictions in the Commonwealth of Virginia and the State of North Carolina. He has contributed to over 100 presentations and peer-reviewed publications and is a full member of the Society of Forensic Toxicologists. Dr. Wolf is a Fellow of the American Board of Forensic Toxicologists (ABFT) and has been certified by ABFT since 2001. He was a member of the group that received the 2007 Educational Innovation Award from the School of Medicine at the Medical College of Virginia campus of Virginia Commonwealth University for their work on developing and maintaining an online continuing education program for the chronic nonmalignant pain management curriculum. In 2017, Dr. Wolf received a grant from the National Institute of Justice to study the matrix effects that liver tissue has on the analysis of opiates using 10 different sample preparation techniques.

NOTES