For the first time in decades, we are witnessing a revolution in forensic DNA testing that promises to bring closure to the tragic number of cold cases currently stalled at some point in the investigative process. There are hundreds of thousands of cold cases in the United States alone. The National Institute of Justice calls it a silent mass disaster. Cold cases in the United States and worldwide continue to accumulate, the vast majority of which will not be solved using traditional forensic DNA testing frameworks. One such framework is the Combined DNA Index System (CODIS), a Federal Bureau of Investigation program that supports DNA databases and infrastructure for using these databases to search unknown DNAs against a catalog of known felons.

While CODIS will remain a critical and irreplaceable component of forensic DNA testing in the foreseeable future, countless solvable cases remain unsolved due to the simple fact that CODIS was designed from the start—when DNA testing was in its infancy—to identify those individuals who had already been identified by other methods. While effective in tracking repeat crime by convicted criminals, CODIS is ineffective for cases such as unidentified remains, as many of them are victims and not criminals. Of course, CODIS will not reveal the identification of all criminals either. Many perpetrators of crimes have yet to have been caught, and even those who are caught (and even convicted) can accidently be missing from CODIS.

In the past few years, incredible advances in forensic genetic testing have transformed what forensic professionals can learn from DNA left at crime scenes. A growing number of seemingly “unsolvable” cases are now being closed—most notably the capture of the Golden State Killer in April 2018. Testing was pivotal in finding the killer and ensuring his life sentence, delivered in August 2020.

These newer DNA testing methods, of which there are many, rely on “reading” tens to hundreds of thousands of DNA markers across the genome. In comparison, a full DNA profile for CODIS contains just 20 core markers—or 20 sites on the human genome. When a CODIS profile is entered into CODIS, a match can be made to someone already in the database. In some states, CODIS can be used to search immediate family relationships, such as parent–offspring, with a technique called “familial DNA testing.” However, to detect the sorts of distant genetic relationships used to catch the Golden State Killer, a much richer genomic profile is needed, comprising as many as hundreds of thousands of DNA markers. Measuring these markers requires new methods typically unavailable at laboratories that offer conventional CODIS testing. The foundation for these new methods comes from consumer, research, and medical DNA testing applications over the past decade.

As this cutting-edge technology is new for most criminal investigations, there are not many resources available to guide investigators and forensic professionals through the process. What cold cases are best for these advanced forms of DNA testing? What are the considerations, trade-offs, and risks? Which scientific methods should be used for which applications? Most importantly, how do you return the most value to forensic professionals while consuming the least amount of evidence and budget?

**Journal Entry**

*Forensic Genomics* is an exciting new peer-reviewed journal from Mary Ann Liebert, Inc., which has decades of publishing experience, particularly in cutting-edge DNA techniques. Starting with *Human Gene Therapy* in 1990, Mary Ann Liebert, Inc., has had a penchant for identifying exciting new areas of research and technology, including recent launches such as *The CRISPR Journal* and PHAGE.

*Forensic Genomics* addresses how advances in genetic testing and genomic analysis can enable investigators to break through previously impenetrable forensic DNA barriers. Our goal is to accelerate the validation and adoption of new methods to support investigations that would be otherwise stall with traditional forensic testing methods.

To accomplish this goal, *Forensic Genomics* will be organized into three complementary sections: emerging...
technologies and inference tools; the practical impact of these technologies on current forensic casework; and a third that seeks to provide a path forward for the expanded utilization of these technologies in current casework.

The journal will be published quarterly, with the first issue appearing in the first quarter of 2021. We are a hybrid journal, which provides authors with maximum flexibility in publishing their work. Manuscripts can be submitted through the traditional model, with access to the manuscript provided via subscription to the journal, or the manuscript can be designated open access via an article processing charge.

I am proud to have joined Forensic Genomics as Editor-In-Chief, and I couldn’t be more excited. I have obsessed about genetics and DNA testing for more than two decades. I got my start in the Human Genome Project at the UT Southwestern Medical Center, and received my PhD in Molecular Biophysics from Baylor College of Medicine. I worked with John Wilson, PhD, and studied DNA repair and gene editing. Massively parallel sequencing was just taking off as I completed my graduate work, and I pursued postdoctoral training with Richard Gibbs, PhD, at Baylor’s Human Genome Sequencing Center. I later started my own research program at Virginia Tech as an associate professor, and remained engaged with many genomics initiatives such as the 1000 Genomes Project.

My work eventually took me away from academic biomedical research and into the consumer genetics testing arena. I built a genomics start-up company called Arpeggi, which was acquired by Gene by Gene, and its flagship brand, Family Tree DNA. I joined as Chief Scientific Officer and immersed myself in genealogical, ancestry, and other interesting applications of consumer genetic testing. I have been on many adventures in the genomics industry since then, but helping people solve family mysteries with DNA testing remains a highlight.

More recently, I founded and am CEO of Othram, a DNA testing laboratory and software company based in The Woodlands, Texas, which enables human identification from difficult evidence such as touch DNA, rootless hair, and decades-old bones. Othram is the first forensic laboratory to integrate a genome-wide test and a human identification solution vertically. The team works with academic researchers, forensic scientists, medical examiners, and law-enforcement agencies to achieve results when other approaches have failed. While my day job involves working with law enforcement to tackle “unsolvable” cases, our team members, much like myself, are academics at heart. We have developed educational programs with MD Anderson Cancer Center in Houston to train the next generation of scientists who will perform these DNA testing techniques, and we are very excited to promote and support the growth of this journal, which will be a leading forum for discussion in this field.

**Building the Team**

I am grateful to be joined on this journey by some exceptional talents who have committed their lives to growing this field and to serving as Associate Editors for Forensic Genomics. Joining the leadership team are Bruce Budowle (UNT Health Science Center), CeCe Moore (Parabon Nanolabs), Amy Michael (University of New Hampshire), Bobby LaRue (Verogen, Inc.), Denise Syndercombe-Court (King’s College London), and Robert Bever (Bode Cellmark Forensics). Their contributions are invaluable and a reflection of their confidence in what we can achieve working together for the field.

There is simply no journal like Forensic Genomics, combining forensic testing with the promise of genomics and genome-wide test methods. We hope to attract stakeholders in academia and private forensic lab companies around the world. We want to hear from researchers and professionals who are innovators in isolating, enriching, and analyzing human DNA; laboratory professionals who push the limits of what sorts of DNA inputs can be used in genome-wide testing—such as the ability to produce DNA profiles from a single strand of rootless hair or touch DNA. We will seek out contributions from bioinformatics and data science professionals that refine our ability to sort out complex mixtures of human genomes and ultimately enable us to produce accurate genomic profiles that can be used to measure precise genetic relationships. Forensic Genomics will also be home to genealogy research, which has been used for decades to solve mysteries in families and now needs to be adapted as a forensic process that will one day be tested in a court of law.

Our field needs reference materials, standards, benchmarks, and frameworks to advance our work in the context of ethical, social, and societal considerations.
Lastly, we need to hear from victims of crimes, from their families, and from those who advocate for them. Science can move unbounded in many directions, and it is important to ensure that research and work product eventually tie back to the goal of solving cold cases and reducing or preventing future crime.

The analytical and bioinformatics tools available to forensic professionals today are unprecedented. We must continue to hone and refine these tools and do so responsibly. Fully consuming evidence using an inappropriate or inadequate method can truly render a cold case unsolvable—the stakes are great, but the reward for solving a case is great as well.

I hope you will find our new journal *Forensic Genomics* just as exciting! I encourage you to contact your institution’s collections librarian to recommend including this key title in their holdings for 2021 and beyond. If you are a forensic or law-enforcement professional outside academia, please contact Wendy News-ham (wnewsham@liebertpub.com) for information on subscribing.

Most importantly, please spread the news about *Forensic Genomics* and bring your research to our journal so that we can learn together and truly make the world a better and safer place.

David Mittelman, PhD
Editor-in-Chief