W13 Moving From the Combined Probability of Inclusion (CPI) to Probabilistic Genotyping for DNA Mixture Interpretation

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After attending this presentation, attendees will understand the current limitations of interpreting DNA mixtures using "binary" approaches in which alleles are either "included" or "excluded" from analysis. Attendees will develop an understanding and overview of probabilistic approaches that consider missing data (allele drop-out) or spurious alleles (allele drop-in) to interpret DNA profiles.

This presentation will impact the forensic science community by providing an overview of the limitations of current statistical approaches and promises for the future of DNA mixture interpretation for forensic DNA analysts, DNA technical leaders, laboratory directors, prosecutors, defense attorneys, and judges.

This workshop is targeted to attendees that have not committed to a probabilistic genotyping software but would like to have an introduction to improve their knowledge base.

Several high-profile closures of forensic DNA laboratories in the United States over the past few years have now focused the forensic DNA community on the challenges associated with the interpretation of mixtures. Many of these challenges involve the use of the CPI or the Combined Probability of Exclusion (CPE) on complex mixtures where allele drop-out is reasonable. In 2010, the Scientific Working Group on DNA Analysis Methods (SWGDAM) published a set of guidelines for autosomal Short Tandem Repeat (STR) interpretation, updated in January of 2017. The SWGDAM guidelines, along with the recommendations of the International Society for Forensic Genetics (ISFG) in 2006, have recommended the use of a stochastic threshold to consider the possible loss of alleles in a DNA profile (i.e., allele drop-out).

With the recent improvements in both STR multiplex chemistry and Capillary Electrophoresis (CE) instrumentation, the interpretation of highly complex mixtures such as "touch" items with (1) two or more contributors, and/or (2) low-level contributors with possible dropout has become a greater challenge for the analyst to interpret. Methods that treat alleles probabilistically instead of with a threshold-based approach have gained acceptance around the world over the past few years as a way forward for DNA mixture interpretation. The statistical output of a probabilistic genotyping software is the Likelihood Ratio (LR), which evaluates the evidence under two mutually exclusive hypotheses.

This workshop is targeted for laboratories considering a move to a probabilistic genotyping system for mixture interpretation or for individuals in the legal community wanting to learn more about this approach compared to the current methods of interpretation. This workshop will begin with a general review of probability, provide an introduction of the LR, and examine the limits of CPI, the modified Random Match Probability (RMP), and the binary LR. This workshop will work specific examples by hand, so attendees are encouraged to bring a calculator or have a calculator app on their smartphone. Finally, attendees will examine two approaches to probabilistic interpretation: the discrete (semi-continuous) and the fully continuous methods of interpretation.

DNA Mixture Interpretation, Likelihood Ratio, Probabilistic Genotyping

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