B139 Testing, Comparing, and Validating Traditional and Emerging Number Of Contributors (NOC) Systems for Forensic DNA Purposes

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Learning Overview: After attending this presentation, attendees will better understand the *A* Posteriori Probability distribution on n (APP(*n*)) and become aware of methods by which to validate and benchmark NOC systems.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by summarizing the results acquired from a developmental validation of a method that estimates the APP(*n*) and by demonstrating that it significantly outperforms the allele counting method and an Artificial Neural Network (ANN).

Forensic DNA signal is notoriously challenging to interpret and requires the implementation of computational tools that support its interpretation. While data from high-copy, low-contributor samples result in electropherogram signal that imparts informative and unambiguous weights of evidence, electropherogram signal from forensic stains are often garnered from low-copy, high-contributor-number samples that are often obfuscated by allele sharing, allele drop-out, stutter, and noise peaks. Since forensic DNA profiles are often too complicated to quantitatively assess by manual methods, continuous, probabilistic frameworks that draw inferences on the NOC and compute the Likelihood Ratio (LR) given the prosecution's and defense's hypotheses have been developed.

This presentation summarizes the validation results acquired from the NOCIt inference platform, which determines an *a* posterior probability distribution on the number of contributors given an electropherogram (APP(*n*)). NOCIt is a continuous inference system that incorporates models of peak height (including degradation and differential degradation), forward and reverse stutter, noise, and allelic drop-out while considering allele frequencies in a reference population. The system's performance was assessed by evaluating the APP(*n*)'s unimodality, sensitivity, fall-out (i.e., number of incorrect *n* included in downstream LR determinations), repeatability, and runtime for 815 publicly available PROVEDIt samples (lftdi.com), consisting of degraded, Ultraviolet (UV) -damaged, inhibited, differentially degraded, or uncompromised DNA mixture samples containing up to five contributors. This probabilistic system makes repeatable and reliable inferences about the NOCs and significantly outperforms traditional counting methods that render minNOC. For example, the proportion of samples for which the maximum APP(*n*) was at *n*= TrueNOC was 0.80, while the proportion of samples for which minNOC = TrueNOC was 0.56. The APP(*n*) was also compared to a fast and repeatable emerging technique—an ANN—which resulted in a wide distribution on *n* making the system highly sensitive but with high fall-out.

Lastly, unlike counting or ANNs, the APP(*n*) can be used in conjunction with a downstream Likelihood Ratio (LR) inference system that employs the same probabilistic model, allowing for a full evaluation across multiple contributor numbers. This presentation will, therefore, illustrate the power of modern probabilistic systems to report a reasonable and contiguous range of *n* that explains the evidence, while introducing the automated features designed to ease burdens associated with artifact filtering.

Forensic DNA, Number of Contributors, Validation

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