COMPARISON OF THREE CALCULATORS FOR COMPLEX LOW LEVEL MIXTURES

Mark Powell, Rebecca Schultheiss Mikulasovich, Katelyn Weymouth, Roger Kahn, Harris County Institute of Forensic Sciences

Frequently, forensic DNA test results produce partial, complex mixtures which, depending on a lab's approach, may be reported as inconclusive. When an association is made between the evidence DNA profile and a reference sample, the reported statistics generally discard much of the available data or ignore loci with exclusionary information based on an analyst's subjective interpretation of drop-out. Furthermore, inclusion/exclusion determinations are made using methodologies more suited to single source or simple mixtures.
More sophisticated approaches to mixture interpretation are available although their use is not yet widespread. We compared three software systems designed to aid in the interpretation and comparison of complex DNA mixtures, TrueAllele, Forensim and LabRetreiver, using a sample set comprised of seven reference samples and six complex mixture samples. These tools increase the available information from complex mixtures, differing somewhat in their approaches.

This presentation will provide an overview of each of the calculators, including the models on which they are based. The results of each sample and reference comparison will be presented, highlighting similarities and differences between the programs. Ease of use, understanding and presentation will be compared and a path to implementation will be proposed including system work flow, component of validation and analyst training regimes.