B28   A New Expert Systems Software Package for Rapid STR Data Analysis

Curtis D. Knox, BS, Kimberly Huston, BS, and Joseph Bessetti, MS, Promega, 2800 Woods Hollow Road, Madison, WI 53711*

After attending this presentation, attendees will have information regarding a newly released expert systems software package, including detailed information on the unique features offered by this software.

This presentation will impact the forensic community and/or humanity by highlighting a new tool for the DNA laboratories.

The goal of this presentation is to describe a newly released expert systems software package, including detailed information on the unique features offered by this software.

With the advent of automation and other solutions to reduce backlogs in sample processing from extraction to amplification and typing, data review has now become a bottleneck that laboratories need to address. Software-directed allele calls do not address the actual quality of the data; therefore, at least a short manual review of the data for each sample is nec- essary. An expert systems software package not only provides a second set of independent allele calls, but also gives the analyst the confidence to not examine sample data that the software has judged to be of high quality. This allows analysts to more efficiently spend their time concentrating on "problem" samples.

In addition to evaluating data for quality, there are other review func- tions that are time consuming or difficult to perform. Mixture analysis is labor intensive, and potential bias is a concern of both the DNA analyst and the attorney. A software package that has the ability to perform two-person mixture deconvolution in an unbiased, efficient fashion will free up ana- lysts' time and will provide a validated method for laboratories to rely on in court.

Sample-to-sample contamination is also of considerable concern to DNA typing laboratories, especially in light of advancements in automation that utilize open-well plates for various steps of the typing process. Examining blank samples for the presence of types is an important step in this process, but this does not account for the possibility of minor DNA components being introduced into samples that already contain DNA. A software package capable of comparing every sample within a batch to every other sample in the batch will aid laboratories in checking for potential contamination events and provide a further level of analyst confi- dence when presenting data in court.

The FSS-i3™ ("i-cubed") expert systems software consists of three functional components integrated into one package. The first component, "i-STRess," provides confirmation of previous allele calls as well as an extensive analysis of the quality of the data. The second component, "i-STReam," performs the mixture analysis, and the third component, "i-ntegrity," performs the within-batch contamination check. The software allows the user to optimize a large number of settings to best suit the laboratory's unique DNA interpretation protocols.

Given the need for data tracking and validation of any new software that is implemented in a forensic laboratory, strategies for performing the validation and automatically generating audit trails will be discussed in this presentation. Functionality of the software, basic optimization procedures for the individual user, and potential workflow enhancements that a labo- ratory may realize upon adoption of the software will also be presented.

Expert Systems, STR Data Analysis, DNA Mixture Analysis