A79 New York State Police Validation of a Statistical Tool for Genotype Inference and Match That Solves Casework Mixture Problems

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After attending this presentation, attendees will have a better understanding of how expert system software for forensic genetic identity testing laboratories can facilitate analytical workflow by automating data interpretation and eliminating case file technical review bottlenecks while, at the same time, reducing examiner bias, introducing greater standardization, and preserving more identification information.

This presentation will impact the forensic science community by introducing them to the objectivity, time savings, and accuracy an expert software system for forensic DNA data interpretation can lend to their lab.

In today's forensic laboratory, a greater range of crime classifications are being considered for DNA analysis (i.e. property crimes) and ever more challenging evidence items are being submitted (i.e., low copy number). Many labs have responded to this increase in submissions by introducing automation into their workflow. The resultant increase in analytical capacity, in turn, has created bottlenecks at the data interpretation and case file technical review steps. To resolve these bottlenecks, the New York State Police Forensic Investigation Center has undertaken to test whether expert system A is capable of unattended STR DNA data review and interpretation.

In this validation study, re-analysis was made on forty-one adjudicated cases previously analyzed by qualified DNA analysts at the Forensic Investigation Center. To span the range of interpretation challenges commonly encountered in forensic casework, these 41 cases were distributed relatively equally between sexual assaults containing victim and suspect reference samples along with various evidence swabs; and more complex multiple-victim homicides involving upwards of twenty evidence items. A broad spectrum of samples commonly submitted as evidence ranging from vaginal swabs, anal swabs, oral swabs, penile swabs, dried secretions, blood stains, and semen stains; to weapons, cigarette butts, condoms, human hair, bite marks, and fingernail scrapings were included in the study (368 items in total).

The original data files generated by the NYSP were uploaded to expert system A, analyzed, and the data was then returned to the authors for retroactive comparison to the data gleaned from the corresponding case reports issued by the NYSP. Allele concordance was analyzed for all 368 items of evidence, monitored expert system A's ability to deconvolute mixtures across a range of mixing weights and complexities, evaluated the mixing weight percentages determined by expert system A, and compared the statistical weight obtained by traditional means (NYSP protocol) to those calculated by the software.

In this study, 4,958 alleles were first analyzed in 202 single-source profiles in forty one previously adjudicated cases, and found the genotypes inferred by the expert system to be in complete concordance. The results of deconvolution of a wide range of mixtures, whether in simple or complex cases, were in accord with those determined using standard validated procedures at the SP Crime lab. Without prior information concerning the STR profile of the suspect, the software effectively ascertained the profile of the perpetrator and, commonly, provided more profile information than the standard non-automated manual process. The software automatically provided likelihood ratios and, in every case examined, preserved more identification information as measured by comparison of match likelihood ratios.

The software conveniently utilizes STR DNA data accepted from in- house genetic analyzers, and, as intended, has demonstrated the potential to relieve bottlenecks due to increased automation. The interpretation of STR DNA data by expert system A offers enhanced objectivity through reduced examiner bias in forensic DNA casework. The software allows the genetic testing laboratory workflow to be designed so that there is no previous exposure of the reporting analyst(s) to the DNA profiles of a suspect or pool of suspects until the laboratory report is prepared. The software achieves greater resolution in deconvolution of mixture profiles than current standard practices. Most importantly, the software offers increased statistical strength.

Bottleneck, Mixture Deconvolution, Expert System

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