B75 Quantifying the Impact of Post-Validation Modifications to Forensic Statistical Tool (FST)

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Learning Overview: After attending this presentation, attendees will better understand the significance of seemingly minor algorithmic and source code modifications made to a probabilistic genotyping system in use for over seven years, the Forensic Statistical Tool (FST), developed by the New York City Office of the Chief Medical Examiner (OCME).

Impact on the Forensic Science Community: This presentation will impact the forensic science community by quantifying, characterizing, and discussing the impact of post-validation software modifications made to FST on likelihood ratios reported by the system. By examining over 400 samples used for validation (with comparisons to over 1,000 known non-contributors), these relevant communities will be better able to evaluate the impact of source code modifications on likelihood ratios in reported results.

FST was brought online for casework in April 2011, and has been used over in over 1,300 cases in about fifty jurisdictions. In April 2011, FST was brought offline for software maintenance, at which time its likelihood ratio algorithm and corresponding source code were modified. Rather than including all loci in all calculations, FST's post-modification version removes data for loci where frequencies of observed alleles across all replicate amplifications summed to ≥97% in any of FST's four reference populations.

Several factors (including the use of minimum allele frequencies, multiple amplifications, four reference populations, and the occurrence of drop-in) resulted in more than 23% of evaluated 2- and 3- person mixtures to have one or more loci removed from consideration after the source code was changed.

For reporting FST results in casework, the OCME utilizes a verbal equivalency scale for reporting. Categories of support for the prosecution or defense hypotheses include limited, moderate, strong, and very strong. This presentation will describe changes in verbal equivalency category for more than 100 Hp-true and 100,000 Hd-true analyses affected by locus-dropping behaviors.

Changes to the FST software are followed by "performance check" regression tests. In 2011, these checks compared pre- and post-modification likelihood ratios for twelve samples, two of which exhibited locus-dropping at one locus each. In 2013, these checks were expanded to include four additional samples, none of which exhibited locus-dropping behaviors. This presentation will describe changes to the likelihood ratios for known contributors to more than 100 mixtures where the locus-dropping behavior occurred.

Findings will be described as both general trends and breakdowns of trends by sample category, (e.g., number of contributors, amplification protocol, and template amount). To-date, no public study has been described for the modified FST algorithm or any comparison of pre- and post-modification versions of FST.

FST, Validation, Probabilistic Genotyping