A154 Using Simulation to Improve Understanding of Likelihood Ratio Results

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After attending this session, attendees will understand issues involved in presenting Likelihood Ratios (LRs) to non-scientists, such as judges and juries, and will see how simulation can be used to help explain the strength of an LR.

This presentation will impact the forensic science community as communication of results in court is an integral part of a DNA analyst's job. The topic should be of broad interest since many laboratories use LRs and wrestle with proper presentation of results in court.

An LR can be used to assign a statistical weight to a comparison between a DNA mixture obtained from an item of evidence and the DNA profile of a known individual, such as a suspect. The Office of Chief Medical Examiner (OCME) of New York City computes LRs using an in-house program, the Forensic Statistical Tool (FST), which models allelic drop-out and drop-in. This is the recommended approach for analysis of complex DNA mixtures by the DNA Commission of the International Society of Forensic Genetics.[1]

To help interpret LRs, a qualitative scale of "limited," "moderate," "strong," or "very strong" support for one hypothesis over the other is used. Even with these qualifiers, it may be difficult for jurors to understand the strength of a result. In addition, the weight may vary depending on the model used, for example two-person versus three-person models, or with or without including a known contributor in the model. One piece of information that may be helpful in understanding the strength of a result would be the probability of obtaining such a result if the suspect is not a contributor to the mixture. In other words, what is the chance that a randomly chosen non-contributor would generate an LR at least as high as the one obtained for the suspect? Simulation and testing of non-contributor profiles can be used to estimate such a probability for a given result with a specific mixture. Others have explored this idea, using simulated profiles to show the distance between a suspect-generated LR and a set of non-contributor LRs.[2]

Estimating the probability of obtaining an LR at least as high as the suspect's requires that one or more simulated non-contributor LRs meet or exceed the LR computed for the suspect. With a low suspect LR, analysis of several thousand non-contributors may be sufficient. But, with a high suspect LR, several million non-contributors may be required in order to find any with LRs in the range of that of the suspect. While millions of non-contributor profiles can be simulated in seconds, the time required to perform LR analysis of those profiles may be a limiting factor. As a solution, many non-contributor profiles can be simulated and those with the fewest alleles missing from the casework mixture can be identified. These represent the non-contributors most likely to generate high LRs.

For example, with one two-person mock casework sample analyzed, one "suspect" generated an LR of 8.5, which would constitute limited support for the suspect, rather than an unknown, unrelated person, contributing to the mixture. Simulation and testing of 10,000 non-contributors yielded two profiles that generated LRs of 8.5 or more. Thus, the probability of obtaining an LR of at least 8.5 for this mixture is about one in 5,000. Using the same sample, another "suspect" generated an LR of 750, which would be classified as strong support for the scenario involving the suspect, over the scenario without the suspect. One million non-contributors were simulated and the top ten thousand were identified, five of which generated LRs greater than 750. Thus, the estimated probability of obtaining an LR of at least 750 for this mixture is estimated at one in 200,000.

The relationship between the number of missing alleles and the LR can be used to determine the appropriate cutoff value such that no high LRs are missed, but the number of profiles to be analyzed is within the range of feasibility. Regression analysis to determine the appropriate cutoff value for the number of missing alleles will be discussed. The cutoff may depend on the number of contributors to the sample and the probability of drop-out used by the LR program. Non-contributor results from analysis of a variety of mock casework mixtures will be presented and ideas for communication of results in court will be discussed.

References:

[1]Gill P, Gusmao L, Haned H, Mayr WR, Morling N, Parson W, Prieto L, Prinz M, Schneider H, Schneider PM, Weir BS. DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods. Forensic Science Int: Genet,

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1. Gill P, Haned H. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci Int: Genet, 2013:7:251-263.

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