LIKELIHOOD RATIOS WITH DIFFERENT NUMBERS OF CONTRIBUTORS

Berdine, Susan G., Denver Police Department Crime Laboratory

Likelihood ratio (LR) calculations for DNA evidence require an assumed number of contributors for each proposition. Estimating the number of contributors to a DNA profile is typically done by maximum allele count or maximum likelihood estimation before comparison to any persons of interest (POI). After comparison to a POI, the evidence profile may support inclusion of the POI only if an additional contributor is assumed. This presents a challenging situation in determining how many contributors to assume in the LR. The number of contributors can be the same or different under the numerator and denominator propositions. The International Society of Forensic Genetics (ISFG, 2006) stated: There is a common misconception that the numbers of contributors under H_p and H_d should be the same. There is no requirement for this… The probability of the evidence under H_p is the province of the prosecution and the probability of the evidence under H_d is the province of the defence. The prosecution and defence both seek to maximise their respective probabilities of the evidence profile.

This presentation provides examples from DNA validation and casework samples where the number of contributors differs under the two propositions in the LR, typically with n contributors in the denominator proposition and n+1 contributors in the numerator proposition. We explore the impact on the resulting LR, which decreases by several orders of magnitude for some profiles when the number of contributors is different. This approach of varying the number of contributors under each proposition has significant implications for using LRs in DNA casework.