



F10 The Elusive Holy Grail of Simple Yet Adequate DNA Mixture Evaluation Method, or How to Frame a Suspect?

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Learning Overview: After attending this presentation, attendees will appreciate that highly prosecution-biased DNA mixture analysis is still thriving and dangerous.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by alerting it the existence of an ongoing subversion of justice via misrepresentation in the court of DNA evidence, leading some suspects to be unfairly convicted based on inadequate evidence, likely including some who are factually innocent.

For 25 years, the forensic community has sought a simple but adequate method for evaluating mixtures. Some folks promoted Combined Probability of Inclusion—the idea of distilling the DNA data down to an unfortunately elusive concept of “inclusion” or not—as filling the bill. For several reasons, it was never good; finally the general understanding of the necessity of dealing with dropout turned the tide against it. The essence of “dealing with dropout” is being able to calculate the probability of some suspect allele to be missing from the mixture data even while hypothesizing that the suspect did contribute.

At present, the general consensus is to confront dropout head-on with a “continuous” approach modeling the phenomenon of peak height stochastic uncertainty. This presentation argues that a continuous model can be simple and elegant in concept, but recognizes that it is tedious to compute. It needs a computer. Hence the less comprehensive “semi-continuous” approach has its adherents and perhaps provides a useful compromise dropout capability.

At a recent murder trial, a Dr. X, expert witness for the prosecution, presented a surprising and unfamiliar mixture calculation method that purports to be the long-sought holy grail of adequate but simple. Dr. X deems a mixture locus to be “informative” if all expected alleles, especially those of the suspect, are observed. Simple binary Likelihood Ratios (LRs) are computed and accumulated across the “informative” loci. The remaining loci are discarded (conveniently evading the difficulty of a dropout calculation); Dr. X testified that omitting them is to omit further evidence against the suspect, hence omitting them favors the suspect.

That is, of course, well-known to be too good to be true. The truth is the opposite. The so-called “non-informative” loci are where the strong exculpatory evidence for an innocent suspect comes from. (Not seeing a suspect’s bootprints on the burgled property is evidence he wasn’t there.) Omitting them is cherry-picking that frames the suspect. Dr. X’s computation will *never* produce a suspect-benefitting $LR < 1$. It can only deliver a number that, to a small or large extent, hurts any suspect.

This is notable because, per Dr. X, Dr. X has testified upward of 1,000 times. If 50 out of each 100 cases rested significantly on the DNA evidence and had less than 100% of the suspect’s profile recorded in the mixture, then those 50 cases need re-evaluation. A handful will be actually innocent. It is likely that numerous innocent people are in prison because courts were gulled by this enticing but anti-mathematical method

DNA, Injustice, Frame