B38   A Two-Trace Problem in Probabilistic Genotyping: Should the Evidence Be Combined or Not?

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Learning Overview: After attending this presentation, attendees will develop an understanding of the trade-offs between reporting comparisons of a person of interest to multiple evidential profiles separately or jointly.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by raising awareness about the benefits and pitfalls of combining DNA evidence.

Casework laboratories routinely perform comparisons of persons of interests to DNA profiles obtained from crime scenes using probabilistic genotyping. When two evidential profiles are obtained from a single crime scene, it is standing practice in most laboratories to report a likelihood ratio statistic for each evidential sample measuring the degree of support for the person of interest contributing DNA to that sample. Although each of the two statistics can be used to evaluate support for contribution to one sample at a time, the two statistics do not necessarily give enough information to evaluate whether or not the Person Of Interest (POI) contributed to both samples. In the simplest case, we can consider two evidence samples that yield a complete profile that match each other and a person of interest. Considering this evidence jointly has been referred to as the two-trace problem, and evaluation in this framework has previously been explored.[1,2] A more complex extension is to consider partial or mixed DNA profiles, and the potential for a POI to have donated to a component of neither, one, or both profiles. These propositions can be investigated using a statistic that considers the two evidential profiles jointly.[3] Depending on case circumstances, the joint-contribution proposition may or may not be a more relevant proposition for a finder of fact. This two-trace problem is explored in this presentation using an example illustrating the trade-offs involved in deciding between reporting separate statistics, a joint statistic, or both.

Assume that two traces are obtained from a crime scene and that it is not certain whether or not these two traces originate from the same source. Both traces are only weakly informative of the genotype of the donor(s) because of low quantity or quality of the DNA. A suspect is apprehended and a reference profile is compared to each of the two traces. Because the evidential traces are of low quality, the two likelihood ratios are only weakly informative. Although it is possible to compute a statistic for joint contribution to both samples, the suspect does not have to concede in court that the two traces are of common origin. Moreover, it may be anti-conservative toward a defendant to wrongly assume a common origin. This suggests that presenting statistics combining evidence in court can be problematic. On the other hand, it is shown that if a common origin is correctly assumed, the joint statistic is more powerful, meaning that unrelated persons can be excluded more strongly. Specifically, it is shown that it is possible for the suspect to be categorically excluded as a donor to both samples while the two separate statistics are inclusionary. This means that it is not conservative either to only present the individual statistics, nor would it be conservative to present a minimum of the individual statistics. In conclusion, it depends on case circumstances as to whether or not the evidence should be combined.

Reference(s):

1.   I.W. Evett. On meaningful questions: A two-trace transfer problem. *Journal of the Forensic Science Society* 27 (1987) 375-381. https://doi.org/10.1016/S0015-7368(87)72785-6.
2.   Gittelson S., Biedermann A., Bozza S., Taroni F. Modeling the forensic two-trace problem with Bayesian networks. *Artificial Intelligence and the Law* 21(2) (2013) 221-252. https://doi.org/10.1007/s10506-012-9136-5.
3.   Taylor D. and Kruijver M. Combining evidence across multiple mixed DNA profiles for improved resolution of a donor when a common contributor can be assumed. *Forensic Science International: Genetics* 49 (2020), https://doi.org/10.1016/j.fsigen.2020.102375.

Combining Evidence, Probabilistic Genotyping, DNA Mixtures

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