A111 The Mythical "Exclusion" Method for Analyzing DNA Mixtures — Does it Make Any Sense at All?

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After attending this presentation, attendees will be properly sceptical of the popular "exclusion" paradigm for analyzing DNA mixtures because the usual claims in its favor do not survive careful analysis.

This presentation will impact the forensic science community by warning attendees of the weakness of one popular approach for the specific question of DNA mixture analysis. More generally a collection of disconnected plausible-seeming intuitions are not a sufficient basis for any analytic method. Instead there should be a clearly stated foundation and chain of reasoning to support it.

Two different approaches to DNA mixture analysis and computation are commonly called the "exclusion" and "likelihood ratio" methods. These are fundamentally different paradigms. Though the so-called likelihood ratio method is agreed to be more flexible and theoretically grounded, the exclusion method is often touted as adequate in principle, and preferable for a variety of practical reasons including ease of use and understanding. But critical consideration shows that none of the claimed advantages of the exclusion method hold much water.

1. The claim that it requires **no assumption about number of** three or four obvious and prominent alleles at each locus. A suspect who has other alleles can be excluded of being a conspicuous contributor, but not of being a negligible contributor based on the DNA alone. The standard but unstated assumption that only "conspicuous" contributions are probative is valid if only two contributors can be assumed, but is not valid absent any such adjunct assumption.

2. Similarly the supposed **ease of understanding** by judge or jury is really an illusion; the method is deceptively easy with emphasis on deception. The ease in apparent understanding rests on overlooking the ambiguous and uncertain nature of DNA evidence, especially mixtures. The basis of the "exclusion" method is a negative evidence paradigm, that the evidence against a real or hypothetical suspect is the lack of alleles *not* present in the unknown mixture. In practice, for the hopelessly elusive concept of "not present" the analysis substitutes a criterion such as "not present above 100 RFU" which is measurable but not logically probative. The audience who accepts the substitution has been hoodwinked.

3. **Ease of use** is claimed to be an advantage particularly for complicated mixture profiles, those with many peaks of varying heights. The truth is the exact opposite. The exclusion method is completely invalid for complicated mixtures. The only recourse in such cases is a proper likelihood ratio analysis however difficult that may be. It is only the clear and straightforward cases that might permit logical application of the exclusion method. But those cases are easy by any method.

4. The common belief that the **exclusion method is conservative** is usually true, but not for the expected reason. Calculating examples with moderate peak-height variation shows that against innocent but included suspects, it would usually unfairly exaggerate the strength of the evidence. Since innocent suspects, especially ones who are not excluded, are somewhat rare, this circumstance is unusual. Still, it would not sound good for a supposedly neutral DNA expert to admit in testimony to using a method whose validity depends on the suspect being guilty.

All of the above problems are manifestations of one basic error: the method rests on the false premise that alleles are "in" a mixture when a donor "contributes" them and that we can tell which alleles are "present" and which are not. Of course allele detection is really not so binary. No amount of ad hoc finagling about dropout repairs the fundamental shortcoming that those words in quotes are undefined. Without clear and explicit definitions as a foundation, any analytic method can't be more than guesswork. Certainly no one has laid out an explicit and rigorous chain of reasoning from first principles to support the exclusion method. It is at best guesswork.

DNA Mixture, Exclusion, Logical Foundation