A164 Combining DNA Evidence for Greater Match Information

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Most fields of scientific enquiry routinely combine data from multiple experiments. These experiments can be repetitions drawn from one item, or involve different items entirely. The motivation is to elicit maximal information from an experimental design. The statistical mechanism is the joint likelihood function.

DNA evidence is often challenging to interpret. When a DNA sample has low quantities, is degraded, or contains several individuals mixed together, no single allele pair may be able to explain the STR data. Multiple allele pair possibilities then become feasible, with an associated loss of identification information. It can then become important to use all the available experiment data in order to restore information.

In forensic DNA science, human data interpretation is usually performed on data derived from just one item. This practice is a natural consequence of "thresholds" – applying a preset peak height level to quantitative peak height data in order to simplify human data interpretation, which creates artificial all-or-none qualitative allele possibilities. However, the resulting genetic profiles cannot be mathematically combined. Some groups may heuristically combine profiles after data interpretation to form a "consensus" profile, but this practice has little statistical justification.

Quantitative computer interpretation of continuous electrophoretic STR data signals, however, has no such artificial limitation. It is therefore natural to mathematically preserve identification information by inferring a genotype using a joint likelihood function that examines all the independent data simultaneously.[1]

A likelihood function mathematically quantifies how well alternative hypotheses explain a fixed data result. A joint likelihood function assesses these hypotheses on multiple data items simultaneously. Typically, the data are drawn from independent experiments. Therefore, the joint likelihood simply multiplies together the likelihood numbers from separate experiments, jointly conditioned on a common explanatory hypothesis.

This talk describes the joint interpretation of DNA evidence. It is shown how likelihood functions can be used to rigorously explain DNA evidence, and how joint likelihood functions can combine evidence. Results that show how the number of assumed contributors affects the inferred result, and why appropriately constructed likelihood ratios (LR) do not overstate the inferred DNA match information will be presented. These concepts on representative DNA mixture criminal cases and experiments will be illustrated.

In particular, using a joint likelihood function on DNA mixtures,
we show:

- How a joint examination of the data signals from 10% and 50% mixtures can infer a highly informative genotype, with a combined LR match statistic a million times greater than either separate analysis;
- A criminal case where none of the three data signals from a low- template three person mixture was informative in isolation, but when jointly examined they together produced a DNA match statistic LR over a million; and
- Strategies for effectively combining the data signals of differen mixture evidence (from one or more items) in a joint interpretation that retains more DNA identification information.

Forensic DNA is an information science that centers on inferring genotypes. More informative genotypes can lead to greater match information. By combining DNA evidence, as taught in this presentation, a practitioner can extract more information from their existing data, and make more accurate DNA identifications.

Reference:

[1.] Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. Journal of Forensic Sciences. 2011;56(November): in press.

Combining Evidence, DNA Mixture, Likelihood Ratio

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