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.

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 likelihoods from separate experiments, jointly conditioned on a particular explanatory hypothesis.

In forensic DNA science, human data interpretation is usually performed on data derived from only a single item. This practice is a consequence of thresholding quantitative peak height data into all-or-none qualitative allele possibilities, in order to simplify human review. Combining profiles after interpretation for "consensus" has little statistical foundation.

Quantitative computer interpretation, however, does not share these artificial limitations. It is therefore natural to mathematically preserve identification information by inferring a genotype using a joint likelihood function, examining all the independent data simultaneously.

This talk describes the joint interpretation of DNA evidence. We show how likelihood functions can be used to rigorously explain DNA evidence, and how joint likelihood functions can combine evidence. We present data that shows how the number of assumed contributors affects the inferred result, and why appropriately constructed likelihood ratios cannot overstate the inferred DNA match information. We illustrate these concepts on representative DNA mixture cases and experiments.