A126 Toward Professionalism in Forensic Mathematics

Charles H. Brenner, PhD, 6801 Thornhill Dr, Oakland, CA 94611-1336*

After attending this presentation, attendees will learn basic standards for writing a methodological paper for quantitative analysis of forensic evidence.

This presentation will impact the forensic science community by increasing skepticism for forensic DNA mathematical papers, most of which fall far short of common-sense minimal standards for logical reasoned exposition.

Attendees will learn from this presentation basic standards for writing a methodological paper for quantitative analysis of forensic evidence. They will consequently have a proper scepticism for forensic DNA (in particular) mathematical papers, most of which fall far short of commonsense minimal standards for logical reasoned exposition.

DNA identification is interesting in offering, more than any other forensic area, scope for explicit mathematical treatment. There are various mathematical problems in forensic genetics beginning with straightforward linking suspect to unknown DNA profile, adding difficulties and complications such as rare haplotypes, database search or mixed sample, and identification via kinship with its many attendant intricacies. They can most clearly and usefully be dealt with through a disciplined mathematical exposition which should be precise and logical — clear statement of the problem and of assumptions, deductive progression of ideas, and justification of assumptions.

Mathematics as a tool has several potential attractions and advantages. Because mathematical writing is explicit in definitions and assumptions, it can provide clear unambiguous communication. The reader should know what is being claimed. Mathematical exposition is logical and deductive. Ideally, the reader is led irresistibly along a linear deductive path. If not irresistibly, at least the exact point of resistance is manifest. Then the reader can say “I disagree with your premise” or can argue that step D doesn’t follow from step C; a productive discussion is then possible with a good chance for resolution of disagreement.

The paradigm should be: State the problem, formulate it mathematically, state premises (inevitably including a model, since this is applied mathematics), justify the premises (i.e., validate the model), derive the result. A paper which simply gives a recipe for calculation without any stated justification is professionally deficient. Yet papers meeting even these basic standards are almost non-existent.

SWGDAM instructions on rare haplotype matching don’t even state a problem but instead begin by proposing how to calculate a haplotype frequency.[1] The reader who realizes that (population) frequency is not (matching) probability and that the evidential problem concerns probability, is left slack-jawed at the post with nothing with which to disagree while the paper gallops off into (irrelevant) mentions of formulas and ideas lacking not only foundation but lacking any chain of reasoning.

In the 90s, the exclusion method for mixtures was simple: If a suspect is “included” then report RMNE, calculated per-locus as the squared sum of the allele frequencies for alleles observed above 100 RFU or so. No one actually wrote down the model but the formula is simple enough that it can be reverse-engineered to deduce what the model must be: The formula assumes that all alleles of a donor will be conspicuous (e.g., >100 RFU) and “included” means all of ones alleles are conspicuous in the mixture. Obviously, this is an absurd model. That it survived and was popular and accepted for years—perhaps still—proves the importance of explicitly writing down models and explicitly deriving and justifying the consequences. *With nothing written down, nothing wrong is written down and errors are less obvious.*

The recent appearance of refining the “exclusion” method by adding a second RFU threshold suggests that RMNE enthusiasts have woken up to the folly and unfairness of the original approach.[2,3] They have not, though, woken up to the importance of models, let alone to justifying their work. Several papers give no mathematical analysis at all; only recipes which, apparently, we are supposed to trust.

The point is not that the method fails. The point is that the adherents of a method have a positive responsibility to show why it works. They have not done a respectably professional scientific job if they don’t explain coherently. Otherwise the rest of us—reader, analyst in the laboratory, judge, and accused—ought to be suspicious of the validity of the method.

References:

1. SWGDAM Y-chromosome Short Tandem Repeat (Y-STR) Interpretation Guidelines. http://www.fbi.gov/.../fsc/oct2009/ standards/2009_01_standards01.htm/.
2. Budowle B, *et al*. Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework, J Forensic Sci 2009;54(4):810–21.
3. SWGDAM Interpretation Guidelines for Autosomal STR Typing §3.5. Interpretation of DNA Typing Results for Mixed Samples. http://www.fbi.gov/.../codis/swgdam-interpretation-guidelines.

Standards, Forensic Mathematics, Professionalism

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