guilt, although it would be very strong evidence. If there were identical twins involved, or even siblings, the force of evidence might be reduced. Matching of band weights for several probes does not imply that the entire DNA system is the same. In fact, if only a few probes with few alleles matched, the evidence could be far from overwhelming, even in those cases where there is no error in measurement.

It should be remarked that if Lifecode type bins are used in a nonexclusionary fashion, apparent matching on almost all of the highly polymorphic probes could be strong evidence, even if there were apparent failure to match on one or two probes. The strength of the evidence would depend on the bin sizes and the relative magnitude of the errors of measurement.

Conditioning. One advantage of Bayesian analysis over NP analysis is that, in the former, we can examine the evidence as it arrives. A partial reply involves the use of conditioning. The force of classical inference is sometimes strengthened by using conditioning appropriately. That could be done here, too. For example, once we had measurements on Ponce's blood, we could use those data to help select what constitute effective probes for the comparison.

Comment: Uncertainty in DNA Profile Evidence

D. H. Kaye

Donald Berry's article on inferring identity from DNA profiles presents a method for "direct calculation of the probability that the suspect is guilty" and "the probability that an alleged father of a child is the true father." The method is Bayesian. Berry computes the posterior odds of guilt as the product of the prior odds (assessed on the basis of all the evidence apart from the electrophoretic measurements) and a likelihood ratio for the DNA results. The specific likelihood ratio (R) that he skillfully derives for single-locus restriction fragment length polymorphisms accounts for random measurement error in electrophoresis and for sampling error in a laboratory's data base on the distribution of fragment lengths in the population.

This comment examines, from the perspective of a lawyer, two connected issues: the forensic importance of quantifying measurement and sampling error and the desirability of combining likelihoods and priors for jurors or judges. I try to place Berry's treatment of these matters in the context of the emerging case law on DNA profiling, and I speculate about the advisability of bringing Bayes to the bar. Proceeding on the premise that Berry's mathematics is impeccable, I conclude that if "To bin or not to bin?" is the question, then Berry has the answer.

1. LABORATORY MEASUREMENT ERROR

Berry's analysis handles normally distributed (and log normal) laboratory errors in measuring the position of a perceived band, and he notes that a more complex analysis could handle other continuous error distributions. Yet, much of the criticism of forensic DNA work emphasizes other threats, such as contamination and degradation of samples. Thompson and Ford (1991, page 138), for example, report that missing bands, extra bands and systematically shifted bands are "quite common in the forensic casework."

These types of experimental error have received considerable judicial attention. Virtually all courts in the United States to face the issue have held that DNA findings of identity are potentially admissible, but the degree of experimental rigor actually required for admission varies with the understanding of the court and the persuasiveness of the experts. *People v. Castro* (1989) is remarkable for the extent of the judicial inquiry into

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