convey some sense of the power of the laboratory's evidence.

Second, I worry that forcing jurors to articulate prior odds conditioned on the non-DNA evidence and to multiply this prior by a likelihood ratio may omit (and possibly divert attention from) major uncertainties in the experimental evidence. As indicated in Sections 1 and 2, the likelihood ratio R does not account for the risks of missing bands, extra bands, population misspecification and substructure.

One can respond, as I suspect Berry might, that all conceivable sources of error need not be reflected in a single figure for the posterior odds. One might treat Berry's analysis as conditioned on the absence of experimental embarassments, at least where the laboratory has observed rigorous protocols (compare OTA, 1990). Where it is not clear whether a suspect is homozygous or a fragment has gone undetected, one can compute distinct values of R under each assumption—as in Berry's discussion of *Castro*. Similarly, one can perform multiple computations of R and hence $P(G \mid X)$ for different racial categories.

The final result, however, is no longer a simple posterior probability for guilt or even a single table of posteriors and priors. It is a set of competing numbers or tables—accompanied, quite possibly, by some nagging doubts that must be left out of the equations for want of adequate data or analytic tools. If the residual uncertainty is substantial, then the jury must attend to it in some intuitive fashion anyway. It cannot take $P(G \mid X)$ at face value if the defendant (or the prosecution in a case in which the defendant offers an exculpatory DNA profile) raises serious questions about population structure or other uncertainties not included in sensitivity analysis of R and $P(G)$. And if this situation does materialize, one is left too wonder once again whether the expected payoff from the Bayesian format is worth the demands it places on the experts, the parties and the court.

4. CONCLUSION

As a lawyer, I see in Berry's article a cogent and powerful indictment of the matching and binning reasoning now used in single-locus DNA profiling. Berry builds an impressive case for using likelihoods that (a) make better use of the information in the test results and the population data and that (b) handle more of the uncertainties now present in DNA evidence.

I am less enamored of the strong Bayesian demand that jurors should quantify their prior probabilities and combine them with likelihood ratios based on certain simplifying assumptions to return a verdict of guilt or innocence. Like the courts, however, I am not prepared to say that there is no room for some form of a Bayesian presentation in a criminal trial. Considering the difficulties that many courts, attorneys and jurors face in assessing quantitative evidence, the efforts of Berry and other statisticians (e.g., Kadane, 1990; Fienberg and Kadane, 1983) to develop suitable Bayesian analyses for forensic applications are a most welcome development.

Comment

Ian Evett

Professor Berry's analysis of DNA profiling is elegant and penetrating. I will not discuss the detail of his treatment but will concentrate on issues touched on by the other discussants that are relevant to the work of the forensic scientist.

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First, should the forensic scientist adopt a Bayesian view of evidence evaluation? It has been the convention, from the first glimmerings of the science, to view evidence from a frequentist perspective. Consider a simple case where the evidence consists solely of a blood stain at a crime scene and there is a single suspect who gives a sample of blood. Assuming a system of discrete alleles with no measurement error then, if the suspect's blood and the scene blood are the same type—say X1—the scientist will refer to a data collection of some sort and, as well as reporting a

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