

# Comment

Donald A. Berry

Professor Roeder has presented the issues clearly, intelligently and in a balanced fashion. I agree with nearly everything she says. I will comment on some issues that she considers and address some she does not.

## MATCH/BINNING VERSUS CONTINUOUS MEASUREMENT AND LIKELIHOOD RATIOS

I am happy to see Professor Roeder argue in favor of likelihood ratios tailored to the observed error distributions over a process initiated by declaring whether the suspect and crime samples match. I will say little about this issue here because, as she indicates, I have written about it elsewhere. The match/binning processes used by the FBI and U.S. forensic laboratories are consistent with the state of statistical knowledge before the time of Daniel Bernoulli. They are archaic and serve to handicap a fine technology. Some cases that might be won are lost, and otherwise good cases are not brought to court. The total number of such cases is small, but a few is a few too many. Fortunately, the technology is usually able to survive the primitive statistical methods.

This circumstance might have been avoided had statisticians been consulted during the development of DNA fingerprinting. There are now some excellent statisticians (such as Kathryn Roeder and Bruce Weir in the United States and Ian Evett in the United Kingdom) involved in the process, but momentum is difficult to interrupt (and statisticians are still not allowed in the inner sanctum—as Professor Roeder indicates, the 1992 NRC panel had no statisticians among its members). Instead of trying to patch up its inadequacies, the DNA fingerprinting community should start over from scratch, and this time with statisticians participating in formulating the statistics.

A further point about match/binning: I conclude from discussions with Bruce Budowle of the FBI that some match/binners still do not understand a very important tenet of inference. The matching proportion is a likelihood ratio. As such it can be used as

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a measure of evidence; but the definition of match that is applied to a suspect's profile must be applied as well to profiles in the database to determine a matching proportion. Otherwise the results are not interpretable. The FBI apparently uses different criteria to decide when a suspect matches than they use in calculating match proportions. I do not know whether they are more conservative in the latter than in the former: while they are quite open about the latter, I have never been able to pin them down concerning the former.

## INDEPENDENCE OF ALLELES

The controversy concerning independence of alleles has the wrong focus, as Professor Roeder suggests. The issue should not be whether alleles are independent, but what difference it makes to the conclusions. Usually, differences are minor. There may be correlations among the loci most commonly used, but none I have seen matter much. Some people would have us throw the baby out with the bath water.

In the previous paragraph I am not counting correlations among measurement errors (band shifting). These are very important. They are easy to handle using a continuous measurement, likelihood ratio approach, but not so easy using match/binning.

Assuming independence can make for extremely small match probabilities (or likelihood ratios). Tiny probabilities make me uneasy, as I will indicate below.

## CONVEYING MATCH PROBABILITIES OR LIKELIHOOD RATIOS

According to an article in the *Minneapolis Star Tribune* (December 20, 1991): "If the two samples give the same results when tested, advocates of the [DNA fingerprinting] method say, it means the odds are overwhelming that one person was the source of both samples." This is reversing the conditional. It may be what "advocates of the method say," but it is most assuredly not what "it means." Statisticians have no trouble recognizing this, but almost every nonstatistician I have met has trouble understanding the difference between this and a correct state-