als to discussion of the frequency of the matching genotypes, the methods for computing that frequency and the controversy surrounding those methods may reinforce the powerfully prejudicial suggestion that false positives are a minor issue and that the frequency of the matching genotypes is the issue on which the value of DNA evidence will turn. In fact, where false positives are possible, the frequency of matching genotypes may have no relationship to the likelihood ratio that describes the value of the DNA evidence for proving two samples have a common source. Hence, it is at best an unhelpful statistic and at worse seriously misleading. Whether it should even be presented to juries is a question that I hope Kathryn Roeder, and her readers, will ponder.

Comment

B. S. Weir

Roeder has provided a useful review of the statistical issues involved in studies of human identification. She makes the distinction between objections to certain assumptions that might be raised in theory and the numerical consequences of those assumptions not being completely true in practice. A related issue is that of statisticians not taking into account all the relevant biological factors, and Roeder pointed to work of Geisser and Johnson (1992, 1993) in that context.

As Roeder explained, Geisser and Johnson explored the consequences of discretizing VNTR fragment lengths into a set of quantile bins, rather than the bins defined by viral fragment lengths as used by the FBI. Both binning strategies are adhoc, but the quantile bins lead to simpler analyses since each bin and each pair of bins is equally frequent. Roeder pointed out that the analyses of Geisser and Johnson have little relevance in the forensic debate since the problem of the unknown cause for single bands was ignored. The same point was made by Weir (1993), who also demonstrated that different numbers of bins, let alone different binning strategies, can lead to different conclusions regarding the independence of pairs of fragments in samples. The phenomenon has been well-documented in the population genetics literature.

Roeder herself might have referred to previous literature in her discussion of hierarchical Bayesian methods that invoke the Dirichlet distribution. Other authors have sought to use this distribution in the population genetics context (Rothman, Sing and Templeton, 1974; Spielman, Neel and Li, 1977), and there may be instances where it provides useful approximations. The current problem is to determine the conditional probability of a genotype, or VNTR profile, when that genotype has already been observed (for the perpetrator of a crime). Such conditional probabilities require the joint probabilities of *genotypes*, whereas Roeder in her equation (8) works with the joint probabilities of *alleles*. The joint genotypic frequencies require information about the relations between four alleles (two per genotype) rather than just two. Nichols and Balding (1991), in the paper that presented Roeder's equations (18), also ignored the relations between alleles considered three or four at a time. It is possible to approximate the necessary four-gene measures of identity with the two-gene measure called θ_s by Roeder, and θ or F_{ST} by others (Weir, 1994).

A deeper question concerns estimation procedures for θ. This quantity provides the correlation for alleles within the same subpopulation, and consequently it provides the component of variance between subpopulations in an analysis-of-variance setting. Evidently such a parameter cannot be estimated from data in one subpopulation (e.g., Weir and Cockerham, 1984), or even from data from the whole population without knowledge of subpopulation structure. Apparently, Roeder et al. (1993) overcome this logical barrier in arriving at estimates by assuming a distribution for allele frequencies, in contrast to the approach of Cockerham (1969) that regards the true allele frequencies as unknown.

The problem with taking genotypic frequencies to have a Dirichlet distribution is that results contrary to genetic expectations can result. Jiang and Cockerham (1987) simulated populations subject to genetic drift and compared a moment estimator of θ derived from an analysis-of-variance viewpoint with

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