the "RST" estimator that Rothman, Sing and Templeton (1974) derived from a Dirichlet model. The moment estimator was essentially unbiased for their parameter values whereas the RST estimator had about a 50% bias. The RST estimator had a standard deviation about half that of the moment estimator. Jiang and Cockerham concluded that the Dirichlet model performed poorly for the genetic drift process, and were concerned that the model may not be broadly useful.

Notwithstanding these comments, the paper by Roeder is a welcome addition to the literature. It illustrates the role statisticians have to play in addressing societal issues.

Rejoinder

Kathryn Roeder

I would like to thank the discussants for their lively remarks, even those wide of the mark. Because of the subject of my review, I am not surprised by some of the emotional arguments put forth, although they seem out of place in *Statistical Science*. As Professor Lempert comments, "there is a kind of passion to each side, which sometimes seems, however politely, to amount to questioning the bona fides of the other." Before discussing the commentators' remarks in detail, I will outline their points.

The discussants broach several interesting issues that are far afield from the points covered in my review. The statistical issues in human population genetics, the core of my review, have been the focus of controversy in the courts and the scientific literature for the last few years. Professors Berry, Lempert and Weir agree with me that the criticisms leveled at the standard paradigm for estimating DNA profile probabilities, while sometimes sound in theory, have a negligible impact on the calculations in practice. Professors Balding, Donnelly and Nichols (BDN) and Professor Lewontin continue to question some population genetic assumptions upon which the probability calculations are based. Professor Sudbury stands alone in questioning the need for the paradigm. The adequacy of the genetic model and the importance of the choice of reference population are elaborated in Sections 1 and 4 of my rejoinder.

Several commentators raise concerns about laboratory error, something I did not discuss in depth in my original paper. They worry that samples will be mixed up in the laboratory, resulting in the suspect's sample being compared with itself, rather than with the crime sample. Another concern they raise is cross-contamination, which could also lead to an erroneous match. Professor Lewontin says that the danger of this is greater when a molecular technique known as PCR is used. I think that the danger of error depends more strongly on laboratory protocol than on the molecular technique.

From his comments, it seems that Professor Lewontin is unfamiliar with the protocol and methodology generally used by forensic scientists. He asserts that crime scene samples, being of limited quantity, are amplified using PCR. In fact, PCR is generally not used for the purpose he describes, and the genetic evidence presented at trial is usually not the product of PCR amplification. The major forensic testing laboratories (FBI, Lifecodes and Cellmark) do not regularly use PCR now, let alone in the past [Ivan Balazs, Director of Research at Lifecodes, and Bruce Budowle, Director of Research at the FBI Laboratory (Balazs and Budowle, 1993)]. Although PCR is sometimes used for an initial screening, for the bulk of cases forensic testing laboratories ultimately use a less sensitive method called RFLP typing via Southern blotting (NRC, 1992). Perhaps Lewontin's remarks are aimed at what he envisions for the future. Indeed RFLP analysis will eventually be replaced by some amplification process because results for the latter can be obtained almost immediately, whereas results for any RFLP analysis require four to six weeks or more.

Professors Thompson, Lempert and Berry believe that the average probability of a laboratory error should place a lower bound on the probability of a match. I disagree. A case-specific, posterior probability of a laboratory error is the appropriate calculation. Such a calculation, if admissible in court, should be presented separately from the probability of a match. Relying on the NRC report, Professor Thompson argues that the probability of a laboratory error should be estimated using proficiency testing. From the statistical perspective, it is clear that proficiency testing is not an efficient means of estimating a small probability. In Section 5, I discuss laboratory error in general, including methods of estimating the probability of error.

BDN voice concern about likelihood ratio statistics that calculate the probability of a match between un-