For $n = 16$, the maxima are $K = 4.90$ and $K_1 + K_2 = 4.51$. Thus, there is only a slight loss in information in using two independent loci.

To summarize verbally the above mathematics, a locus with n alleles is maximally informative when all alleles are equally frequent in the underlying population. The condition of equally frequent alleles is admittedly extreme, but one might approximate it by the appropriate choice of test loci. Under the assumption of maximum information, two loci with $\sqrt{n}$ alleles each are jointly about as informative as a single locus with n alleles. If the more informative single locus suffers from band overlap, its information content is diminished. One can take the approach of Berry and try to extract the most information by dealing with the quantitative measures directly. By comparison, the FBI's method of preset bins loses some information in discretizing the problem. According to the above mathematical argument, these bins should be equally probable rather than equally spaced.

In closing, let me stress that the rapid rate of innovation in molecular genetics is apt to overcome the technical problems such as band overlap associated with the current DNA fingerprint loci. These loci are typed by a procedure called Southern blotting. The alternative PCR techniques advocated by Weber and May (1989) and Budowle, Chakraborty, Giusti, Eisenberg and Allen (1991) are exquisitely sensitive to minute amounts of DNA and can avoid the problem of band overlap. However, PCR sensitivity can be so extreme that contamination by exogeneous DNA is troublesome. It is not now clear which technology will prevail. I prefer the PCR technology since it permits more loci to be typed from a small crime sample. As I have attempted to argue, most of the controversies over Hardy–Weinberg equilibrium and, particularly, linkage equilibrium will dissipate with better defined loci. In any event, we should welcome the inevitable improvements in technology even if the statistical issues become less interesting. Justice will be better served by greater genetic clarity.

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Comment

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1. INTRODUCTION

Berry sets two objectives in his abstract. One is to introduce the Bayesian approach to the forensic use of DNA evidence, and the other is to compare that approach with that of "match/binning." The latter is criticized as giving results that are too extreme and for failing to distinguish, in principle, between results that barely fail to fall in the appropriate bin and those that are way out. As he points out, two potential observations that are very close to one another could lead to drastically different conclusions. As I understand it, he seems to suggest that the users of this approach may have recognized this problem in the Castro case and reacted by an ex post facto widening of the bin when the observation barely failed to fall in a bin suggesting guilt.

In my opinion the Bayesian approach is well suited for this subject and deserves to be developed as a useful tool. This approach has several difficulties, some of which are addressed by Berry. One of these is that of educating the members of the legal system and the potential jurors. Another is the use of density estimation to determine the frequency distribution of band weights.

Several issues will be discussed here. The match/binning approach, as described, doesn't make much inferential sense, and if the Bayesian approach should be compared with something, it should be with a more or less classical significance or frequentist Neyman–Pearson (NP) competitor. While binning does replace a continuous analysis by a discrete analysis that leads to aggravating discontinuities, one ought to evaluate the resulting cost in loss of efficiency before outlawing the practice of binning. To do so, we shall review briefly

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