
Legal Standards and the Significance of DNA Evidence

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Abstract Most human biologists are aware of controversies regarding the use of DNA profiles in the courtroom. Much attention has been given to estimating the probability of obtaining matches between DNA samples from an innocent suspect and those from a crime scene, but considerably less attention has been given to the critical issue of determining the probability of guilt given a match. Using Bayes' rule and simple algebra, we develop a measure of the strength of DNA evidence that indicates the amount of incriminating evidence needed in combination with DNA match evidence to meet a given conviction standard. Based on current standards and practices, we use this measure to demonstrate that (1) the amount of non-DNA evidence needed to convict, given a DNA match, generally is quite small, even if errors can occur in the processing of DNA evidence; (2) DNA match evidence alone is insufficient to convict, even for the lowest recognized conviction standards; (3) failure to match DNA evidence samples should be exculpatory unless laboratory proficiency is poor; and (4) if errors in handling evidentiary samples occur (even rarely) that tend to produce a false DNA match, then the legal significance of DNA evidence is remarkably insensitive to estimates of chance match probability.

Forensic applications are rapidly emerging as one of the most recognized practical uses of human genetic data. The role of DNA profiles in establishing guilt or innocence in a legal setting has been controversial, attracting the attention of most human biologists. Although many of the technical objections to forensic uses of DNA evidence appear to be settled (Lander and Budowle 1994), there is still considerable discussion—and sharp differences of opinion—concerning how such evidence should be presented and interpreted in legal settings. Rather than advocating one side in the debate, we present an approach that can be used to assess the legal value of DNA evidence that in

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combination with numerical values greatly clarifies critical elements of the debate. Because others have raised most of the points we discuss, our treatment is essentially a selective review of the issues from a unique vantage point. For two recent in-depth overviews see Roeder (1994) and Weir (1995).

It has been argued that an appropriate assessment of the legal significance of DNA evidence should be based directly on its bearing on the guilt or innocence of a suspect [e.g., Berry (1991), Kaye (1993), Koehler (1993b), Balding and Donnelly (1994), and Robertson and Vignaux (1995)]. Bayes' rule provides a logical framework for forming opinions about the likelihood of a suspect's guilt or innocence based on multiple sources of evidence (Lindley 1977; Evett 1983). The Bayesian approach relies on the probability of (or, more accurately, the belief in) guilt exclusive of DNA evidence. If this so-called prior probability of guilt is low, then a DNA match need not imply guilt beyond a reasonable doubt. The critical question we address here is, How large must the prior probability of guilt be for DNA evidence to establish a belief in guilt beyond a given conviction standard? Here, we develop a simple, general procedure that answers this question, in effect providing an informal measure of the legal value of DNA evidence. Our measure is unique in that it relies explicitly on a given conviction standard. We illustrate the utility of this measure by considering some specific numerical cases.

We stress that our purpose here is not to advocate that expert witnesses testify using our Bayesian based method, nor are we proposing the Bayesian decision process as a model of how jurors do (or ought to) form opinions about guilt or innocence [for discussions, see Kaye (1993), Koehler (1993b), and Matthews (1994)]. Furthermore, our intent is not to argue for or against the suitability of our methods for real legal applications; such issues (which fall well outside our expertise) must ultimately be settled by forensic scientists and legal experts. Rather, we view our procedure as a straightforward way in which interested readers of *Human Biology* can easily appreciate the strengths and weaknesses of DNA evidence without being confined by strict legal conventions.

Materials and Methods

Bayes' Rule and the Probability of Guilt Given a DNA Match. Bayes' rule provides a logical procedure by which DNA and other evidence can be used to quantitatively alter degrees of belief in guilt or innocence of a suspect. The degree of belief in a suspect's guilt or innocence is often called the probability of guilt or innocence. We refer to the degree of belief in guilt (or innocence) formed without using DNA match evidence as the *prior* probability of guilt (or innocence); the *posterior* probability of guilt (or innocence) refers to the degree of belief in guilt (or innocence) given the DNA and other evidence combined.

Table 1. Computations Needed to Determine the Posterior Probabilities of Guilt and Innocence Using Bayes' Rule

| | Prior Probability | $Pr\{\text{DNA Profile Match}\}$ | Product | Posterior Probability |
|-----------|----------------------|----------------------------------|------------|-----------------------|
| Guilt | g | $1 - e$ | $g(1 - e)$ | $G = g(1 - e)/T$ |
| Innocence | $1 - g$ | f | $(1 - g)f$ | $1 - G = (1 - g)f/T$ |
| Total | 1 | | T | 1 |

The posterior probability of guilt or innocence given a match between DNA profiles of a defendant and an evidentiary sample can be computed using Bayes' rule (Linden et al. 1978; Balding and Donnelly 1994). Table 1 summarizes the computations involved. In the present application Bayes' rule relies on three basic pieces of information: (1) the prior probability of guilt g , (2) the probability e that a laboratory fails to detect a match between two samples with identical DNA marker genotypes (i.e., e = probability of a false mismatch), and (3) the probability f that DNA samples derived from two different individuals are reported to have the same marker genotype (i.e., the probability of a false match). Later in this section, we discuss potential sources and probabilities of false matches and possible values of g and e .

The posterior probability of guilt, denoted G , is (Table 1)

$$Pr\{\text{guilt}|\text{DNA profile match}\} \equiv G = \frac{(1 - e)g}{(1 - e)g + f(1 - g)}. \tag{1}$$

Equation (1) can be viewed as giving a revised probability of guilt in light of DNA match evidence; however, G is no more meaningful than the parameters from which it is computed. Of course, jurors would be the ones who ultimately set, perhaps implicitly, the relevant values of g , e , and f in a legal setting.

An alternative form of Bayes' rule, often used in forensic contexts [e.g., Walsh et al. (1994)], represents Eq. (1) in terms of the odds against guilt and a likelihood ratio. The odds-based Bayes' rule is mathematically more elegant than Eq. (1). However, we believe that probabilities are somewhat more intuitive than odds, which is why we have chosen to work with the slightly more cumbersome Eq. (1). In any case, the alternative forms of Bayes' rule are completely interchangeable, and the translation from probability to odds is mathematically trivial.

Minimum Non-DNA Evidence Needed for Conviction Given a DNA Match. In a legal setting the main interest is in whether or not $Pr\{\text{guilt}|\text{DNA match}\}$ is sufficiently high to convict. Let G_{convict} represent the minimum probability of guilt considered to be "beyond a reasonable doubt" (or whatever legal burden of proof applies). For any given conviction standard

G_{convict} , the Bayesian formula (1) can be inverted to determine g_{min} , the minimum prior probability of guilt required to ensure a posterior probability of guilt that exceeds the conviction standard:

$$g_{\text{min}} = \frac{fG_{\text{convict}}}{fG_{\text{convict}} + (1 - e)(1 - G_{\text{convict}})}. \quad (2)$$

That is, if $g \geq g_{\text{min}}$, then $G \geq G_{\text{convict}}$; the total evidence is sufficiently strong to convict. The minimum prior probability of guilt g_{min} can thus be thought of as a heuristic indicator of the strength of DNA match evidence: The smaller the value of g_{min} , the stronger the value of the DNA match evidence. [Ours is essentially an extension of a procedure described by Berry (1990, p. 25) for paternity analysis.] Another advantage of g_{min} —especially for jurors—is that the prior probability g need not be precisely known, so deciding whether the evidence is sufficient to convict would simply reduce to determining whether g is greater than g_{min} .

As can be inferred from Eq. (2), g_{min} increases with increasing conviction standards G_{convict} and decreases with decreasing false match probabilities f . A higher probability of a false DNA mismatch e inflates g_{min} , but our analyses indicate that this effect is negligible compared with those of G_{convict} and f for realistic parameter values.

False Matches. A false match of DNA evidence collected from a defendant and the crime scene can arise in two ways. First, two different individuals (e.g., the defendant and another person who left DNA evidence at the crime scene) may by coincidence have identical genotypes at the marker loci being used in a forensic test. Although this involves a real match between the test loci from two samples, it is false in the sense of implying that both samples are from the same individual. Second, different individuals with distinct marker genotypes may be erroneously scored as a match as a result of handling errors that occur in the course of collecting and analyzing DNA samples. Types of handling error include contamination, mislabeling of samples, gel loading errors, bleeding between gel lanes, and clerical mistakes [for further discussion, see Thompson and Ford (1989)]. Note that deliberate “errors,” such as malicious evidence planting, would also fall within this category, as would deposition of the suspect’s DNA at the crime scene through innocent means.

The probability of a false match f can be decomposed into components reflecting these two sources. If p_{chance} denotes the probability of a false match resulting from coincidence and p_{handling} is the probability that a false match arises through handling errors, then

$$f = (1 - e)p_{\text{chance}} + (1 - p_{\text{chance}})p_{\text{handling}}. \quad (3)$$

Using parameter values (discussed later), we substitute this expression into

Eq. (2) to assess the relative impact of chance and handling errors on g_{\min} , our measure of the probative value of DNA match evidence.

Posterior Probability of Guilt Given a DNA Mismatch. Bayes' rule can also be used to determine the posterior probability of guilt given a *mismatch* between the DNA profiles obtained from a suspect and a crime scene. The derivation parallels that of $\Pr\{\text{guilt}|\text{DNA match}\}$ in Table 1:

$$\Pr\{\text{guilt}|\text{DNA mismatch}\} = \frac{eg}{eg + (1 - f)(1 - g)}. \quad (4)$$

As we argue, this posterior probability generally falls below most reasonable conviction standards G_{convict} . However, if the probability of a false mismatch e is sufficiently high, DNA mismatch evidence may not be exculpatory because for sufficiently high prior probabilities of guilt $\Pr\{\text{guilt}|\text{DNA mismatch}\}$ may still be greater than G_{convict} .

Parameter Values. The basic information needed to apply our heuristic measure [Eq. (2)] of the value of DNA evidence consists of the probability of a false mismatch (e), the probability of a false match (f), and a conviction standard (G_{convict}). The probability of a false mismatch is reportedly 0.5% or less (Nowak 1994); however, Lewontin (1994) suggested that e may be as high as 12%. The false match probability f has been the focus of much debate [e.g., Chakraborty and Kidd (1991), Lewontin and Hartl (1991), and Weir (1992)], but suggested values range from 10^{-5} to 10^{-9} (Lander and Budowle 1994) when close relatives of the accused can be ruled out as suspects and as high as 0.265 when they cannot [e.g., Evett (1992) and Brookfield (1994b)].

The minimum probability of guilt needed to convict, G_{convict} , depends on both the legally mandated burden of proof and the individual juror. The legal literature documents opinions on values of G_{convict} for various burdens of proof. In a survey conducted by McCauliff (1982), federal judges and justices were asked to assign numerical definitions of certainty (probabilities) required by nine burdens of proof. For brevity we discuss only "beyond a reasonable doubt," but other burdens of proof can easily be used in our formulas. Of the 171 judges that assigned probabilities to "beyond a reasonable doubt" in the survey, the median and modal response was 90%. Over half of the responses were in the range 85–95%. (Twenty-one judges assigned the value 100%. Taken literally, this implies that no evidence could meet their burden of proof because all evidence is subject to some, perhaps unreasonable, doubts.) There is a legal precedent for G_{convict} based on a survey of nine judges in the Eastern District of New York [*United States v. Fatico*, 1978; see also McCauliff (1982) and Gastwirth (1992)]; the probabilities ranged from 75% to 95% with the median and modal value being 85%. Of course, in a real situation G_{convict} must ultimately be determined by the trier of fact. Our formulas allow any particular value of G_{convict} to be used.

Application of Bayes' formula [Eq. (4)] for the posterior probability of guilt given a DNA mismatch requires, in addition to e and f , a value for the degree of belief of guilt formed without using DNA evidence, g . This prior probability of guilt may be near 0 when screening DNA databases for suspects or near 1 if other evidence is strongly incriminating. Evett (1993), Walsh et al. (1994), Berry (1994), and Balding and Donnelly (1995), among others, discuss considerations and procedures for determining prior probabilities.

If one wants to explicitly consider the two sources of a false match [Eq. (3)], then values for p_{chance} and p_{handling} are also needed. In previous work the false match probability f was essentially identified with p_{chance} . This suggests that p_{chance} ranges from 10^{-5} to 10^{-9} (Lander and Budowle 1994). If, however, close relatives of the accused cannot be ruled out as suspects, then p_{chance} can be of the order of 0.1 or more for a single locus (Evett 1992; Brookfield 1994b).

Although forensic experts and laboratories may argue that mistakes in handling DNA evidence are impossible (thus implying that p_{handling} is 0), there are many steps in the processing of evidence at which handling errors can (and have been known to) occur, which suggests that nonzero values of p_{handling} may be more realistic [for discussion see Thompson and Ford (1989), Koehler (1993a,b), Lempert (1993), Devlin et al. (1994), and Thompson (1995)]. In fact, p_{handling} can be quite high if there is a strong suspicion that the DNA evidence was planted or tampered with or was left at the crime scene through innocent means. In what follows we determine what values of p_{handling} significantly affect the value of DNA match evidence.

In a legal setting a juror may use the testimony of forensic experts to form opinions about the relevant values of e , f , p_{chance} , and p_{handling} . All the parameters—including G_{convict} , of course—are open to interpretation by a juror (Kaye 1993). For example, the results of proficiency tests could be presented as evidence of a laboratory's probability of reporting a false mismatch (e). However, an expert might testify that the laboratory has corrected problems that led to a relatively high reported value of e . It would be up to the juror to adjust (or not) the value of e in light of such testimony. Likewise, expert witnesses may argue convincingly that the collection and analysis of the DNA evidence in a particular case was done flawlessly, implying that p_{handling} is negligible. However, if a juror believes that the DNA evidence was planted before its collection, then the relevant value of p_{handling} in the juror's deliberations may actually be near 1. The probability of a coincidental DNA match between two individuals p_{chance} has been the subject of much scientific deliberation; yet it too is open to interpretation by a juror. This is because any computed value of p_{chance} depends on a number of assumptions that could be questioned by a juror, such as the composition of the reference population or the degree of population substructuring [for discussion and further references see Nichols and Balding (1991), Roeder (1994), and Brookfield (1995)].

The essential point is that the parameter values we discuss here may only roughly reflect those that could be relevant in a legal setting. However, given our more modest goal of heuristically exploring the legal significance of DNA evidence, we use the parameter ranges given earlier. We believe that much insight can be gained by doing so. In any case, the formulas are completely general and can be used with parameter values that are not considered here.

Results

Minimum Prior Probability Needed to Convict. The minimum prior probability needed to convict with DNA match evidence [Eq. (2)] depends on the probability f that a reported match is false and on the value of G_{convict} (Figure 1). When close relatives of the accused can be eliminated as suspects, the minimum prior probability of guilt needed to convict will, in general, be small (Figure 1A). This suggests that, given a match, the non-DNA evidence need not be strong to convict. For example, if $G_{\text{convict}} = 99\%$ (the most stringent feasible guilt standard of those cited), $e = 12\%$ (indicating poor laboratory proficiency), and $f = 10^{-5}$ [a high-end estimate of the false match probability, according to Lander and Budowle (1994)], then the minimum prior probability needed to convict is only $g_{\text{min}} \approx 0.1\%$. Such a prior probability of guilt, although low, might not be met in some cases, for example, if DNA match evidence is the sole source of evidence linking a suspect to a crime (Koehler 1993b; Lempert 1993; Brookfield 1994a).

If close relatives of the accused cannot be excluded from the suspect pool, then the minimum prior probability needed to convict may, in principle, be much higher (Figure 1B). For example, if $G_{\text{convict}} = 99\%$ and $e = 12\%$ but the probability of a false match is $f = 0.1$ because close relatives (such as siblings) are prevalent in the suspect population, then $g_{\text{min}} \approx 92\%$. This means that DNA match evidence only slightly increases the probability that the accused is guilty. If a lower conviction standard were used, the impact of a DNA match could be substantial, even with relatives being among the potential suspects. For instance, if conviction standard $G_{\text{convict}} = 90\%$, $e = 12\%$, and $f = 0.1$, then $g_{\text{min}} \approx 51\%$, whereas if $G_{\text{convict}} = 75\%$, then $g_{\text{min}} \approx 25\%$, suggesting that a DNA match may still be strong evidence of guilt, even if it is not overwhelmingly so. Although the issue of relatives can clearly be important in certain cases (Evetts 1992; Brookfield 1994b), to simplify our presentation, we focus on situations in which close relatives of the accused can be excluded from the suspect pool.

Mismatch Evidence. It is often taken for granted that if a suspect's DNA profile does not match that of the crime scene evidence, then the suspect could not be the source of the crime scene material. In agreement with this,

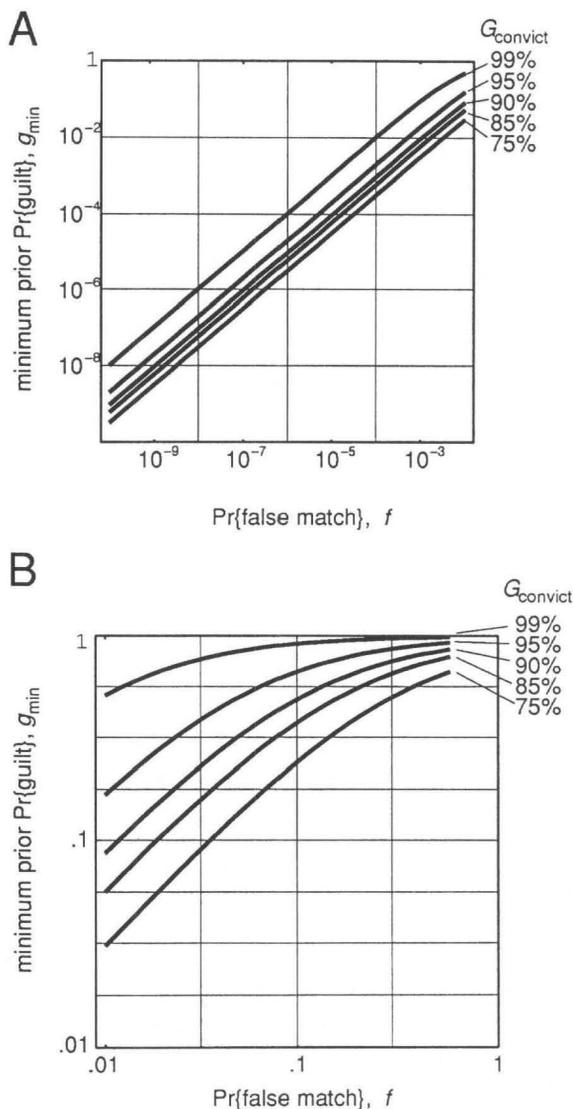


Figure 1. Log-log plots of the minimum prior probability of guilt (g_{\min}) needed to convict with DNA match evidence as a function of the probability of obtaining a false match (f). Curves are shown for five conviction standards. These five standards span the dominant range (75–95%) and upper limit (99%) of feasible values reported by McCauliff (1982) and *United States v. Fatico* (1978). All curves assume $e = 5\%$. A prior probability of guilt that lies above g_{\min} for a given conviction standard and false match probability implies that there is sufficient evidence to convict at that standard. (A) Relevant range of false match probabilities f if close relatives of the accused can be excluded as suspects. (B) Possible range of f if close relatives of the accused figure prominently in the suspect pool. Analogous curves for $e = 12\%$ and $e = 0.5\%$ are higher and lower, respectively, than those shown—but almost indistinguishably so.

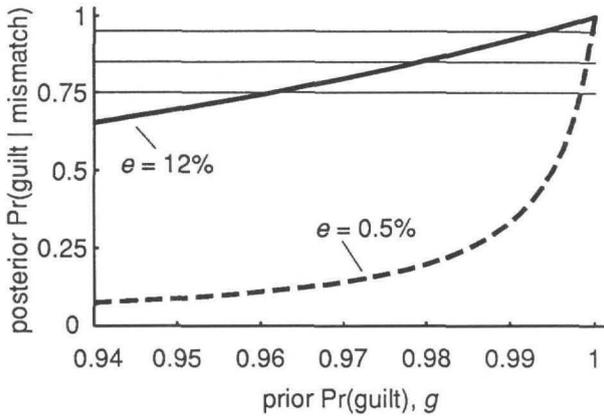


Figure 2. Semi-log plot of the posterior probability of guilt given a mismatch between the DNA profiles of a suspect and an evidentiary sample as a function of the prior probability of guilt for two laboratory error rates suggested in the literature, $e = 0.5\%$ and $e = 12\%$. The horizontal lines indicate the minimum, maximum, and modal conviction standards cited in *United States v. Fatico* (1978).

Figure 2 shows that the posterior probability of guilt given a DNA mismatch [Eq. (4)] is, in general, below conviction standards unless the prior probability of guilt g and the probability of a false mismatch e are both large. For example, if $g = 99\%$, $e = 0.5\%$, and $f = 10^{-5}$, the probability of guilt given a reported DNA mismatch is less than 33%, well below any of the cited standards required to convict. This supports the usual exculpatory interpretation of DNA mismatch evidence. However, if e is as large as 12% (Lewontin 1994), then $\Pr\{\text{guilt}|\text{DNA mismatch}\} = 92\%$, which is greater than the median conviction standards cited in *United States v. Fatico* (1978) and McCauliff (1982).

Chance Matches and Handling Errors. Using only chance match probabilities to indicate the significance of DNA evidence (Lander and Budowle 1994) essentially equates f with p_{chance} in Eqs. (1), (2), and (4). However, if p_{handling} (the probability of a false match resulting from handling errors) is larger than p_{chance} , then the minimum prior probability of guilt needed for conviction g_{min} may be increased by several orders of magnitude, reflecting the reduced impact of DNA evidence (Figure 3A). Even for values of p_{handling} larger than p_{chance} , g_{min} may not be exceptionally high (Figure 3A). For example, if $p_{\text{handling}} = 5\%$, $p_{\text{chance}} = 10^{-5}$, and $e = 5\%$, then g_{min} is about 23% when $G_{\text{convict}} = 85\%$, the median and modal value cited in *United States v. Fatico* (1978). So, despite the sensitivity of g_{min} to p_{handling} , the complete absence of handling error, although desirable, is not absolutely essential for the forensic relevance of DNA evidence. A similar qualitative argument has

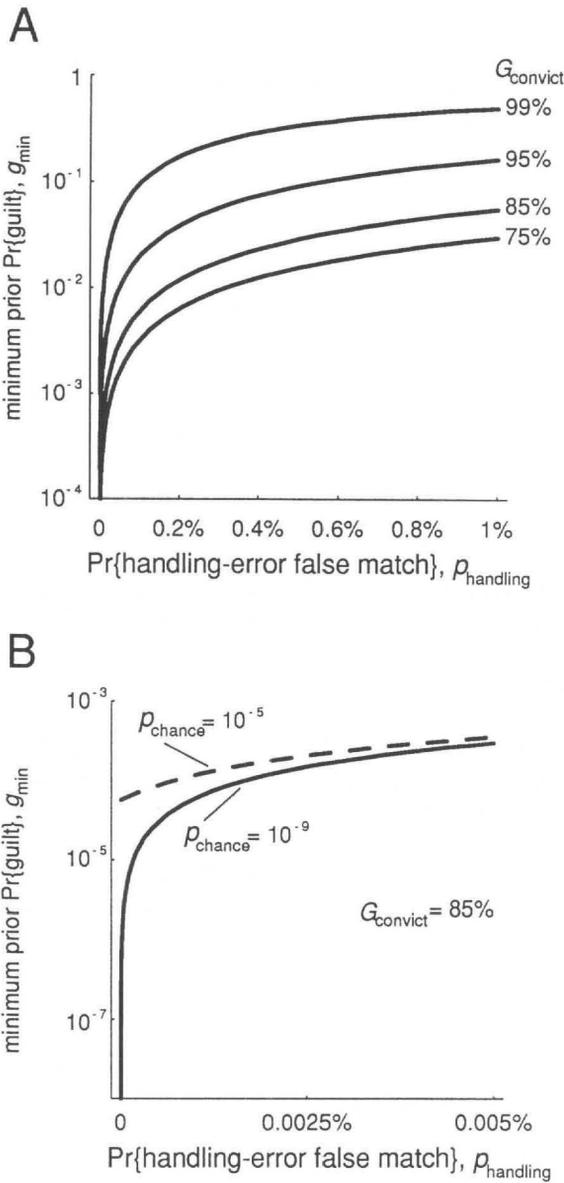


Figure 3. Semi-log plot of the minimum prior probability of guilt (g_{\min}) needed to convict with DNA match evidence as a function of the probability of a false match arising from handling errors (p_{handling}) for the conviction standards used in Figure 1. (A) Plot assumes $e = 5\%$ and $p_{\text{chance}} = 10^{-5}$. At this scale the four curves are virtually indistinguishable from analogous curves produced using smaller match probabilities, even $p_{\text{chance}} = 10^{-9}$. (B) Scale at which the chance match probability p_{chance} has a perceptible impact on g_{\min} . Curves show g_{\min} as a function of p_{handling} , assuming that $G_{\text{convict}} = 85\%$ and $e = 5\%$ for $p_{\text{chance}} = 10^{-5}$ and $p_{\text{chance}} = 10^{-9}$.

been made by Lempert (1993). (Note that this conclusion depends on the applicable guilt standard; if G_{convict} were 99% in the last example, then $g_{\text{min}} \approx 83\%$.) Of course if p_{handling} is large, perhaps because of a strong suspicion of evidence tampering, then DNA match evidence has little legal significance. For example, $g_{\text{min}} \approx 75\%$ when $p_{\text{handling}} = 0.5$, $p_{\text{chance}} = 10^{-5}$, $e = 5\%$, and $G_{\text{convict}} = 85\%$.

Interestingly, if p_{handling} were even an order of magnitude larger than the larger values suggested for p_{chance} ($\sim 10^{-5}$), then the controversy involving population genetics [e.g., Chakraborty and Kidd (1991), Lewontin and Hartl (1991), Weir (1992), Hartl (1994), Lander and Budowle (1994), and Lewontin (1994)] would be irrelevant to the practical forensic significance of DNA evidence (Figure 3B). That is, the minimum prior probabilities required to reach a given conviction standard assuming $p_{\text{chance}} = 10^{-5}$ versus assuming $p_{\text{chance}} = 10^{-9}$ are nearly identical when p_{handling} is greater than 10^{-5} (see Figure 3B). Although laboratory protocols and checks undoubtedly reduce the likelihood of handling errors, we know of no studies designed specifically to determine p_{handling} for the entire sequence of evidence processing (from crime scene collection to laboratory analysis to data entry and statistical analysis); however, values of p_{handling} as low as 10^{-5} would be difficult to estimate with accuracy. We stress that the relevant value of p_{handling} must refer to handling errors that might occur not only in a forensic laboratory but also before DNA evidence ever reaches such a lab.

Our analyses are in accord with suggestions made by Lewontin and Hartl (1991), Lewontin (1994), and others that handling errors may be more important in the legal interpretation of DNA evidence than the population genetics issue of how often different individuals happen to share an identical DNA marker genotype. This argument supports the recent contention of Lander and Budowle (1994) that the population genetics controversy surrounding the forensic use of DNA evidence is over, but for a different reason: If handling errors occur (even below statistically detectable levels), then the population genetics argument over whether $p_{\text{chance}} = 10^{-5}$ or 10^{-9} (or some other small value) is largely academic (see Figure 3B).

Discussion and Conclusions

We have presented a simple heuristic way to assess the legal significance of DNA match evidence. Our measure describes how much evidence, in addition to the DNA evidence, is required to reach or surpass a standard for conviction. Unlike other indicators of the weight of DNA evidence, our Bayes' rule-based measure explicitly acknowledges the legal decision process, including subjective opinions of a trier of fact. As such, it is more than likely not an appropriate measure for use by expert witnesses (Kaye 1993; Koehler 1993b). Moreover, the logic of Bayes' rule might not be used by a

real juror (Kaye 1993; Lempert 1993). However, outside a formal legal setting our measure provides much insight into the potential value of DNA evidence. It may be possible to use our measure in a legal setting, but that issue is well beyond the scope of this paper and our expertise. We have introduced Bayes' rule in university statistics classes and found that even this highly selected subset of the general public has difficulty with the general concepts. (Our measure is completely general and, in principle, can be used to evaluate the legal significance of any type of evidence.)

A unique feature of our measure is its explicit reliance on quantification of the burden of proof. Obviously, such a conviction standard must be determined by an individual juror; however, our results based on values reported in the legal literature illustrate the heuristic value of considering specific numerical examples of potentially representative standards and the other necessary parameters. Our results indicate that the belief in guilt based on non-DNA evidence need not be exceptionally high for DNA match evidence to indicate a probability of guilt above even high conviction standards. At the same time, the requirement for evidence in addition to a DNA match is sufficiently great that our results support arguments against the use of DNA evidence to convict in the absence of other evidence, as may be the situation when searching DNA databases for suspects [e.g., Balding and Donnelly (1994) and Brookfield (1994a)]. The need for at least some additional evidence is especially critical if close relatives of the accused cannot be excluded from the suspect pool or if handling errors occur (even rarely) that tend to produce false matches.

The logic of Bayes' rule can also be used to assess the importance of DNA mismatch evidence. Our findings reveal that such evidence is likely to be exculpatory under most circumstances, supporting the interpretation that is often used by default. However, if laboratory proficiency is low and other evidence is strong, then DNA mismatch evidence may not be sufficient for an acquittal.

Finally, we examined the impact of handling errors that tend to result in false DNA matches on the significance of DNA evidence. Our notion of handling errors includes the probability of an anomaly (unintentional or not) in the process of collecting, handling, and analyzing DNA evidence as well as the possibility that the DNA evidence was left innocently at the crime scene. Our results indicate that even if handling errors occur sometimes, DNA match evidence can still represent powerful evidence of a suspect's guilt. Finally, our results strongly suggest that disagreements about computing the probability of a chance match may be largely academic if handling errors occur even at levels that would likely be below detection.

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