

Koehler, J. J. (1993). DNA matches and statistics. Important questions, surprising answers. Judicature, 76, 222-229.

DNA MATCHES AND STATISTICS:

IMPORTANT QUESTIONS SURPRISING ANSWERSⁱ

Jonathan J. Koehler

University of Texas

November 23, 1992

Since its introduction at trial in a Florida case in 1987, DNA profiling evidence has been used to convict defendants in more than a thousand criminal and civil cases. Initially received by the courts and news media as a nearly foolproof means of identifying (a) vicious criminals who left blood, hair or semen at the scenes of their crimes,ⁱⁱ and (b) biological fathers implicated in paternity lawsuits, there is now an increased awareness that DNA analyses are subject to error and more deserving of careful scrutiny.ⁱⁱⁱ

This article asks and answers questions related to the probative value of a reported DNA match.^{iv} None of the questions concern the validity of the underlying genetic theory or the biological protocol practiced by the DNA laboratories. (See Sidebar #1 for a brief nontechnical overview of the DNA typing procedure.) Instead, the focus is on the meaning and significance of a reported match, and the role that the possibility of error should play evaluating this evidence. These issues are not well understood by attorneys, judges, jurors, or, in many cases, the DNA experts themselves.

I. MEANING OF A MATCH

Based on my examination of transcripts from criminal cases involving DNA evidence, it is clear that defense attorneys are greatly concerned with such issues as the procedural details of the DNA identification process, the acceptability of the technology in the scientific community, the size of the data bases that are used to make probabilistic estimates, and the credentials of the prosecution's expert witnesses. To be sure, there are some useful points to be made with respect to each of these issues. However, defense attorneys are often so preoccupied with the scientific procedures that generated the DNA evidence that they fail to pursue important points related to the validity of the inferences that are drawn from the evidence. Defense attorneys who understand the limited meaning of a reported match and the accompanying frequency statistics, and who work to impress such an understanding on factfinders, are likely to experience greater success at trial.

The answers to some of the questions asked below may surprise you. For example, it will be explained that there is a world a difference between (a) a reported DNA match between a suspect and a sample of trace evidence, and (b) a conclusion about the likelihood that a defendant is the source of that trace. Simply put, *a DNA expert cannot identify the probability that a defendant is the source of a hair, bloodstain or semen stain recovered from the scene of a crime.* The expert can--with varying degrees of accuracy--estimate the frequency with which various characteristics might be expected to be found in a human blood or hair sample. This information is probative, to be sure, but an estimate of the probability that a defendant is the source of a particular trace requires an estimate about the strength of the relevant nongenetic information as well. The failure to understand this principle probably has been (and will continue to be) responsible for the conviction of people who would not have been convicted if the evidence were presented in a proper form.^v

DNA Matches

Question: Is DNA matching evidence probative?

Answer: Yes. In most cases, a reported DNA match is extremely probative with respect to the questions "Is the defendant the source of the trace?" and "Is the defendant guilty as charged?" That is, after learning that a laboratory report indicates that trace evidence recovered from a crime scene matches the DNA profile of a defendant, factfinders generally should strengthen their beliefs in the propositions (a) the defendant is the source of the trace, and (b) the defendant is guilty of the crime.^{vi}

Having said this, it is important to note that a reported DNA match does not require a belief in either proposition. First, the reported match may not be a "true" match--laboratories sometimes make mistakes (see section II). Second, even a rare DNA pattern may be shared by several others (particularly by a relative of the defendant). Third, even if the defendant is the source of the trace, there may be an innocent explanation. A Good Samaritan may run into the woods to save a woman screaming for help, cut himself on a tree branch, and bleed on the woman while trying to save her. Finally, other evidence may suggest that the defendant is neither the source of the trace nor guilty of the crime. An eyewitness may report that the defendant was not the one he or she saw at the scene of the crime. This report remains relevant no matter what results the DNA analyses yield. Indeed, a final judgment about whether a person is the source of an evidentiary trace or guilty of a crime must be based both on the laboratory report and all other relevant evidence.

Question: What does it mean when a DNA expert declares a match between a suspect and trace evidence recovered from the scene of a crime?

Answer: When scientists declare a DNA match between a person and an evidentiary trace, they are saying that the person might be the source of that trace. Another way of saying this is that the person cannot be excluded as a possible source. But a match report does not necessarily mean that the matching person is the source of the trace, or even that a probability that the matching person is the source can be determined.

Question: Then what does the small probability that usually accompanies expert testimony of a DNA match mean?

Answer: The probability that accompanies a reported DNA match is the theoretical likelihood that a randomly selected person from the general population (or from the population of certain large ethnic or racial groups) would genetically match up with the trace evidence as well as the defendant. This probability, which may be referred to as the "*random match probability*" (see Sidebar #2), often (but not always--see Relatives and Subgroups section below) helps factfinders assess the probative significance of a match.

It is important to be clear about what the random match probability does not reflect. It does

not tell us the "*source probability*," i.e., how likely it is that the defendant is the source of the trace, and it most certainly does not tell us the "*guilt probability*," i.e., how likely it is that the defendant committed the crime in question (see Sidebar #2). To assume otherwise is to commit the error of assuming that because it is known that (a) Jack the Ripper was left handed, (b) 10% of the population is left-handed, and (c) I am left-handed, there must therefore be a 10% chance that I am not Jack the Ripper. The fallacy here, of course, is in translating the handedness match evidence directly into a probability of innocence without considering the strength of other evidence for and against the proposition that I am Jack the Ripper. This same error is made when experts, attorneys or judges identify the probability that a defendant is guilty based solely on DNA random match frequencies.^{vii}

Paternity

DNA analyses are frequently used in paternity cases as well. In the typical case, laboratories perform genetic tests on the mother, the child, and the alleged father to arrive at a so-called "*paternity index*." The paternity index is a measure of the strength of the genetic evidence against the alleged father, where higher numbers are more probative of paternity than lower numbers. Essentially, it is a ratio of the probability that the alleged father would transmit the genetic markers observed in the child if he really were the father to the probability that such markers would be passed along by a randomly selected man from the reference population if he were the father. Thus, if an alleged father has a paternity index of 82, he is 82 times more likely than a randomly selected man to produce children that have the genetic pattern of the child in question. Some alleged fathers will be excluded as possible fathers of the child in question by these tests because they do not possess the requisite genetic markers. For these men, a paternity index generally is not computed and the laboratories report the exclusion result. For nonexcluded men, the laboratories report the paternity index. In addition, most laboratories provide a so-called "*probability of paternity*" that is based partly on the paternity index and partly on an assumption about the strength of the nongenetic evidence against the accused father.

Question: Does the "paternity index" tell us how likely it is that an alleged father is the true father of a particular child?

Answer: No. Paternity indexes, like random match probabilities in criminal cases, identify the theoretical probability that a randomly selected person from a particular population would match so well. This information can be helpful to factfinders, but it should not be mistaken for an estimate of the probability that an alleged father is the true father of a particular child.

Question: Does the "probability of paternity" statistic supplied by the laboratories tell us how likely it is that an alleged father is the true father?

Answer: No. Despite the facts that many laboratories routinely provide a "*probability of*

paternity," and many courts support admission of this probability value into evidence, the laboratories are not in a position to supply such an estimate.

Question: Can you give an example to clarify this point?

Answer: Certainly. Imagine two paternity cases, A and B. In case A, the alleged father denies having sexual relations with the mother at or near the time of conception. The mother says otherwise. DNA blood analyses do not exclude the defendant as a potential father and yield a paternity index of 1000. This means that the alleged father is 1000 times more likely than a randomly selected man from the general population to produce children that have the genetic pattern of the child in question. Reflect for a moment on how likely you believe it is that the alleged father is the true father of the child.

Now consider Case B. Case B is identical in all respects, right down to the paternity index of 1000. But here, an experienced physician testifies that the defendant had a vasectomy prior to the time of conception, and that follow-up tests indicate that he could not have fathered this or any other child. How likely do you believe it is that the alleged father is the true father?

If you believe that the alleged father in case B is less likely to be the true father than the alleged father in case A, you should be able to see why a laboratory analysis does not, by itself, determine the probability of paternity. A reasonable estimate of the probability of paternity can only be made after considering all relevant evidence. And certainly proof of a successful vasectomy provides at least some relevant evidence in case B.^{viii} Failure to assign different subjective probability of paternity estimates for cases A and B would suggest that the vasectomy evidence has zero probative value.^{ix}

The Insidious 50% Prior Probability Assumption

Question: But if a probability of paternity computation requires knowledge of all relevant evidence--both genetic and nongenetic--how are paternity laboratories able to estimate this value?

Answer: As noted above, the laboratories compute probabilities of paternity by making a critical assumption about the strength of the nongenetic evidence. They assume that the combined strength of all nongenetic evidence in every paternity case indicates that there is exactly a 50% chance that the defendant is the father of the child. This 50% estimate, also known as a "*prior probability*" (*i.e., probability of paternity prior to the introduction of laboratory evidence*) is then combined with the paternity index to yield a probability of paternity. The combination is achieved by a mathematical technique called Bayes' Theorem.^x

Question: Is the 50% prior probability assumption reasonable?

Answer: No. The practice of assuming a 50% prior probability is misleading and potentially prejudicial to defendants.^{xi} The laboratories have no reason to assume that, prior to forensic analysis, there is a 50% chance that an alleged father is the true father of a particular child?^{xii}

Ideally, the scientists who conduct paternity tests should know nothing about the nongenetic evidence in the case so that their own analyses remain untainted.

Question: How do the laboratories justify the use of a 50% prior probability?

Answer: The laboratories argue that the 50% prior probability of paternity is "a neutral assumption" because it does not indicate whether the proposition is more likely true or false.

But why should an assumption be made when there is real evidence to be heard? Depending on the case, the nongenetic evidence may suggest probabilities that are much higher or lower than 50%. Use of the 50% prior says, in essence, that the nongenetic evidence in a case--including evidence of sterility or other possible fathers--is irrelevant!

There is also a legal objection to the 50% prior probability assumption. Even if forensic scientists were in a position to assess the strength of the nongenetic evidence in a case, it is not their function to do so. It is the factfinders' job alone to combine the strength of both the genetic and nongenetic evidence to arrive at a final judgment in each case.

Question: Does the 50% prior probability assumption arise in criminal contexts as well?

Answer: It does when forensic scientists testify about source probabilities or guilt probabilities (i.e., the probability that a defendant is the source of recovered trace evidence or the probability that a defendant is guilty of a particular crime). The major difference is that, in criminal cases, statements pertaining to source and guilt probabilities are made without explicit reference to the 50% prior probability assumption. The result is that judges and jurors are never told that the probability values they hear require an assumption about something the forensic scientist does not and should not know anything about.

Question: Why do the laboratories continue to compute probabilities that require use of the controversial 50% prior probability assumption?

Answer: It is hard to know for sure, but ignorance may be the best explanation. Laboratory analysts are often unfamiliar with the subtle statistical issues related to the interpretation of genetic matches. A less charitable explanation is that laboratory analysts provide probabilities of paternity and source probabilities because they expect these to have a greater impact in court than other, more appropriate, characterizations of their findings. This increased impact lends power, prestige and financial reward to the forensic science profession.

Question: Is there evidence that source probability characterizations (or rather,

mischaracterizations) of forensic matching evidence increase the odds that jurors will return verdicts against defendants?

Answer: Yes. My own empirical research with mock jurors shows that when factfinders are provided with source probability statements in a hypothetical murder case, they are more likely to vote to convict the defendant.^{xiii} As the figure below indicates, this is particularly true when relatively less extreme probabilities are involved.

In one study, subjects were provided with forensic matching evidence in one of two presentation modes (random match probability, source probability) at one of two probability levels (one in a thousand, one in a billion). For probability levels of one in a thousand, commission of the "*source probability error*"--reframing a source probability statement as a random match probability statement--dropped the conviction rate from 40% to 18%.^{xiv}

Insert Figure About Here

Question: This graph also shows that reframing a source probability statement as a random match probability statement made little difference when the probability level was one in a billion. Because so many DNA cases include probability values in the billions, won't the impact of the source probability error be minimal in practice?

Answer: No. The National Academy of Sciences recently proposed a set of guidelines for computing DNA match probabilities that are more conservative than those previously used.^{xv} As these guidelines gain acceptance in the courts, we can expect to see fewer extremely small probabilities than we have seen thus far. Consequently, the empirical results associated with the source probability error will become increasingly relevant.

Relatives and Subgroups

Question: Are there grounds for disputing the DNA frequency statistics in cases where a source probability error is not committed?

Answer: Yes. An important criticism of DNA frequency statistics is that they fail to take into account the population of interest. The frequency statistics computed by most laboratories compare the defendant to a randomly selected person in some general population (e.g., North American Caucasians). Sometimes, these estimated frequencies are not as probative as the laboratories would have us believe. The main reason is that the general population may not be a fair genetic representation of the *potential source population*, i.e., the group of people who might reasonably be the source of the recovered trace evidence.

Question: What difference does this make?

Answer: It can make a big difference in cases where there is reason to believe that members of the potential source or suspect populations^{xvi} are genetically similar to the defendant. Imagine a case in which the authorities strongly suspect that a rape was committed by one of three biological brothers. Imagine further that one of the brothers is charged with the crime, and that a three probe^{xvii} DNA analysis reveals that the frequency of the genetic pattern identified in both the defendant's blood and a sample of recovered semen is 1 in 1,000,000.

At first blush, the one in a million match statistic appears to provide nearly conclusive proof that the defendant is the source of the recovered semen. However, one must bear in mind that the probability that blood from one of the other brother-suspects would genetically match the recovered semen is far greater than the 1 in 1,000,000 chance that a randomly selected person from the general population would match. According to genetic theory, the probability that at least one of the two brothers would also match on the three probe analysis is more than 3%.^{xviii} The fact that the pattern is rare in the general population makes little difference. Far more important is that the population of potential donors of the trace evidence consists, at least in part, of people who are much more likely than a random person from the general population to have genotypes that match those of the defendant.

In short, the probabilities ordinarily generated by DNA laboratories make no allowance for possible genetic similarities among members of the potential source or suspect populations. This diminishes their usefulness in cases where the potential source population contains untested relatives of a defendant.^{xix} In such cases, the probative value of the probabilities may well be outweighed by its potential to mislead jurors.

Question: What about cases in which the potential source population does not contain siblings or other close relatives?

Answer: Even in these cases, genetic sub-populations or substructures exist that may call into question the accuracy of general frequency statistics.^{xx} At present, there is substantial disagreement about how seriously these substructures undermine the general population frequency statistics.^{xxi}

II. ERROR

There is great controversy about the role that error can and does play in the DNA typing process. Two major categories of error exist: false positives and false negatives. For our purposes, a false positive error occurs when a laboratory erroneously reports that a defendant is the source (or likely source) of a matching trace. A false negative error occurs when a laboratory erroneously reports that a defendant is not the source of a trace. Most of the discussion of laboratory error to date has focused on the possibility of false positive error. On the one side, DNA experts testifying for the prosecution argue that it is impossible or nearly impossible to obtain a false positive error.^{xxii} Such testimony appears to be motivated

by definitions of false positive error that exclude consideration of human error or coincidental matches. On the other side, some defense experts argue that errors not only can and do occur, but that the forensic science community has conspired to cover them up.^{xxiii}

Question: Why should we worry about the possibility of false positive errors when we are provided with probabilities that are as small as those typically encountered in DNA cases (e.g., 1 in a million, 1 in a billion)?

Answer: As discussed earlier, there is sometimes good reason to question the relevance of reported DNA probabilities that are based on general populations. But even when the reported probabilities are regarded as accurate indicators of a chance match in the relevant population, these values are not synonymous with the false positive error rate.

The frequency with which a genetic pattern occurs corresponds with one type of false positive error, namely, coincidental match. But what we would really like to know is the error rate across all types of false positive errors. As noted above, we wish to know how often a laboratory declares a match between two samples when, in fact, the samples are from different sources. In order to answer this question, the possibility of a variety of human errors must be considered. These errors--many of which have been documented--include transcription errors, sample mix-ups, measurement errors, tampering, fraud,^{xxiv} etc.

Question: How can we measure the aggregate false positive error rate (i.e., the error rate that takes into account both the probability of coincidental matches and all forms of human error in DNA testing)?

Answer: Blind proficiency tests. Laboratories can be provided with known pairs of samples, ostensibly as part of their routine case work, and asked to make match/non-match judgments about them. The false positive error rate is the proportion of sample pairs that were not produced from a common source, but that are reported as matches by the laboratories. Unfortunately, few proficiency tests have been conducted to date, and those that have been conducted were generally nonblind.

Question: What's wrong with nonblind proficiency tests?

Answer: Nonblind proficiency tests may not provide a good indicator of the error rate in actual case work because the technicians may be unusually diligent and cautious when they know they are being observed and tested. Specifically, the observed technicians may be reluctant to declare matches in ambiguous situations to avoid the stigma of having committed a false positive error.

Question: Can the false positive error rate of a particular DNA laboratory or laboratory technician be determined in the absence of data from blind proficiency tests?

Answer: Not exactly, but there are ways to handle this problem. Here is one idea. The results of nonblind proficiency tests that have been performed may be combined and averaged to provide a lower bound estimate of the false positive error rate (i.e., a minimum error rate) for a laboratory or laboratory technician whose error rate is unknown. Thus, if the average error rate in testing is 2%, then it should be concluded that laboratories make errors at least 2% of the time.

There are several reasons why the proficiency test error rate should be used as a lower bound estimate rather than as a best estimate. First, as noted above, the openness (as opposed to blindness) of the tests makes them less sensitive to false positive error. The probability of false positive error is also diminished in many proficiency tests because the samples used are generally easier to work with and to analyze than those in actual case work. Finally, as a matter of legal policy, defendants should be given the benefit of the doubt when it comes to estimating the error rate associated with the analyses that matched their own blood with an incriminating trace.

A related idea is to report the false positive error rate as the largest false positive error rate that is consistent with the combined false positive error rates obtained in proficiency tests. The advantage of this approach is that it contains an incentive for DNA laboratories to submit to, and to perform well in, large scale proficiency tests.^{xxv} The burden would then shift to the individual laboratories to present evidence that their own false positive error rates are lower than this value.

Question: According to proficiency test data conducted to date, what is the false positive error rate of DNA analyses?

Answer: First it must be noted that proficiency test results to date are extremely limited. Much more proficiency testing under reasonably realistic conditions is needed before confident estimates can be made. But based on the little evidence available to date, a reasonable estimate of the false positive error rate is 1-4 percent. In 1987 and 1988, the California Association of Crime Laboratory Directors (CACLD) conducted proficiency tests with 3 DNA laboratories. In an initial study, two out of 110 reported matches were false positives. In a follow up study, one out of an estimated 120 reported matches were false positives.^{xxvi} More recent proficiency tests involving many more laboratories reflect a similar or slightly higher false positive error rate.^{xxvii} It should be noted that many laboratories conduct internal proficiency tests and report that errors are rare. However, these tests are generally shrouded in so much secrecy^{xxviii} and are so obviously self-serving that it is hard to know how to assess their significance. After considering all available evidence, the bottom line is that the laboratories seem to make many more accurate match declarations than inaccurate ones. But before you decide that an error rate of, say, 1% is acceptable or even "good," consider the error rate that you would tolerate in a commercial airliner (where an "error" is defined as a mistake that could cost you your life). Even seemingly low rates of error may be intolerable when the cost of the error is sufficiently high.

Question: What is an appropriate legal policy for divulging DNA laboratory error rates at trial?

Answer: A good argument can be made for requiring DNA laboratories to provide factfinders with conservative estimates of their false positive error rates whenever they provide testimony about genetic matches. By the same token, laboratories should be required to divulge their estimated false negative error rate in cases in which exclusions are reported.^{xxix}

III. CONCLUSION

DNA identification evidence has been, and probably will continue to be, extremely valuable in obtaining criminal convictions. When such evidence is presented, jurors frequently report that it was convincing.^{xxx} In many cases, this is as it should be. DNA evidence can provide a powerful link between a defendant, a crime scene, and a victim. However, it is imperative that attorneys, factfinders, and experts understand the meaning of a reported match and the conditions under which it should have more and less impact on judgments. Experts must be discouraged from overstating the probative significance of a match (i.e., no source or guilt probability statements), and encouraged to discuss the significance of relatives and subpopulations in the potential source population. They should also provide candid testimony about the potential for error in DNA analyses. But when zealous experts are not forthcoming about the limitations and shortcomings of DNA evidence, defense attorneys must be prepared to identify and explicate the relevant issues in cross-examination and with experts of their own.

i. Research on this article was supported by grant #SES-9209544 from the National Science Foundation and a Summer Research Award from the University Research Institute at the University of Texas at Austin. This research was conducted, in part, during the summer of 1992 while the author was a visiting scholar in the psychology department at Stanford University. Thanks are due to Sam Lindsey for his research assistance and to David Kaye, Bernard Robertson, Michael Saks and two anonymous reviewers for comments on an earlier version of this paper. Correspondence should be addressed to Jonathan J. Koehler, MSIS Department, CBA 5.202, University of Texas, Austin, TX 78712 (e-mail: Koehler@utxvm.cc.utexas.edu).

ii. Some courts were in awe of DNA evidence: "It is the enormous degree of identity that DNA profiling provides . . . that makes DNA profiling the most important advance in forensic science since the advent of fingerprinting. . . . [T]he current reliability and accuracy of DNA profiling justifies an aura of amazement" (U.S. v. Jakobetz, 747 F.Supp 250, 258, 263 D.Vt. 1990); "In short, if DNA Fingerprinting works and receives evidentiary acceptance, it can constitute the single greatest advance in the 'search for truth,' and the goal of convicting the guilty and acquitting the innocent, since the advent of cross-examination" (People v. Wesley, 140 Misc. 2d 306, 533 N.Y.S. 2d 643, 644 Albany County Ct. 1988).

Exaggerated claims about the power of the new technology were made in the popular press as well: Warren, S. (1/23/88). DNA 'fingerprints' may identify rapist, Houston Chronicle, p. 1, 12 ("In a rape case, for instance, semen samples taken from a rape victim could be compared to a blood sample from a suspect. If the DNA matches, police know they have the rapist"); Begley, S. (10/26/87). Leaving Holmes in the Dust, Gene prints unravel crime and paternity puzzles, Newsweek, p. 81 ("Genetic fingerprinting offers proof positive").

iii. False positive and false negative errors by DNA laboratories have been documented and discussed. See Ford, S. & Thompson, W. C. (Jan/Feb 1990). A question of identity: Some reasonable doubts about DNA 'fingerprints'. The Sciences (NY Academy of Science), 30(1), 37-43; Lander, E. S. (1989). DNA fingerprinting on trial. Nature, 339, 501-505; Shapiro, M. M. (1991). Imprints on DNA fingerprints. Nature, 353, 121-2; Thompson, W. C. & Ford, S. (1991). The meaning of a match: Sources of ambiguity in the interpretation of DNA prints. In M. A. Farley & J. J.

Harrington (Eds.). Forensic DNA Technology, Chelsea, MI: Lewis Publishers; DNA Technology in Forensic Science, Board on Biology, Commission on Life Sciences, National Research Council, National Academy Press, Washington D.C. 1992, Prepublication manuscript, 4/16/92 ("Presentations that suggest to a judge or jury that DNA typing is infallible are rarely justified and should be avoided," p. S-27).

Some courts have expressed skepticism about DNA frequency statistics as well. See People v. Alt, No. K4-90-1437, Minnesota District Court, Fourth Judicial District, 5/29/92, Order Limiting the Use of DNA Test Results; Commonwealth v. Curnin 565 N.E.2d 440, 445 Mass. 1991;

Commonwealth v. Lanigan 596 N.E.2d 311, Mass. 1992.

The new skepticism has also been documented in the popular press. See Merrifield, B. (6/9/92). Microbiologist challenges results of FBI DNA tests in Moore case. Chicago Tribune, p. 3 Zone D; Kolata, G. (4/14/92). U.S. Panel seeking restriction on use of DNA in courts: Labs Standards faulted: Judges are asked to bar genetic 'fingerprinting' until basis in science is stronger. New York Times, p. A1, A6; Nesmith, J. (9/22/91). Bias charged in DNA 'fingerprints', Emory researcher says technique slanted against defendant. Austin American Statesman; Kolata, G. (2/14/91). Gene test barred as proof in court: DNA fingerprinting requires more scientific scrutiny, Arizona judge rules. New York Times, p. 1; Montgomery, L. (10/14/90). DNA test accuracy on trial: Method is subject to error, critics say. Dallas Times, p. A1, A12; Labaton, S. (6/22/90). DNA fingerprinting is facing showdown at an Ohio Hearing. New York Times, p. A1, B11; Thompson, M. (5/3/89). DNA 'fingerprints' may be smudged: Labs doing genetic matching for police aren't perfect and aren't eager to have their methods scrutinized. Newsday, p. 65.

iv. Although the emphasis here is on DNA matches, the principles apply equally to other forms of identification evidence.

v. A different issue, and one that is not addressed here, is how the genetic evidence should be framed to create an appropriate balance between the risk of convicting an innocent defendant and the risk of setting a guilty defendant free.

vi. Sometimes the discovery of a DNA match between a trace sample and a defendant should have only a minimal impact on one's belief that the defendant is guilty. For example, when there is reason to believe that the trace may have been left by the defendant before or after the commission of the crime, the significance of the reported match is reduced.

vii. Consider the following exchange between an attorney and a DNA expert in one recent Texas case (State v. Bethune, 821 S.W. 2d 222 (Tex.App. 1991), transcript, p. 2327):

Q: Is that correct? So that in the event that the accused sitting in this chair would happen to be White, you're telling the members of this jury that there would [be] a one in 5 billion chance that anybody else could have committed the crime; is that correct?

A: One in 5 billion, correct.

viii. The situation described in case B is not unrealistic. There have been several cases in which large paternity indexes were obtained despite evidence of a successful vasectomy prior to conception. See e.g., Cole v. Cole, 328 S.E.2d 446 (N.C.App. 1985); O'Bannon v. Azar, 435 So.2d 1144 (La.App. 4 cir 1983).

ix. For those of you who discount the vasectomy testimony altogether, you may wish to consider a case C in which an alleged father yields a paternity index of 100, despite the fact that he died several months before conception. In this case, the probability of paternity is extremely low, laboratory evidence notwithstanding.

x. Bayes' theorem is a general method for updating probabilistic beliefs in the face of new evidence. It is based on the tenets of elementary probability theory. The odds form of Bayes' theorem is as follows:

$$\frac{P(H/E)}{P(-H/E)} = \frac{P(H)}{P(-H)} \times \frac{P(E/H)}{P(E/-H)}$$

P(H) and P(-H) refer to the unconditional probabilities that a hypothesis H is true and false respectively. These probabilities are commonly referred to as "prior probabilities" and their ratio is the "prior odds." P(E/H) and P(E/-H) refer to the information value of the evidence E if hypothesis H is true and false respectively. P(E/H) and P(E/-H) are called likelihoods and their ratio is the "likelihood ratio." P(H/E) and P(-H/E) are the probabilities that the hypothesis H is true and false in light of the evidence E. Their ratio is the "posterior odds," and it may be computed by multiplying the prior odds by the likelihood ratio.

In paternity cases, the 50% prior probability assumption is P(H), the paternity index is the likelihood ratio, and the odds in favor of paternity are the posterior odds ratio. Now, because the sum of two mutually exclusive and exhaustive outcomes equals 100%, if P(H)=50%, then P(-H)=50%. And when P(H)=50%, the prior odds ratio is 1, and the odds in favor of paternity are identical to the paternity index.

Returning to the example in the text, the odds in favor of paternity are:

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Error! Main Document Only.posterior odds of paternity

correspond with a probability of paternity of 99.9%. Under the 50% prior probability assumption, the probability of paternity would be identical for Cases A and B in the text, despite their obvious evidentiary differences.

xi. Professor David Kaye has criticized the use of a 50% prior probability estimate as well. See Kaye, D. H. (1989). The probability of an ultimate issue: The strange case of paternity testing. Iowa Law Review, 75, 75-109; Kaye, D. H. (1988). Plemel as a primer on proving paternity. Willamette Law Review, 24, 867-883. Unfortunately, a majority of jurisdictions encourage, allow, or require (!) the 50% prior probability estimate in paternity cases.

xii. An argument could be made that the true prior probability of paternity is substantially higher than 50% based on studies showing that approximately 70% of alleged fathers are, in fact, "guilty" of paternity (see Ellman, I. M. & Kaye, D. (1979). Probabilities and proof: Can HLA and blood group testing prove paternity? New York University Law Review, 54, 1131-1162, 1150). But Ellman and Kaye (1979) argue that there are serious legal problems associated with using this general base rate as an estimate of an alleged father's prior probability of paternity (p. 1151-2).

xiii. More than three hundred jury-eligible students enrolled in graduate and undergraduate business law classes at the University of Texas participated as mock jurors in these experiments. Subjects were provided with a one page description of a hypothetical murder case and asked to (a) render a verdict, and (b) estimate the numerical probability that the defendant killed the victim. Subjects were told that the evidence must satisfy them beyond a reasonable doubt in order to render a guilty verdict.

Brief summaries of prosecution and defense arguments were included. Most subjects read that forensic tests on a blood trace detected beneath the victim's fingernail could not rule out the defendant as a possible source of the evidence. Next, the test results were presented in terms of either a random match or source probability, and included probability values at either the one in one thousand or one in one billion levels. Subjects who did not receive forensic identification evidence were in the control group.

The statistics provided in Figure 1 are the result of a loglinear analysis on the verdicts. The probability data, which were analyzed using analysis of variance, reflected a similar pattern. A complete experimental report is in preparation and may be obtained from the author.

xiv. The hypothetical case used was purposefully designed to reflect a rough balance of incriminating and exculpatory evidence. Consequently, the conviction rates may be lower than might be expected in a typical murder case involving DNA evidence.

xv. The National Academy of Sciences initiated a study in January, 1990 to examine the complex issues surrounding DNA evidence. The final report, issued in April, 1992, recommended the use of more conservative techniques for estimating random match probabilities. Unless offset by an increase in the number of genetic characteristics examined, this will reduce the number of extremely small probability values produced by DNA laboratories. See DNA Technology in Forensic Science, Board on Biology, Commission on Life Sciences, National Research Council, National Academy Press, Washington D.C. April, 1992, chapter 3.

xvi. Although the potential source population is the population of interest, the suspect population will often be an acceptable substitute. The exception occurs when there are members of the potential source population who, for whatever reason, happen to be ruled out as suspects in the crime.

xvii. Probes are fragments of radioactive DNA material that have been designed to attach to particular sections of DNA. After treatment, each probe produces one or two bands (resembling supermarket bar codes) that represent distinctive parts of a person's DNA pattern.

xviii. The general formula for computing the probability of a match between brothers is $(.25 + .5p + 2p^2)^k$ where p = the average probability that two alleles will match, and k = the number of probes sites examined (DNA Technology in Forensic Science (1992), p. 3-16). For DNA profiles consisting entirely of rare alleles, p approaches zero and there is a 1/4 probability that two brothers will share a set of alleles at each probe site. In these cases, $P(\text{At least 1 of 2 brothers will also match on all 3 probes}) = 1 - P(\text{Neither brother matches on all 3 probes}) = 1 - [1 - (1/4)^3]^2 = 1 - (63/64)^2 = 3.1\%$. For alleles that are less rare, p is greater than zero and the probability that two brothers will share a set of alleles at each probe site is greater than 1/4. In these cases, $P(\text{At least 1 of two brothers will also match on all 3 probes})$ may be considerably greater than 3.1%.

xix. Wherever possible, DNA analyses should be performed on the blood of close relatives who are members of the suspect population.

xx. See Lempert, R. (1991). Some caveats concerning DNA as criminal identification evidence: With thanks to the Reverend Bayes. Cardozo Law Review, 13, 303-341.

xxi. Devlin, B. Risch, N. & Roeder, K. (1992). Forensic inference from DNA fingerprints. Journal of the American Statistical Association, 87, 337-350; Risch & Devlin (1992). On the probability of matching DNA fingerprints. Science, 255, 717-720; Lewontin, R. C. & Hartl, D. L. (12/20/91). Population genetics in forensic DNA typing. Science, 254, 1745-1750; Chakraborty, R. & Kidd, K. (12/20/91). The utility of DNA typing in forensic work. Science, 254, 1735-1739; Devlin, B., Risch, N. & Roeder, K. (1990). No excess of homozygosity at DNA fingerprint loci. Science, 249, 1416-1420; Cohen, J. E. (1990). DNA Fingerprinting for forensic identification: Potential effects on data interpretation of subpopulation heterogeneity and band number variability. American Journal of Human Genetics, 46, 358-368; Cohen, J. E. (1990). DNA fingerprinting: What (really) are the odds? Chance, 3(3), 26-32; Lander, E. (1989). DNA fingerprinting on trial. Nature, 339, 501-505.

xxii. State v. Jones, 569 So. 2d 1234, Fla. 1990, transcript, p. 677 ("[I]t is technically impossible to make a false/positive identification"); State v. Kelly, 792 S.W.2d 579 Tex.App. Forth Worth 1990, transcript p. 919 ("There is no way to get a false positive with this technology"); State v. Yelder, No. 3 Div 212 Court of Criminal Appeals, Ala. 1991, transcript, p. 84 ("[T]here's no way to make or create a false positive with this test"); State v. Pierce, 597 N.E.2d 107 Ohio, 1992, transcript, p. 431 ("You can't get a false positive"); State v. Cobey, 559 A. 2d 391, 392 Md.App. 1989, (An Incorrect match is an impossible result); People v. Fishback, 829 P.2d 489, 495 Colo.App. 1991, (DNA analysis is "failsafe").

xxiii. Ford, S. & Thompson, W. C. (Jan/Feb, 1990). A question of identity: Some reasonable doubts about DNA 'fingerprints.' The Sciences (NY Academy of Science), 30(1), 37-43, 41; Thompson, W. C. & Ford, S. (1991). The meaning of a match: Sources of ambiguity in the interpretation of DNA prints. In M. A. Farley & J. J. Harrington (Eds.), Forensic DNA Technology (pp. 93-152). Chelsea, MI: Lewis Publishers, p. 144, fn. 122.

xxiv. I mention the possibility of fraud not because it is likely or well-documented, but because it will always be a possibility, particularly in situations where the incentive to produce a match is high.

xxv. See Saks, M. J. & Koehler, J. J. (1991). What DNA "fingerprinting" can teach the law about the rest of forensic science. Cardozo Law Review, 13, 361-372, 369-70.

xxvi. In a letter to the author dated August 3, 1992, the Chair of the CACLD studies, Margaret Kuo, disputes the characterization of one these two errors as a false positive error, preferring to regard it as more similar to a false negative error. The CACLD report classified this particular error as an "incorrect match," which resulted when "a semen stain [was reported] as DQ-alpha type 3,3 instead of the correct type 1.3,3" (California Association of Crime Laboratory Directors, DNA Committee Report #6, October 1, 1988, p. 5). Because there are only 21 possible classifications using this method (Kuo letter, p.1), this type of error can easily lead to both false positives and false negative errors in actual case work. For further discussion of errors by DNA laboratories in proficiency tests and actual case work, see DNA Technology in Forensic Science (1992), *Supra*, p. 3-17 - 3-18; Giannelli, P. C. (1991). Criminal discovery, scientific evidence and DNA. Vanderbilt University Law Review, 44, 791-825, 794-797; Thompson & Ford (1991), *Supra*, 141-6; Anderson, A. (1989). DNA fingerprinting on trial. Nature, 342, 844.

xxvii. Data collected by Collaborative Testing Services (CTS) indicate that at least three, and possibly four, out of thirty-eight DNA laboratories committed some form of false positive error on a non-blind proficiency test that included two matching samples. There were approximately 75 match declarations in this study, three of which were incorrect. This yields a false positive error rate of 4.0%.

Two comments about the CTS proficiency test report are in order. First, CTS does not believe that their proficiency tests reflect "an overview of the quality of work performed in the profession" (DNA Profiling, Report No. 91-15, Introduction). Second, my interpretation of the CTS data is different from CTS's interpretation. CTS concludes that "there were no false matches" (p. 2). But I found that incorrect matches were made by laboratories 1504, 1528, 1532, and, possibly, 1518.

xxviii. The reluctance of the FBI to make the results of its internal proficiency tests public is documented by Thompson and Ford (1991), *Supra*, p. 145.

xxix. False negative errors (i.e., false exclusions) can be as serious as false positive errors for several reasons. First, rapists, robbers and killers may be returned to the streets to harm other innocent people when DNA laboratories mistakenly exclude them as possible sources of recovered trace evidence. Second, if the DNA sample is used up during testing (a frequent occurrence) in cases involving false exclusions, an innocent person may then be arrested and convicted (without DNA evidence). Thus, a false negative error by a DNA laboratory can easily lead to the erroneous conviction of an innocent defendant. The plausibility of this scenario is heightened by the fact that DNA evidence is often used in high profile cases in which there is pressure to obtain a conviction.

xxx. Dizon, L. (6/30/92). DNA data helps convict Buena Park man of 8 rapes. Los Angeles Times, Part B, p. 4 ("The DNA evidence was overwhelming. The fact that there were nine sets of [DNA sample patterns] and they all match with Mr. Harris--that's just impossible to defend against"; "Without DNA evidence, there clearly was no case. We became numbed by the number of witnesses and the story they had to tell, but it wasn't the great decider of the case."); Thompson, M. (5/3/89). DNA 'fingerprints' may be smudged: Labs doing genetic matching for police aren't eager to have their methods scrutinized. Newsday, p. 65 ("You can't really argue with science"; the DNA evidence "was very conclusive the way the experts explained it.").