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Forensic DNA Evidence

The Myth of Infallibility

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PROMOTERS OF FORENSIC DNA testing have claimed from the beginning that DNA evidence is virtually infallible.¹ In advertising materials, publications, and courtroom testimony they have claimed that DNA tests produce either the right result or no result. These claims took hold early in appellate-court opinions, which often parroted promotional hyperbole. They were bolstered by the impressive “random-match probabilities” presented in connection with DNA evidence, which suggest that the chances of a false match are vanishingly small. They were reinforced in the public imagination by news accounts of postconviction DNA exonerations. Wrongfully convicted people were shown being released from prison, while guilty people were brought to justice, all on the basis of DNA tests. With prosecutors and advocates for the wrongfully convicted both using DNA evidence successfully in court, who could doubt that it was in fact what its promoters claimed: the gold standard, a “truth machine”?²

The rhetoric of infallibility proved helpful in establishing the admissibility of forensic DNA tests and persuading judges and jurors of its epistemic authority.³ It has also played an important role in the promotion of government DNA databases.⁴ Innocent people have nothing to fear from being included in a database, promoters claim. Because the tests are infallible, the risk of a false incrimination must necessarily be nil. One indication of the success and influence of the rhetoric of infallibility is that until quite recently concerns about false incriminations played almost no role in policy discussions. For example, David Lazer’s otherwise excellent edited volume, *DNA and the Criminal Justice System*, which offers a broad assessment of ways in which DNA evidence is transforming the justice

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system, says almost nothing about the potential for false incriminations.⁵ The infallibility of DNA tests has, for most purposes, become an accepted fact—one of the shared assumptions underlying the policy debate.

In 2009 the National Research Council (NRC) released a scathing report on the status of forensic science. The report found serious deficiencies in the scientific foundations of many forensic science disciplines. It also found that procedures used for interpretation lack rigor, that analysts routinely take inadequate measures to avoid error and bias, and that they testify with unwarranted certainty. But the report pointedly excluded DNA testing from these criticisms. It held DNA testing up as the shining exception—an example of well-grounded forensic science that other forensic disciplines should emulate—further reinforcing DNA's status as a gold standard.⁶

In this chapter I will challenge the assumption that DNA tests are infallible. I will show that errors in DNA testing occur regularly and that DNA evidence has falsely incriminated innocent people, causing false convictions. Although I agree with the 2009 NRC report's conclusion that DNA testing rests on a stronger scientific foundation than most other forensic science disciplines, I will argue that many of the problems identified in the NRC report also apply to DNA evidence. In particular, DNA analysts take inadequate steps to avoid bias and to assess the risk of error, and they frequently overstate the statistical value of test results. Although DNA tests undoubtedly incriminate the correct person in the great majority of cases, the risk of false incrimination is high enough to deserve serious consideration in public policy debates, particularly in debates about expansion of DNA databases and debates about the need for governmental oversight of forensic laboratories. My key point is that the risk of error is higher than it needs to be. I will argue that forensic laboratories often compromise scientific rigor and quality control in order to achieve other goals, and they sometimes suppress evidence of problems in order to protect their credibility and maintain the public perception of DNA's infallibility.

Erroneous Matches

When DNA evidence was first introduced, a number of experts testified that false matches were impossible in forensic DNA testing. The claim that DNA tests are error free has been a key element of the rhetoric of infallibility surrounding DNA evidence. According to Jonathan Koehler, these experts engaged in “a sinister semantic game” in which they distinguished error by the test itself from error by the people administering

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and interpreting the test. They acknowledged (if pressed) that human *error* could produce false reports of DNA matches, but they emphasized that the tests themselves are error free.⁷

Sinister or not, the distinction between human error and test error is artificial and misleading, given that error-prone humans are necessarily involved in conducting and interpreting DNA tests. For those who need to assess the value of DNA evidence, such as judges, jurors, and policy makers, what matters is not whether errors arise from human or technical failings, but how often errors occur and what steps are necessary to minimize them.

The 2009 NRC report agreed that it is vital to know the error rate of forensic tests. It recognized that errors in DNA testing can occur in two ways: “The two samples might actually come from different individuals whose DNA appears to be the same within the discriminatory capability of the tests, or two different DNA profiles could be mistakenly determined to be matching.” The report declared that “both sources of error need to be explored and quantified in order to arrive at reliable error rate estimates for DNA analysis.”⁸ This is certainly true. But I believe that the NRC report erred when it went on to assert that sufficient evidence is now available to assess the probability of a false match in DNA testing. One of the reasons that DNA testing is stronger than other forensic disciplines, according to the NRC report, is that “the probabilities of false positives have been explored and quantified in some settings (even if only approximately).”⁹ But the NRC report provided no citations to support this assertion, and I know of none. The only quantification of error rates in DNA testing that I know of concerned proficiency-testing errors in the late 1980s, which have little relevance to current practices.¹⁰ I believe that the NRC report confused rhetoric with reality when it discussed this issue.

What little we know about the potential for error in DNA testing comes almost entirely from anecdotal reports about false matches. These reports are sufficiently numerous to refute claims that errors are extremely rare or unlikely events. They are also useful for illustrating the ways in which errors can occur. But anecdotal data do not provide an adequate basis for assessing the rate of error because it is impossible to know what proportion of the errors in casework are detected—the errors we know about may be the tip of an iceberg of undetected or unreported error.

Types of Errors

One cause of false DNA matches is cross-contamination of samples. Accidental transfer of cellular material or DNA from one sample to another

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is a common problem in laboratories and can lead to false reports of a DNA match between samples that originated from different people. Scotland's High Court of Justiciary quashed a conviction in one case in which the convicted man (with the help of sympathetic volunteer scientists) presented persuasive evidence that the DNA match that incriminated him arose from a laboratory accident.¹¹ Cross-contamination is also known to have caused a number of false cold hits. For example, while the Washington State Patrol Crime Laboratory was conducting a "cold-case" investigation of a long-unsolved rape, it found a DNA match to a reference sample in an offender database, but it was a sample from a juvenile offender who would have been a toddler at the time the rape occurred. This prompted an internal investigation at the laboratory that concluded that DNA from the offender's sample, which had been used in the laboratory for training purposes, had accidentally contaminated samples from the rape case, producing a false match.¹² Similar errors leading to false database matches have been reported at forensic DNA laboratories in California, Florida, and New Jersey, as well as in New Zealand and Australia.¹³ Three separate cases have come to light in which cross-contamination of samples at the Victoria Police Forensic Services Centre in Melbourne caused false cold hits. Two of those cases led to false convictions.¹⁴

Perhaps the most telling contamination incident occurred in Germany, where police invested countless hours searching for a mysterious woman known as the "Phantom of Heilbronn" whose DNA profile was found in evidence from a surprising variety of crimes, from murder to larceny. Her DNA was found on "guns, cigarette packs, even nibbled biscuits at crime scenes." Police sought public assistance in identifying this menace to society, and a bounty of 300,000 euros was placed on her head. It turned out that the woman in question was not a criminal at all but an employee involved in manufacturing the cotton swabs that crime laboratories use to collect DNA from crime scene samples. Accidental contamination of crime-scene samples with her DNA (which was on the swabs) caused her to be falsely implicated in dozens of crimes.¹⁵

A second potential cause of false DNA matches is mislabeling of samples. In 2011 the Las Vegas Metropolitan Police Department acknowledged that a mix-up of DNA samples in its forensic laboratory had caused a false conviction. The lab mistakenly switched reference samples of two men who were tested in connection with a 2001 robbery. One of the men may well have been involved in the robbery—his DNA profile matched an evidentiary sample from the crime scene. Because of the sample switch, however, this suspect was mistakenly excluded while the

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second man was falsely linked to the crime. Although the police now acknowledge that he was innocent, the second man was convicted and served nearly four years in prison. The error came to light when the first man's DNA profile was entered into a government offender database after he was convicted of an unrelated crime in California, and it produced a cold hit to the crime-scene sample from the 2001 Las Vegas robbery. When investigators realized that the Las Vegas lab had earlier excluded the same man as a source of that sample and had matched the sample to a different man, they realized that an error had occurred.¹⁶

Similar sample-labeling errors have caused false DNA incriminations in cases in California and Pennsylvania, as well as in an earlier case in Las Vegas.¹⁷ These cases came to light during the judicial process and before conviction, but only because of fortunate happenstances. There have also been reports of systemic problems with sample labeling in Australia. A review of DNA testing by an ombudsman in New South Wales discovered that police had incorrectly transferred forensic data to the wrong criminal cases in police computer records, which on two occasions produced false DNA database matches that led to people being incorrectly charged with a crime.¹⁸ One man was convicted before the error was discovered. Doubt was also cast on a number of convictions in Queensland when a forensic scientist who had previously worked for a state forensic laboratory publicly expressed concerns about the reliability of the lab's work. He told the *Australian* newspaper that it was not uncommon for the lab to mix up DNA samples from different cases. He said that although many such errors were caught, sample limitations made it impossible to resample or retest in some questionable cases.¹⁹

A sample-switch error caused a tragic delay in apprehension of a man who is believed to be the notorious Night Stalker, a serial rapist who committed over 140 sexual assaults in London. Although police became suspicious of this man relatively early during their investigation of the attacks, they did not arrest him because a DNA-testing error involving a switch of reference samples caused him falsely to be excluded as the source of biological samples found on the crime victims. The error caused a "match" to another man with the same name, but he had a solid alibi. The Night Stalker's crime spree continued for months until police eventually realized that reference samples of the two men had been switched.²⁰

A third potential cause of false DNA matches is misinterpretation of test results. Laboratories sometimes mistype (i.e., assign an incorrect DNA profile to) evidentiary samples. If the incorrect evidentiary profile happens to match the profile of an innocent person, then a false incrimination may result. Mistyping is unlikely to produce a false match in cases

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where the evidentiary profile is compared with a single suspect, but the chance of finding a matching person is magnified (or, more accurately, multiplied) when the evidentiary profile is searched against a database.

A false cold hit of this type occurred in a Sacramento, California, rape case. A male DNA profile was developed from a swab of the victim's breast. The profile was searched against a California database. The search produced a cold hit to the profile of a man who lived in the Sacramento area, but the resulting police investigation apparently raised doubt about his guilt.²¹ At that point a laboratory supervisor reviewed the work of the analyst who had typed the evidence sample. According to a report issued by the laboratory director, the supervisor determined that the analyst had "made assumptions reading and interpreting the profile of the breast swab sample that were incorrect" and "had interpreted the profile as being a mixture of DNA from a male and female, when in fact the mixture was of two males."²²

Interpretation of DNA mixtures can be challenging under the best of circumstances, but it is particularly difficult when the quantity of DNA is limited, as was true in the Sacramento case. Under these conditions DNA tests often fail to detect all of the contributors' genetic alleles (a phenomenon known as "allelic dropout") and can sometimes detect spurious or false alleles (a phenomenon known as "allelic drop-in").²³ Determining which alleles to assign to which contributor can also be difficult, particularly when there is uncertainty about the number of contributors and whether alleles are missing. Interpretations made under these conditions are inherently subjective and hence are subject to error.²⁴

A 2011 study highlighted the degree of subjectivity involved in DNA mixture interpretation and the potential it creates for false incriminations. Itiel Dror and Greg Hampikian asked seventeen qualified DNA analysts from accredited laboratories to evaluate independently the DNA evidence that had been used to prove that a Georgia man participated in a gang rape. The analysts were given the DNA profile of the Georgia man and the DNA test results obtained from a sample collected from the rape victim, but they were not told anything about the underlying facts of the case (other than scientific details needed to interpret the test results). The analysts were asked to judge, on the basis of the scientific results alone, whether the Georgia man should be included or excluded as a possible contributor to the mixed DNA sample from the victim. Twelve of the analysts said that the Georgia man should be excluded, four judged the evidence to be inconclusive, and only one agreed with the interpretation that had caused the Georgia man to be convicted and sent to

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prison—that is, that he was included as a possible contributor to the DNA mixture. The authors found it “interesting that even using the ‘gold standard’ DNA, different examiners reach conflicting conclusions based on identical evidentiary data.” Noting that the analyst who testified in the Georgia case had been exposed to investigative facts suggesting that the Georgia man was guilty, they suggested that this “domain irrelevant information may have biased” the analyst’s conclusions.²⁵ The potential for bias in DNA testing and ways to deal with it are discussed further in “Gross Negligence, Scientific Misconduct, and Fraud” below.

How Errors Are Detected

Proving that an error has occurred in DNA testing is not always easy. DNA evidence has such authority that doubts often arise about other evidence that contradicts it. Consider, for example, the case of Timothy Durham, who was accused of raping a young girl in Oklahoma City. At his trial Durham produced eleven alibi witnesses, including his parents, who all testified that he was with them attending a skeet-shooting competition in Dallas at the time at which the rape occurred. Durham also produced credit-card receipts for purchases he made in Dallas on that day. But the prosecution had something stronger: the young victim’s identification and DNA evidence. Durham was convicted and sentenced to 3,000 years in prison.²⁶

How can we know whether a DNA test is wrong? One way is to do additional DNA testing. Luckily for Durham, a portion of the incriminating evidence was available, and his family could afford to have it retested. The new DNA test not only excluded him as the source of the semen found on the victim but also showed that the previous DNA test had been misinterpreted. Durham is one of three men in the United States who have been convicted and sent to prison on the basis of erroneous DNA matches but later exonerated by additional DNA testing. (The other two are Josiah Sutton, who was falsely incriminated because of an error in interpretation, and Gilbert Alejandro, who was falsely incriminated because of fraud by a DNA analyst.)²⁷ It is important to understand, however, that retesting cannot catch every error. Some errors arising from cross-contamination of evidence, mislabeling of samples, and coincidental matches are undetectable during retesting because the new tests simply replicate the erroneous result of the first. In some cases the initial tests exhaust the available evidentiary samples and leave nothing to retest. And many defendants who are incriminated by DNA evidence find it difficult to obtain a retest even when evidence is available.²⁸

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A second way DNA-testing errors come to light is when laboratories make an admission of error, typically by withdrawing an erroneous laboratory report and issuing a revised report with different results. An interesting example occurred in Philadelphia in 2000. The city's crime laboratory tested samples from a rape victim and from a suspect named Joseph McNeil. The lab's initial report stated that DNA profiles matching McNeil's were found in three evidentiary samples: a vaginal swab, a cervical swab, and a seminal stain on the victim's underwear. McNeil was charged with rape and taken into custody. Although McNeil adamantly denied the crime and rejected a favorable plea bargain, his lawyer could not conceive that a DNA tests could be wrong about three different samples. After an independent expert noted some discrepancies in the lab report, however, he sought access to his client's DNA for an independent test. At that point the police lab realized that an error had been made and issued a new report exonerating McNeil. In its initial test the lab had mixed up the reference samples from McNeil and the victim. What the lab had mistakenly reported as McNeil's profile in samples found on the victim was in fact the victim's profile.²⁹

A third way laboratory errors come to light is through proficiency testing. In accredited DNA laboratories analysts must take two proficiency tests per year. Generally this involves comparison of samples from known sources. The analysts typically know that they are being tested but are not told the correct results until after they have reported their conclusions. These tests have been criticized as too easy to detect problems that might arise in actual casework. Nevertheless, errors occasionally occur, generally arising from cross-contamination or sample-labeling problems, sometimes from misinterpretation of partial or degraded DNA profiles.³⁰ Many laboratories treat proficiency-test results as confidential records, which makes details about the frequency and nature of errors difficult to obtain.

Perhaps the best source of information on the nature and frequency of laboratory foul-ups is "contamination logs" and "corrective action files" that are maintained by some DNA laboratories. Guidelines issued by the FBI's DNA Advisory Board in 1998 recommend that forensic DNA laboratories "follow procedures for corrective action whenever proficiency-testing discrepancies and/or casework errors are detected" and "maintain documentation for the corrective action."³¹ Although many laboratories have ignored these guidelines, some laboratories (probably the better ones) have kept records of instances in which, for example, samples are mixed up or DNA from one sample is accidentally transferred to another sample, causing a false match. These records are generally treated as con-

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fidential but occasionally become public when they are released under court order as part of the discovery process in criminal cases, or when news organizations file public records act requests for them.³²

Some labs have voluminous corrective action files that show that errors occur regularly. Files from Orchid-Cellmark's Germantown, Maryland, facility, for example, showed dozens of instances in which samples were contaminated with foreign DNA or DNA was somehow transferred from one sample to another during testing. Files from the District Attorney's Crime Laboratory in Kern County, California, a relatively small lab that processes a low volume of samples (probably fewer than 1,000 per year), showed an array of errors during an eighteen-month period, including multiple instances in which (blank) control samples were positive for DNA, an instance in which a mother's reference sample was contaminated with DNA from her child, several instances in which samples were accidentally switched or mislabeled, an instance in which an analyst's DNA contaminated samples, an instance in which DNA extracted from two different samples was accidentally combined in the same tube, falsely creating a mixed sample, and an instance in which a suspect tested on two different occasions did not match himself (probably because of another sample-labeling error).³³

In 2008 the *Los Angeles Times* obtained corrective action files from several California labs and found many instances of cross-contamination, sample mislabeling, and other problems. For example,

Between 2003 and 2007, the Santa Clara County [California] district attorney's crime laboratory caught 14 instances in which evidence samples were contaminated with staff members' DNA, three in which samples were contaminated by an unknown person and six in which DNA from one case contaminated samples from another. The records also revealed three instances in which DNA samples were accidentally switched, one in which analysts reported incorrect results and three mistakes in computing the statistics used in court to describe the rarity of a DNA profile.³⁴

The errors documented in these files have typically been detected by laboratory staff—often, but not always, before a mistaken report was issued. Consequently, forensic scientists sometimes argue that the problems recorded in corrective action files are “not really errors” because they were caught by the lab. They argue, with some justification, that these files are evidence that the laboratory's quality-control system is working to detect and correct errors when they occur. The problem with this analysis is that errors often are caught because of circumstances that are not always present when such errors occur. It will not always be the case, for

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example, that mistaken cold hits will implicate offenders who were too young to have committed the crime, nor will it always be the case that cross-contamination of DNA samples will produce unexpected results that flag the error. If DNA from a suspect is accidentally transferred into a “blank” control sample, it is obvious that something is wrong; if the suspect’s DNA is accidentally transferred into an evidentiary sample, the error will not necessarily be obvious because there is another explanation—that the suspect contributed DNA to the evidentiary sample. The same processes that cause detectable errors in some cases can cause undetectable errors in others. Although laboratories should be encouraged to keep careful records of “unexpected events” and should be commended for doing so, the extensive catalogs of error recorded in existing files can hardly be taken as reassuring evidence that laboratory quality-control systems are working. They are a warning signal that we need to worry about similar errors that labs do not catch, although the frequency of such errors is obviously difficult to estimate.

Moreover, there is great variation among labs in the size and scope of their corrective action files. Some labs (again, probably the better ones) have extensive files documenting numerous problematic incidents and steps taken to deal with them, but other labs either fail to maintain such files or claim that their files are empty because they have never, ever had a problem requiring corrective action. Given the high frequency of incidents warranting corrective action in some very reputable DNA laboratories, it strains credibility to believe that such incidents never occur in other laboratories. A more likely explanation is that these labs choose not to document errors in order to maintain a pretense of infallibility.

An embarrassing episode at the San Francisco police crime laboratory, which came to light in 2010, supports this interpretation. An anonymous person sent letters to the San Francisco Public Defender’s Office and to the American Society of Crime Laboratory Directors’ Laboratory Accreditation Board (ASCLD-LAB), which had issued a “certificate of accreditation” to the San Francisco laboratory. The letters alleged that laboratory managers had inappropriately covered up a sample-switch error that had occurred when the lab was processing DNA evidence in a homicide case. In response to an inquiry from the ASCLD-LAB, the laboratory managers wrote a letter denying that any such error had occurred. During a subsequent inspection of the laboratory, however, representatives of the ASCLD-LAB found evidence that the error had indeed occurred and that the laboratory staff had falsified laboratory records to cover it up. It is not clear that the error materially affected the test results in the homicide case. Nevertheless, the lab managers seemed intent on

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preventing defense lawyers from discovering that a problem had occurred. In order to avoid disclosing a seemingly minor problem, the lab managers contravened an important quality-control procedure recommended by the FBI's DNA Advisory Board and lied to their accrediting agency.³⁵ This is a clear instance of a laboratory putting the appearance of infallibility ahead of good laboratory practice (and basic honesty). Similar incidents in which laboratory managers suppressed evidence of DNA-testing errors have been reported at the Maine State Police Crime laboratory, the U.S. Army Criminal Investigation Laboratory, the North Carolina State Bureau of Investigation, and the Houston Police Department Crime Laboratory.³⁶

Gross Negligence, Scientific Misconduct, and Fraud

Since the mid-1990s news reports have offered a continuing stream of stories about gross negligence, scientific misconduct, and fraud in forensic laboratories.³⁷ A number of these problems have affected DNA testing, including the following:

- The Houston Police Department shut down the DNA and serology section of its crime laboratory in 2003 after a television exposé revealed serious deficiencies in the lab's procedures that were confirmed by an outside audit. Two men who were falsely convicted on the basis of botched lab work were released from prison after subsequent DNA testing proved their innocence. In dozens of cases DNA retests by independent laboratories failed to confirm the conclusions of the Houston lab. An independent investigation found that the laboratory had failed for years to employ proper scientific controls, had routinely misrepresented the statistical significance of DNA matches, and in some cases had suppressed exculpatory test results.³⁸ The unit reopened under new management in 2006. In 2008, however, the head of the DNA unit was forced to resign in the face of allegations that she had helped DNA analysts in the unit cheat on proficiency tests.³⁹
- In Virginia postconviction DNA testing in the high-profile case of Earl Washington Jr. (who was falsely convicted of capital murder and came within hours of execution) contradicted DNA tests on the same samples performed earlier by the State Division of Forensic Sciences. An outside investigation concluded that the state lab had botched the analysis of the case, had failed to follow proper procedures, and had misinterpreted its own test results.⁴⁰ In a second

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capital case postconviction reviews found that the state lab had overstated the value of the DNA evidence that incriminated the defendant and had improperly dismissed as inconclusive results that were strongly exculpatory.⁴¹ In a third capital case the state analyst grossly overstated the statistical significance of a DNA match.⁴²

- In North Carolina the *Winston-Salem Journal* published a series of articles in 2005 documenting numerous DNA-testing errors by the North Carolina State Bureau of Investigation.⁴³ In 2010 an independent audit of this lab by two FBI laboratory supervisors found that lab analysts had withheld or misrepresented the results of tests for the presence of blood in more than 200 cases.⁴⁴
- A multi-year investigation by the McClatchy news organization, beginning in 2005, revealed that an analyst at the U.S. Army Criminal Investigation Laboratory had a history of cross-contaminating samples, had violated laboratory protocols, and had falsified test results. An independent investigation found significant problems in one-quarter of all the cases this analyst had handled. Laboratory managers failed to disclose these problems to lawyers involved in the relevant cases and took other steps to cover up these problems.⁴⁵
- DNA analysts at a number of other laboratories have been fired for falsification of test results, including labs operated by the FBI, Orchid-Cellmark, the Office of the Chief Medical Examiner in New York City, and Bexar County, Texas. Fraud allegations were also leveled against an analyst at the Chicago Police Department Crime Laboratory.⁴⁶

The most common form of misconduct in DNA testing is shading of scientific findings to make them more coherent or more consistent with what the analyst believes to be true. For example, the analyst may fail to report minor (or seemingly minor) discrepancies between profiles, problems with controls, or other inconsistencies among findings and may justify this as an effort to avoid confusing lawyers and jurors with “irrelevant” information. The problem with this practice is that the analyst’s conception of what is true (and therefore what is “relevant” and “irrelevant”) is often colored by investigative facts communicated by police officers and prosecutors. When I asked one analyst to explain why she had decided to disregard a discrepancy between two “matching” DNA profiles in a rape/robbery case, she responded: “I know it’s a good match—they found the victim’s purse in [the defendant’s] apartment.”

DNA analysts are often well informed about the underlying facts of the cases they process—as those facts are reported by the police. In cases

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I have reviewed, there often are comments in the case file such as the following (from a rape case in Virginia): “This [man] is suspected in other rapes but they can’t find the [victims]. Need this case to put [him] away.” Or this, from an aggravated assault case in California: “Suspect—known crip gang member—keeps ‘skating’ on charges—never serves time. This robbery he gets hit in head with bar stool—left blood trail. Miller [the deputy district attorney who was prosecuting the case] wants to connect this guy to scene w/DNA.”

Information of this type may well influence analysts’ interpretations of test results, particularly in cases where the results are somewhat ambiguous or otherwise problematic. Because interpretive bias of this kind can operate unconsciously, I hesitate to label it scientific misconduct, although the failure of forensic scientists to implement rigorous procedures to guard against such bias is surely bad scientific practice. The 2009 NRC report recognized that interpretive bias is a significant problem in forensic science as a whole but did not acknowledge that it is also a problem for forensic DNA testing.

Procedures have been proposed for reducing bias by temporarily “blinding” analysts to unnecessary information when they are analyzing and interpreting DNA tests, but the forensic science community has yet to accept that such procedures are necessary or even desirable. Part of the problem is confusion over the forensic scientist’s role in the judicial process. Some believe that it is appropriate to consider a broad range of investigative facts (such as the purse in the apartment) in drawing conclusions about forensic evidence. As one put it, “if this ‘bias’ leads to the truth, is it really a bias?” Others believe (implausibly) that they can control any bias by act of will.⁴⁷

Bias shades into intentional scientific misconduct when analysts begin suppressing or misrepresenting their findings. An independent investigation of the Houston Police Department Crime Laboratory found many instances of this type.⁴⁸ Some of the problems in Virginia and North Carolina and at the U.S. Army DNA laboratory also fall into this category. The guilty analysts appear to have been motivated partly by a desire to help police and prosecutors convict the “right” people and partly by a desire to cover up shortcomings in their own scientific work.

Production pressures are also an important factor. Several of the analysts who were fired for fraud were caught falsifying laboratory records in order to cover up the failure of scientific controls in their assays, and particularly to hide the presence of positive results in blank samples that are included in the assays to detect contamination. As discussed earlier, cross-contamination of samples is a common event in forensic laboratories, but

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it can be embarrassing for analysts, particularly if it happens too often, because it raises questions about their technical competence and care in handling samples. Furthermore, because the entire assay must be redone if a control sample signals the presence of contaminating DNA (even if the contamination appears to have affected only the control), these incidents are important setbacks for an analyst trying to keep up with a demanding workload.⁴⁹ There is evidence that the army analyst who falsified results was striving to maintain his reputation as the most productive analyst in the laboratory.⁵⁰ A colleague of the Orchid-Cellmark analyst who was fired for falsifying results told me that the analyst in question strove always to be at or near the top of a chart posted on the laboratory wall that tracked analysts' productivity (measured by samples and cases successfully completed).

Analysts working in a pressured environment may be tempted to cut corners in order to keep on schedule and thereby make themselves look good, particularly if they know (or think they know) on the basis of other investigative facts that they have reached the correct conclusion about which samples match. Analysts in the Houston Police Department Crime Laboratory simply dispensed with running blank control samples in their assays, which is clearly a dangerous and unacceptable scientific practice but undoubtedly sped up their work: there is no need to redo assays when controls fail if one has no controls. From misconduct of this sort it is perhaps not a very big step to the more blatant falsifications of analysts like Fred Zain, Joyce Gilchrist, and Pamela Fish, who are alleged to have faked or misrepresented results of entire tests in order to incriminate people they thought were guilty.⁵¹

For a number of years I have urged forensic scientists to adopt blind procedures for interpreting DNA test results. My main concern is with unconscious bias in interpretation, which I believe is a widespread problem. But I believe that blind procedures would also reduce the temptation to falsify DNA data, misrepresent findings in laboratory reports, and ignore evidence of problems in assays. Analysts who do not know whether their tests point to the "right" person will (I believe) be more cautious and rigorous in their interpretations and more honest in acknowledging uncertainty and limitations in their findings.

Coincidental Matches

The impressive numbers that accompany DNA evidence contribute greatly to its persuasive power. Often called random-match probabilities (RMPs), the numbers represent the frequency of a particular DNA pro-

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file in a reference population. Statistician Bruce Weir has estimated that the average probability that two unrelated people will have the same thirteen-locus DNA profile is between 1 in 200 trillion and 1 in 2 quadrillion, depending on the degree of genetic structure in the human population.⁵² Numbers this small make it seem that the chances the wrong person will “match” are unworthy of consideration. But this impression is incorrect for several reasons.

First, RMPs describe only the chances of a random unrelated person having a particular DNA profile; they have nothing to do with the likelihood of the wrong person being reported to match for other reasons, such as cross-contamination of samples, mislabeling of samples, or error in interpreting or recording test results. RMPs quantify the likelihood of one possible source of error (coincidental matches) while ignoring other events that can also cause false incriminations and often are more likely to do so.

Second, extremely low RMPs, like those computed by Weir, apply only in the ideal case in which the lab finds a match between two complete single-source DNA profiles. The evidence in actual cases is often less than ideal. Evidentiary samples from crime scenes frequently produce incomplete or partial DNA profiles that contain fewer genetic alleles (characteristics) than complete profiles and are therefore more likely to match someone by chance. A further complication is that evidentiary samples are often mixtures. Because it can be difficult to tell which alleles are associated with which contributor in a mixed sample, there often are many different profiles (not just one) that could be consistent with a mixed sample, and hence the chances of a coincidental match can be much higher.

To illustrate these points, consider the DNA profiles shown in Table 15.1. Forensic laboratories typically “type” samples using commercial test kits that can detect genetic characteristics (called alleles) at various loci (locations) on the human genome. The most commonly used forensic DNA tests examine loci that contain short tandem repeats (STRs), which are sections of the human genome where a short sequence of genetic code is repeated a number of times. (They are called short *tandem* repeats because these short repeating units occur on both sides of the DNA double helix). Although everyone has STRs, people tend to vary in the number of times the genetic code at each STR repeats itself, and each possible variant is called an allele. Generally there are between six and eighteen possible alleles at each locus. Each person inherits two of these alleles, one from each parent, and the pair of alleles at a particular locus constitutes a genotype. The complete set of alleles detected at all loci for a given sample is called a DNA profile.⁵³

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Profile A in Table 15.1 is a complete thirteen-locus DNA profile, while profiles B and C are partial profiles of the type often found when a limited quantity of DNA, degradation of the sample, or the presence of inhibitors (contaminants) makes it impossible to determine the genotype at every locus. Because partial profiles contain fewer genetic markers (alleles) than complete profiles, they are more likely to match someone by chance.⁵⁴ The chance that a randomly chosen U.S. Caucasian would match the profiles shown in Table 15.1 is 1 in 250 billion for profile A, 1 in 2.2 million for profile B, and 1 in 16,000 for profile C.⁵⁵

Because profiles D and E contain more than two alleles at some loci, they are obviously mixtures of DNA from at least two people. Profile A is consistent with profile D (i.e., every allele in profile A is included in profile D), which means that the donor of profile A could be a contributor to the mixture. But many other profiles would also be consistent. At locus D3S1358, for example, a contributor to the mixture might have any of the following genotypes: 15,16; 15,17; 16,17; 15,15; 16,16; 17,17. Because so many different profiles may be consistent with a mixture, the probability that a noncontributor might by coincidence be included as a possible contributor to the mixture is far higher in a mixture case than in a case with a single-source evidentiary sample. Among U.S. Caucasians approximately 1 person in 790,000 has a DNA profile consistent with the mixture shown in profile D. Thus the RMP for mixed profile D is higher than the RMP for single-source profile A by five to six orders of magnitude. When partial profiles like profiles B and C are also mixtures, the RMPs can be high enough to include thousands, if not millions, of people as possible donors. RMPs greater than 1 in 100 are sometimes reported in such cases.

A third important caveat about extremely low RMPs like those reported by Weir is that they are estimates of the probability of a coincidental match among random individuals who are unrelated to the donor of the sample in question. In actual cases the pool of possible suspects is likely to contain individuals who are related to one another. For example, a man might falsely be accused of a crime that was actually committed by a brother, uncle, or cousin. In such cases the probability of a false incrimination due to a coincidental match is much higher than the RMP might suggest. Consider again profile A in Table 15.1. Although this profile would be found in only 1 in 250 billion unrelated individuals, the probability of finding this profile in a relative of the donor is far higher: 1 in 14 billion for a first cousin; 1 in 1.4 billion for a nephew, niece, aunt, or uncle; 1 in 38 million for a parent or child; and 1 in 81,000 for a sibling. In cases involving partial and mixed profiles, the chances of a coincidental

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Table 15.1 Matching DNA profiles

Profile	STR locus													
	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	
A	15,16	17,18	21,22	13,14	29,30	14,17	11,12	11,12	8,10	11,12	8,11	6,9	11,12	
B	15,16	17,18	13,14	13,14	29,30	11,12	11,12	11,12	8,10	11,12	8,11			
C	15,16	17	13,14	13,14	30	11,12	11	11	8,10					
D	15,16,17	17,18	21,22	13,14,15	29,30	12,13 14,17	11,12	11,12	8,9, 8,9,	11,12	8,9,11	6,7,9	11,12,13	
E	15,16,17	17,18	21,23	13,14,15	29,30	10,12 12,17	11,12	11,12	8,9,10	11,12	8,9			

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match to a relative of the donor can, commensurately, be higher by orders of magnitude than for a complete single-source profile like profile A.

A fourth important caveat about the impressive RMPs that often accompany forensic DNA evidence is that the risk of obtaining a match by coincidence is far higher when authorities search through millions of profiles in a DNA database looking for a match than when they compare the evidentiary profile to the profile of a single individual who has been identified as a suspect for other reasons. As an illustration, suppose that a partial DNA profile from a crime scene occurs with a frequency of 1 in 10 million in the general population. If this profile is compared with that of a single innocent suspect who is unrelated to the true donor, the probability that it will match is only 1 in 10 million. Consequently, if one finds such a match when one tests an individual who is already suspected for other reasons, it seems safe to assume that the match was no coincidence. By contrast, in searches through a database as large as the FBI's National DNA Index System (NDIS), which reportedly contains over 8 million profiles, there are literally millions of opportunities to find a match by coincidence. Even if everyone in the database is innocent, there is a substantial probability that one (or more) will match the profile with a general-population frequency of 1 in 10 million. Hence a match obtained in such a database search may well be coincidental, particularly if there is little or no other evidence against a matching individual.⁵⁶

When the estimated frequency of the DNA profile is 1 in n , where n is a number larger than the earth's population, some people assume that the profile must be unique, an error that statistician David Balding has called the "uniqueness fallacy."⁵⁷ In such cases the expected frequency of duplicate profiles is less than one, but it never falls to zero no matter how rare the profile is. If the frequency of a profile is 1 in 10 billion, for example, then the expected likelihood of finding a duplication in a population of 250 million unrelated individuals is about 1 in 40. This may sound like a low risk, but in a system in which thousands of evidentiary profiles with frequencies on the order of 1 in 10 billion are searched each year against millions of database profiles, coincidental matches will inevitably be found.⁵⁸

Indeed, a large number of coincidental DNA matches have already been found in database searches. The British Home Office has reported that between 2001 and 2006, 27.6 percent of the matches reported from searches of the United Kingdom's National DNA Database were to more than one person in the database. According to the report, the multiple-match cases arose "largely due to the significant proportion of crime scene sample profiles that are partial."⁵⁹ In other words, officials were frequently searching for profiles like profiles B and C in Table 15.1 that would be

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expected to match more than one person in a database of millions. But the frequent occurrence of DNA matches to multiple people surely makes the point that a DNA match by itself is not always definitive proof of identity.

False incriminations arising from such coincidental matches have occurred in both the United Kingdom and the United States. In 1999 the DNA profile of a sample from a burglary in Bolton, England, was matched in a database search to the profile of a man from Swindon, England. The frequency of the six-locus profile was reported to be 1 in 37 million. Although the Swindon man was arrested, doubts arose about the identification because he was disabled and apparently lacked the physical ability to have committed the Bolton crime. Testing of additional genetic loci excluded him as the source of the sample and proved that the initial 1-in-37-million match was simply a coincidence. As David Balding points out, this kind of coincidence is not particularly surprising because “the match probability implies that we expect about two matches in the United Kingdom (population » 60 million), and there could easily be three or four.”⁶⁰

In 2004 a Chicago woman was incriminated in a burglary by what turned out to be a coincidental cold hit. The woman’s lawyer told the *Chicago Sun-Times* that it was only her strong alibi that saved the woman from prosecution: “But for the fact that this woman was in prison [for another offense at the time the crime occurred] . . . I absolutely believe she’d still be in custody.”⁶¹

A similar error came to light in 2010 in an Ohio burglary prosecution. The homeowner had confronted the burglar, whom he described as short, stout, and balding, and had yanked some hair from his scalp. DNA typing of tissues attached to the hair produced a six-locus partial DNA profile with an RMP of 1 in 1.6 million. Ten years later a database search matched this profile to one Steven Myers, who was described as a tall, skinny 25-year-old and who had no known connection to the town where the burglary had occurred. Despite the mismatch between the homeowner’s description of the burglar and Myers, who would have been only 15 at the time of the crime, Myers was indicted and spent seven months in jail awaiting trial. Luckily for him, the hair samples were still available. Retesting produced results at additional loci that excluded him as the donor, and he was released.⁶²

Misleading Statistics

DNA analysts sometimes present misleading statistics that overstate the value of the DNA evidence. For example, in cases where a suspect’s profile is being compared with a mixture, analysts sometimes present the frequency of the suspect’s profile rather than the frequency of profiles

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that would be included as possible contributors to the mixture. This practice is misleading because the relevant issue in such a case is the probability of a random match to the mixture, not the probability of a random match to the suspect. In a case where a suspect with profile A was matched to a mixture like profile D, the relevant statistic is 1 in 790,000, not 1 in 250 billion.

Before the scandal broke in 2003, the Houston Police Department Crime Laboratory routinely presented the wrong statistic in mixture cases. In the case of Josiah Sutton, for example, the laboratory reported an RMP of 1 in 690,000 (the frequency of Sutton's profile) when the probability of a random match to the mixed evidentiary sample was approximately 1 in 15. (Also, because Sutton was one of two men who were falsely accused of the crime, the chance the lab would find a coincidental match to at least one of them was approximately 1 in 8.)⁶³

Although the proper way to compute statistics in mixture cases has been widely known since at least 1992, when it was discussed in a report by the National Research Council, the practice of presenting the suspect's profile frequency in mixture cases has been surprisingly persistent. I have seen instances of it in many cases, including a capital case in South Carolina that I reviewed in 2010.

A more subtle problem arises when a suspect's profile (such as profile A) is compared with a partial profile in which some of the suspect's alleles are missing (such as profile E). Any true discrepancy between profiles means that they could not have come from the same person, but an analyst may well attribute discrepancies like those between profiles A and E to technical problems in the assay or to degradation of sample E and therefore declare A to be a possible contributor to mixture E despite the discrepancies. The problem then becomes how to assign statistical meaning to such a partial match.

At present there is no generally accepted method. The approach laboratories typically use is to compute the frequency of genotypes at loci where the two profiles match and simply ignore loci where they do not. This approach has been strongly criticized for understating the likelihood of a coincidental match (and thereby overstating the value of the DNA evidence), but it remains the most common approach in cases of this type and is currently used throughout the United States.⁶⁴

Fallacious Statistical Conclusions

Another persistent problem has been fallacious testimony about the meaning of a DNA match. Analysts sometimes give testimony consistent

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with a logical error called the “prosecutor’s fallacy” (or, alternatively, the “fallacy of the transposed conditional”) that confuses the RMP with a different statistic known as the source probability. The RMP is the probability that a random unrelated person would match an evidentiary sample. The source probability is the probability that a person with a matching DNA profile is the source of the evidentiary sample. The RMP can be estimated by the DNA analyst using purely scientific criteria; the source probability can be assessed only on the basis of all the evidence in the case, including nonscientific evidence. Hence, although forensic scientists can properly present RMPs (if they compute them correctly), it is improper for them to testify about source probabilities. But sometimes they do so anyway.⁶⁵

For example, when a defendant named Troy Brown was prosecuted for rape in Nevada, the analyst testified that his DNA profile matched the DNA profile of semen found on the victim, and that the RMP was 1 in 3 million. Prompted by the prosecutor, she went on to testify that this meant that there was a 99.999967 percent chance that Brown was the source of the semen, and only a .000033 percent chance that he was not. On the basis of this testimony, the prosecutor argued that the DNA evidence by itself proved Brown’s guilt beyond a reasonable doubt. When Brown’s case was accepted for review by the U.S. Supreme Court in 2009, a group of twenty “forensic evidence scholars” filed an amici curiae brief discussing problems with the DNA analyst’s testimony. The Supreme Court described those problems correctly in its resulting opinion, although it dispensed with the case on procedural grounds without considering whether fallacious testimony of this type violates a defendant’s constitutional rights.⁶⁶

Statistical Accuracy: Independence Assumptions

Thus far I have been assuming that the statistical estimates computed by forensic laboratories are accurate, but there is still some uncertainty about that due largely to the refusal of the FBI to allow independent scientists to perform statistical analyses of the DNA profiles in the National DNA Index System (NDIS). Forensic laboratories typically base their frequency estimates not on NDIS or any other large database containing millions of profiles but on published statistical databases that contain a few hundred profiles from “convenience samples” of members of each major racial or ethnic group. To generate a number like 1 in 2 quadrillion from a statistical database that consists of a few hundred profiles requires an extrapolation based on strong assumptions about the statistical independence of various markers.⁶⁷

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When DNA evidence was first introduced in the late 1980s and early 1990s, a heated debate arose about the independence assumptions. Although many forensic and academic scientists were comfortable with these assumptions, some prominent critics expressed concern that the independence of the markers might be undermined by population structure—the tendency of people to mate with those who are genetically similar to themselves within population subgroups. By 1992 the dispute about statistical independence had led several appellate courts to rule DNA evidence inadmissible under the *Frye* standard, which requires that scientific evidence be generally accepted in the scientific community as a condition for its admissibility in jury trials.⁶⁸

Although the exclusion of DNA evidence affected relatively few cases, it created a sense of crisis in the forensic science community and led to a flurry of research designed to test the extent of population structure and, by extension, the independence of the markers. By the mid-1990s new data had assuaged the worst fears about the extent of population structure, and criticism began to fade. The 1996 NRC report on DNA evidence recognized the potential importance of population structure, but it concluded on the basis of the data available at the time that the effect was likely to be modest and could be addressed by using a small correction factor, called theta, in computing match probabilities. Since that time statistical estimates based on assumptions of independence have routinely been admissible (with or without the theta correction).⁶⁹

But troubling questions about statistical independence linger for several reasons. First, the growing use of large government databases for identification of unknown profiles has made it more important than it was in the past to know precisely how rare matching profiles are. When the scientific community reached closure on the issue in the 1990s, DNA testing was used primarily for confirming or disconfirming the guilt of individuals who were already suspects. In cases where DNA of a person who is already a suspect is found to match the DNA of the perpetrator, it probably does not matter very much whether the frequency of the matching profile is really 1 in 10 trillion, say, rather than 1 in 10 billion or 1 in 10 million. Any of these probabilities is low enough to effectively rule out the theory of a coincidental match and therefore justify a conviction. When a suspect is identified in a search of a large database, however, the precise rarity of the matching profile is much more important. In such cases the DNA evidence that identifies the suspect may constitute the only evidence against that person. Hence it is crucial to know whether the suspect is the only person with the matching profile. If the frequency is really 1 in 10 trillion, then the likelihood that any other human will

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have the profile is extremely low, but the likelihood is not nearly as low if the frequency is 1 in 10 billion; and if the frequency is 1 in 10 million, then the suspect is certainly not the only person with the matching profile. Hence whether a conviction is justified may well depend on the precise rarity of the profile.

The relatively small size of available statistical databases makes it impossible to perform sensitive tests of the statistical independence of markers across multiple loci. Such tests could be conducted if population geneticists were given access to the DNA profiles (with identifying information removed) in the large offender databases used for criminal identification. For example, Bruce Weir published an analysis of a government database from the state of Victoria, Australia, that contained 15,000 profiles.⁷⁰ He found no evidence inconsistent with the standard assumptions on which statistical calculations are based, but according to one critic, even that database was too small to do “rigorous statistical analysis” of independence across six or more loci. Weir and other experts have suggested that the DNA profiles in FBI’s CODIS system be made available (in anonymized form) for scientific study. Weir told the *Los Angeles Times* that the independence assumptions relied on for computing profile frequencies should be tested empirically using the national database system: “Instead of saying we predict there will be a match, let’s open it up and look.”⁷¹

The 1994 DNA Identification Act, which gave the FBI authority to establish a national DNA index, specifies that the profiles in the databases may be disclosed “if personally identifiable information is removed, for population statistics databases, for identification research, or for quality control purposes.”⁷² Requests for access to anonymized (deidentified) profiles in state databases for purposes of statistical study by independent experts have been made by defense lawyers in a number of criminal cases but so far have been vigorously and successfully resisted. According to the *Los Angeles Times*, the FBI has engaged in “an aggressive behind-the-scenes campaign” to block efforts to obtain access to database profiles or information about the number of matching profiles in databases.⁷³

In December 2009 a group of thirty-nine academics (including the author of this chapter and one of the editors of this volume) signed an open letter published in *Science* calling for the FBI to “release anonymized NDIS profiles to academic scientists for research that will benefit criminal justice.” The letter argued that disclosure of the profiles would “allow independent scientists to evaluate some of the population genetic assumptions underlying DNA testing using a database large enough to

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allow . . . powerful tests of independence within and between loci, as well as assessment of the efficacy of the theta factor used to compensate for population structure.” The letter also pointed to a number of other scientific questions that could be answered through analysis of the NDIS data, including questions about how match probabilities are affected by the number of relatives in the database and questions about the degree to which DNA profiles cluster because of identity by descent. Furthermore, analysis could provide insight into the frequency and circumstances in which certain kinds of typing errors occur. To date the FBI has published no scientific findings derived from the NDIS data and has yet to release the data to any independent scientists for review.⁷⁴

The continuing uncertainty about the accuracy of statistical estimates is not a neutral factor in weighing the chances of a false incrimination due to coincidence. Some people mistakenly assume that statistical uncertainty “cancels out”—that is, that the estimates may be too low but also may be too high, so our ignorance of the truth is unlikely to harm criminal defendants. Statistician David Balding has demonstrated mathematically that this position is fallacious. The extreme estimates produced by forensic laboratories depend on the assumption of perfect knowledge about the frequency of DNA profiles, and to the extent that our knowledge is uncertain, the estimates should be considerably less extreme. Hence Balding declares that “ignoring this uncertainty is always unfavourable to defendants.”⁷⁵

Intentional Planting of DNA

The ability of criminals to neutralize or evade crime-control technologies has been a persistent theme in the history of crime. Each new method for stopping crime or catching criminals is followed by the development of countermeasures designed to thwart it. For example, the development of ignition locks did not solve the problem of car theft because criminals quickly learned to defeat the locks by hot-wiring cars, stealing keys, and other tactics that led to the development of additional protective devices (steering-wheel bars, locator beacons), which eventually proved vulnerable to further criminal countermeasures. The history of safecracking has been a virtual arms race between safe manufacturers looking to build ever-safer boxes and criminals finding more advanced ways to break in. It would hardly be surprising, therefore, if criminals sought ways to avoid being identified by DNA tests.⁷⁶

Police officials have expressed concern about that very issue. Between 1995 and 2006, a period when DNA testing was becoming more com-

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mon, the clearance rate for rape cases reportedly declined by 10 percent. Asked to explain this trend, a number of police officials suggested that criminals have become more sophisticated about evading detection. Police officials have also suggested that television shows like *CSI* can serve as tutorials on getting away with crime, although there is no good empirical evidence to prove this claim.⁷⁷

There are anecdotal reports of criminals trying to throw investigators off the track by planting biological evidence. An accused serial rapist in Milwaukee reportedly attempted to convince authorities that another man with the same DNA profile was responsible for his crimes by smuggling his semen out of the jail and having accomplices plant it on a woman who then falsely claimed to have been raped. It occurred to me, and must have occurred to some criminals, that the rapist would have been more successful had he planted another man's semen on his actual victims. Semen samples are not difficult to obtain. In a park on the campus where I teach, semen samples in discarded condoms can be found regularly (particularly in springtime). Perhaps I have been studying DNA testing too long, but I cannot pass that area without wondering whether the young men who leave those biological specimens could be putting their futures at risk. And there are other items besides semen that might be used to plant an innocent person's DNA at a crime scene. Clothing the person wore, a cigarette the person smoked, or a glass from which the person drank could all, if placed at a crime scene, create a false DNA link between an innocent person and a crime. When such planting occurs, will the police be able to figure it out? Will a jury believe that the defendant could be innocent once a damning DNA match is found? I have strong doubts on both counts and, consequently, believe that intentional planting of DNA evidence may create a significant risk of false incriminations.

As with the other risks, this one is magnified by the growing use of DNA databases. If someone plants your DNA at a crime scene, it might throw police off the trail of the true perpetrator, but it is unlikely to incriminate you unless your profile is in the database. The authorities are likely to search the profile of the crime-scene sample against a database, but if your profile is not in the database, they will find no match and will be left with just another unknown sample. Suppose, however, that you are unlucky enough to have your profile in the database. In that case the police will likely find it, at which point they will have something far better than an unknown sample—they will have a suspect. Given the racial and ethnic disparities that exist in databases, that suspect is disproportionately likely to be a minority-group member.⁷⁸

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The expansion of databases increases the number of people who risk being falsely incriminated in this manner. The seriousness of this risk is obviously difficult to assess. It depends on how frequently criminals engage in evidence planting, whose DNA they plant, how often the planted DNA is detected, and how often its detection leads to criminal charges and conviction, among other factors. One can only guess how often these events occur, but it would be foolish to assume that these events will not occur or have not occurred already. Consequently, this risk is one that must be weighed against the benefits of database expansion.

In the future, more sophisticated criminal countermeasures could compromise the effectiveness of DNA testing as a crime-fighting tool. A researcher at the University of Western Australia has studied the effects of contaminating simulated crime scenes with a concentrated solution of amplicons (short fragments of DNA copied from the DNA in a biological sample). She used a standard test kit of the type employed by forensic DNA laboratories and a procedure known as the polymerase chain reaction (PCR) to create highly concentrated solutions of DNA fragments from the core CODIS loci. She then tested the effects of spraying this solution about a room using a small atomizer. She found, not surprisingly, that the concentrated solution of amplicons was detected by standard STR tests and produced profiles that could easily be mistaken for the profiles of typical forensic samples. What is more interesting (and disturbing) is that the DNA profile of the amplicons was, under some conditions, detected preferentially over the DNA profile of actual biological samples in the room. For example, when amplicons from person A were spritzed with the atomizer over a bloodstain from person B, and a sample from the bloodstain was typed using standard STR procedures, the result sometimes appeared to be a mixture of DNA from person A and person B, but sometimes it appeared to consist entirely of DNA from person A—in other words, the contaminating DNA from the atomizer was the only profile that was detected. This prompted a warning that criminals could use this technique to commit “DNA forgery” and to fraudulently plant DNA with the intention of implicating an innocent person.⁷⁹

Kary Mullis, who invented the PCR, anticipated this potential misuse of the technique. In a conversation I had with him in 1995, Mullis jokingly discussed creating a company called “DN-Anonymous” that would sell highly amplified solutions of DNA from celebrities, or from large groups of people, that criminals could use to cover their tracks. Although

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Mullis was not serious about doing this himself, he predicted that someone would do so within the next ten years. As far as I know, Mullis's prediction has yet to come true, but it may be only a matter of time before materials designed to stymie DNA tests (by planting other people's DNA at crime scenes) become available for sale on the Internet along with kits designed to thwart drug tests.

Improving DNA Evidence

Do innocent people really have nothing to fear from DNA evidence? It should now be clear to readers that this claim is overstated. Cross-contamination of samples, mislabeling, and misinterpretation of test results have caused (and will continue to cause) false DNA matches. Coincidental matches and intentional planting of evidence create added risks of false incrimination. These risks are magnified for people whose profiles are included in government DNA databases. We know less than we should about the nature and scope of these risks, and we have done far less than we should to minimize and control these risks.

The 2009 NRC report identified significant problems with the "culture" of forensic science. It found that the field is too strongly influenced by law enforcement and insufficiently connected to academic science. It recommended that crime laboratories be separated from law-enforcement control and that a new federal agency called the National Institute of Forensic Science (NIFS) be established. The NIFS would oversee the field, fund research designed to improve the validity and reliability of forensic methods, establish best-practice standards, and investigate problems. Although the NRC report pointedly excluded DNA testing from its criticism of other forensic science techniques, I believe that this chapter makes it clear that many of the "culture" problems in other domains of forensic science are also problems for forensic DNA testing. An agency like the NIFS is needed as much to improve DNA testing as it is to address deficiencies in other forensic science disciplines.⁸⁰

The great advantage that DNA testing has over other disciplines is the ability to estimate RMPs. Forensic scientists cannot at present estimate the chances of a coincidental match in latent print analysis, tool-mark analysis, or trace-evidence comparison (or any other forensic discipline) the way they can with DNA evidence. As the NRC report recognized, however, RMPs are only one factor affecting the value of DNA evidence. Even that factor is shadowed by lingering uncertainty, although

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the uncertainty could be resolved if the FBI were willing to give independent scientists access to NDIS profiles.

For DNA evidence to achieve the gold-standard status it purports to have, several steps are necessary. Forensic laboratories need to be more open and transparent about their operations. Independent scientists should be given access to all databases for purposes of scientific study. Laboratories should be required to keep careful records of errors, problems, and other unexpected events, and those events should be investigated carefully. Just as crashes and near misses in aviation are examined carefully (by a government agency) to determine what can be learned from them and how such episodes can be avoided, false incriminations and near false incriminations like the many discussed here should be examined and evaluated.

Greater efforts to assess the frequency and source of errors are also needed. There is no good reason (other than lack of resources) that laboratories are not subjected to realistic external, blind proficiency tests in which analysts must type samples that appear to be part of routine casework without knowing that they are being tested. There should also be a public program of research that monitors the operation of government databases in order to assess the frequency and causes of false cold hits. There is no good reason not to record and disclose information about how many searches are conducted, how discriminating the searches are, and how many produce cold hits, as well as the number of cold hits that are confirmed or disconfirmed by subsequent evidence.

More rigorous standards for interpretation and reporting of test results are also needed, along with a mechanism to enforce them. The failure of forensic scientists to adopt blind procedures for interpretation is a particularly important problem. We also need better mechanisms for monitoring and evaluating expert testimony.

Finally, we need better institutional mechanisms for investigating allegations of serious negligence and misconduct. Inadequate investigative efforts are part of the reason that the scandalous scientific misconduct in the Houston Police Department Crime Laboratory went on for more than a decade without correction. At present, investigations of alleged misconduct are typically conducted by entities that not only lack scientific expertise but also have serious conflicts of interest.⁸¹ The district attorney's office that relied on the evidence to convict defendants is often called on to investigate allegations that the evidence was fraudulent or mistaken or overstated. It would be far better if the investigation could be conducted by an independent state or federal agency with appropriate scientific expertise.

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Whether there is political support for the creation of the NIFS or something like it remains to be seen. An agency of this type would clearly be helpful in achieving the goals just outlined. In the meantime, it is important for the academic community to adopt a more realistic view of DNA evidence. Those who continue to promote the myth of its infallibility may well be undermining efforts to make it better.

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15. Forensic DNA Evidence

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investigation of errors at the laboratory. The author assisted the newspaper in this investigation.

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16. Nurturing Nature

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