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]

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

Table 15.1 Matching DNA profiles

	STR locus												
Profile	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	THO1	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	29,30		11,12	11,12		11,12	8,11		
C	15,16	17		13,14	30		11,12	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, 10,12	11,12	8,9,11	6,7,9	11,12,13
E	15,16,17	17,18	21,23	13,14,15	29,30	12,17	11,12	11,12	8,9,10	11,12	8,9		

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

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

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

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]

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

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

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-

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]

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

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

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.