The Potential for Error in Forensic DNA Testing (and How That Complicates the Use of DNA Databases for Criminal Identification)

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Promoters of forensic DNA testing have, from the beginning, claimed that DNA tests are virtually infallible.[1,2] In advertising materials, publications and courtroom testimony the claim has been made that DNA tests produce either the right result or no result.[3] This rhetoric of infallibility took hold early in appellate court opinions, which often parroted promotional hyperbole.[4] It was supported when the National Research Counsel, in the second of two reports on forensic DNA testing, declared "the reliability and validity of properly collected and analyzed DNA data should not be in doubt."[5] It was further reinforced in the public imagination by news accounts of post-conviction DNA exonerations. Wrongfully convicted people were shown being released from prison, while guilty people were brought to justice, by this marvelous new technology. With prosecutors and advocates for the wrongfully convicted both using it successfully in court, who could doubt that DNA evidence was in fact what its promoters claimed: the gold standard, a truth machine?[6]

The rhetoric of infallibility proved helpful in establishing the admissibility of forensic DNA tests and persuading judges and jurors of its epistemic authority.[7] It has also played an important role in the promotion of government DNA databases. Innocent people have nothing to fear from databases, 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 debates about database expansion. For example, David Lazer's otherwise excellent edited volume, *DNA and the Criminal Justice System* (2004) says almost nothing about the potential for false incriminations.[8]

The infallibility of DNA tests has, for most purposes, become an accepted fact—one of the shared assumptions underlying the policy debate.

In this article, I will argue that this shared assumption is wrong. Although generally quite reliable (particularly in comparison with other forms of evidence often used in criminal trials), DNA tests are not now and have never been infallible. Errors in DNA testing occur regularly. DNA evidence has caused false incriminations and false convictions, and will continue to do so. Although DNA tests incriminate the correct person in the great majority of cases, the risk of false incrimination is high enough to deserve serious consideration in debates about expansion of DNA databases. The risk of false incrimination is borne primarily by individuals whose profiles are included in government databases (and perhaps by their relatives). Because there are racial, ethnic and class disparities in the composition of databases,[9,10] the risk of false incrimination will fall disproportionately on members of the included groups.

This article will discuss major ways in which false incriminations can occur in forensic DNA testing, including coincidental DNA profile matches between different people, inadvertent or accidental transfer of cellular material or DNA from one item to another, errors in identification or labeling of samples, misinterpretation of test results, and intentional planting of biological evidence. It will also discuss ways in which the secrecy that currently surrounds the content and operation of government databases makes these issues difficult to study and assess. It will conclude by calling for greater openness and transparency of governmental operations in this domain and a public program of research that will allow the risks discussed here to be better understood.

Coincidental Matches

A coincidental match between different people who happen to share the same DNA profile is one way a false incrimination can occur. To understand the likelihood of a coincidental match, it is important to understand what a DNA profile is and how DNA profiles are compared. 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 test kits used in the United States generally examine the 13 STR loci selected by the FBI for CODIS, the national DNA database.[11] Some of the newer test kits also examine two additional STR loci.

At each STR locus, there are a number of different alleles (generally between 6 and 18) that a person might have. Each person inherits two of these alleles, one from each parent. Numbers are used to identify the alleles and the pair of alleles at a particular locus constitutes a genotype. Hence, one person can have a genotype (for a locus called D3S1358) of "14,15;" while another person has the genotype "16,17." The complete set of alleles detected at all loci for a given sample is called a DNA profile. When describing DNA profiles, people sometimes mention the number of loci they encompass. For example, Profile A, shown in Table 1, is a 13-locus DNA profile.

In cases I have reviewed over the past few years, evidentiary samples from crime scenes often produce incomplete or partial DNA profiles. Limited quantities of DNA, degradation of the sample, or the presence of inhibitors (contaminants) can make it impossible to determine the genotype at every locus. In some instances the test yields no information about the genotype at a particular locus; in some instances one of the two alleles at a locus will "drop out" (become undetectable). Because partial profiles contain

fewer genetic markers (alleles) than complete profiles, they are more likely to match someone by chance.[1] Profile B and Profile C in Table 1 are examples of partial DNA profiles. In both cases these partial profiles would be deemed to "match" Profile A because every allele in the partial profiles is also found in the full profile. It is important to understand, however, that the probability of a coincidental match is higher for a partial profile than for a full profile. For example, the chance that a randomly chosen U.S. Caucasian would match the profiles shown in Table 1 is 1 in 250 billion for Profile A, 1 in 2.2 million for Profile B and only 1 in 16,000 for Profile C. Accordingly, when discussing the probability of false incrimination due to a coincidental match it important to distinguish between what is commonly called a full-profile match, in which the profiles are identical at 13 or more loci, and a partial profile match involving fewer alleles.

Table 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	6,9.3	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	6,7,9.3	11,12,13

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[1] *In general, as the number of alleles in a DNA profile decreases, the probability that a randomly chosen person will, by coincidence, happen to match that profile increases. Because the alleles vary greatly in their rarity, however, it is possible for a profile containing a few rare alleles to be rarer overall that a profile containing a larger number of more common alleles. Consequently, when discussing the likelihood of a coincidental match it is more helpful to focus on the estimated frequency of the profile than the number of loci or alleles encompassed in the profile.*

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. Consider, for example, Profile D in Table 1. Because it contains more than two alleles at some loci, it is obviously a mixture of DNA from at least two people. Profile A is consistent with 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 non-contributor might, by coincidence, be "included" as a possible contributor to the mixture is far higher in a mixture case than a case with a single-source evidentiary sample. Among US Caucasians, approximately one person in 790,000 has a DNA profile consistent with the mixture shown in Profile D.

Let us ignore for a moment the complications presented by partial profiles and mixed samples and focus on the *ideal* case involving a match between complete, single-source 13-locus STR profiles. It is generally accepted that such profiles are extremely rare and hence that the probability of a coincidental match between different individuals is fantastically small. Statistician Bruce Weir recently estimated that the overall or average probability that two unrelated people will have the same DNA profile at all 13 core CODIS STR loci is between 1 in 200 trillion and 1 in 2 quadrillion, depending on what is assumed about population structure.[12] (Probabilities for particular 13-locus profiles may be higher or low than these averages). Numbers this small make it seem as

if a coincidental match is unworthy of consideration, but in a large population we would expect at least a few coincidental 13-locus matches to occur. In a population of millions of people there are trillions of *pairs* of people to be compared, hence the probability of finding a matching pair somewhere in the population can be relatively high even when the probability of a match between any particular pair is truly tiny. This statistical phenomenon (high probability that *some* pair will match despite a low probability that *any particular* pair will match) is analogous to the well-known "birthday problem" in statistics. There is roughly 1 chance in 365 that any particular pair of individuals will share the same birthday, but the probability of finding a pair of individuals in a group who share the same birthday can be very high because each person in the group has a chance to match every other person. In a group of 23 people there are 253 pairs that can be compared and hence the probability of finding two with a shared birthday exceeds 50%.

Weir made similar computations regarding the population size of unrelated individuals necessary to assure a 50% or higher chance of there being (somewhere in the population) a matching pair of 13-locus DNA profiles. His estimates ranged from 7.7 million to 28 million, depending again on assumptions about population structure. Hence, in populations the size of those in the United States or United Kingdom, it is virtually certain that there are pairs of unrelated individuals with matching 13-locus DNA profiles, although no such match has yet been reported. Since only a few such pairs would be expected in the entire population, however, the probability that any particular 13-locus DNA match found by police will involve one of these coincidental pairs is still small.

Coincidental 13-locus matches are more likely to occur between close relatives. Consider, for example, Profile A shown in Table 1. This is a relatively common profile among Caucasians—the probability of finding this profile in a random Caucasian unrelated to the donor of the profile is 1 in 250 billion. The probability of finding this profile in a relative of the donor is 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 thousand for a sibling. These frequencies suggest that a 13-locus match is most likely to be found between siblings, such as brothers. Given the large number of men who have brothers, it is likely that a considerable number of matching pairs of brothers exist in the United States and United Kingdom, although the probability that any particular pair will fully match is rather low.

A greater risk of false matches arises when the government chooses to search databases for matches to incomplete or mixed DNA profiles. There is no published research from which one could estimate the average coincidental match probability, or the range or distribution of such probabilities, in cold hit cases. My impression is that the range is extremely broad and that database searches routinely involve profiles common enough that coincidental matches would be expected. Indeed, the British Home Office has reported that between 2001 and 2006, 27.6% of the matches reported from searches of the UK National DNA Database (NDNAD) 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."[13]

False incriminations arising from such coincidental matches have occurred in both the UK and the US. In 1999 the DNA profile of a sample from a burglary in Bolton, UK

was matched in a database search to the profile of a man from Swindon, UK.[14] 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, proving that the initial 1-in-37 million match was simply a coincidence. As statistician David Balding points out, this kind of coincidence is not particularly surprising as "the match probability implies that we expect about two matches in the United Kingdom (population $\approx$ 60 million), and there could easily be three or four."[15]. Large DNA databases make it easier for authorities to find one of these matching profiles but do not assure that the first matching profile identified is that of the culprit. In 2008, another database match (between an item found in murder investigation in Surrey and a sample found in a church in Sunderland) was reportedly attributed to coincidence after a police investigation found no connection between the items.[16]

In 2004 a similar incident was reported in Chicago.[17] A six-locus partial DNA profile from the scene of a burglary was searched against a state offender database. The police were told the search had produced a "hit" to a Chicago woman. Police arrested the woman, but released her when she produced a convincing alibi: she had been in custody in a state prison at the time of the burglary. My own review of the evidence [18,19] indicates that the frequency of the six-locus "partial profile" in this case was considerably higher than the frequency of the partial profile in the Bolton case, hence this match appears to be another coincidence (although sample limitations precluded testing that hypothesis by typing additional loci).   Illinois officials have reportedly "changed the

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form that is sent to police to state clearly when a DNA 'hit' is a full match and when it is a partial match."[17] Nevertheless, the danger of false incriminations from such searches is apparent. The woman's lawyer told the Chicago Sun-Times that is was only the strong alibi that saved the woman from prosecution: "But for the fact that this woman was in prison…I absolutely believe she'd still be in custody."[17]

The risk of obtaining a match by coincidence is far higher when authorities search through thousands or millions of profiles 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 to a single innocent suspect, the probability of a coincidental match is only 1 in 10 million. Consequently, if one finds such a match in a single-suspect case it seems safe to assume the match was no coincidence. By contrast, when searching through a database as large as the FBI's National DNA Index System (NDIS), which reportedly contains nearly 6 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 have the 1-in-10 million profile. Hence, a match obtained in a database search might very well be coincidental. Consider that among the 6 billion or so people on planet earth we would expect about 600 to have the one-in-10-million DNA profile; among the 300 million or so in the United States we would expect to find about 30 people with the profile. How certain can we be that the one matching profile identified in a database search is really that of the person who committed the crime?

The answer to this question will depend, of course, on the strength of the other evidence against the matching suspect. As a number of commentators have pointed out, it is impossible to estimate the probability that a person who matches the DNA profile of a piece of evidence is (or is not) the source of that evidence based on the DNA evidence alone.[20,21] People sometimes mistakenly assume that if the frequency of the matching profile is 1 in 10 million, that there is only one chance in 10 million that the suspect is *not* the source of that profile. This is a logical error that has been labeled the *prosecutor's fallacy*.[22] As a matter of simple logic, the DNA evidence cannot distinguish any particular suspect who has the 1-in-10 million profile from the other 600 or so people in the world who have it; hence, without considering *other* evidence for or against a particular suspect, it is impossible to draw any conclusion. If the other evidence against a particular suspect is weak or entirely lacking, or if the suspect has a good alibi, then the odds may be very strongly against his being the source of the evidence, notwithstanding the 1-in-10 million match (and this is why the *prosecutor's fallacy* is fallacious).

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 the profile must be unique, an error David Balding has called the *uniqueness fallacy*.[15] 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 one 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.[2] This may sound like a low risk, but in a system in which

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[2] *If genetic profile G, from a given individual, occurs with probability P_G, then the probability of finding at least one additional individual who has the profile in a population of N unrelated individuals is $1-(1-P_G)^N$. An approximate estimate of this probability can be obtained by the simpler expression NP_G .[23]*

thousands of 1-in-10 billion evidentiary profiles are searched each year against millions of database profiles, coincidental matches will inevitably be found.

Familial Searches

A number of states have recently begun conducting what is known as familial searches.[24,25] In cases where a database search finds no exact match to an evidentiary profile but finds a near match—that is, a profile that shares a large number of alleles but is not identical—authorities seek DNA samples from relatives of the person who nearly matches in the hope that one of the relatives will be an exact match to the evidentiary sample. In several high-profile cases familial searches have identified suspects who were successfully prosecuted.[24] The key questions raised by familial searches, from a civil liberties perspective, are how often they lead to testing of innocent people—i.e., people who do not have the matching profile—and how often they might falsely incriminate innocent people through coincidental matches.

The answer to the first question turns in part on the standard the government uses for invoking a familial search. The key issue is how closely the evidentiary profile must match the profile of a person in the database before the government will begin testing DNA of that person's relatives. A trade-off exists between what statistician call Type I errors (relatives are tested when none of them match) and Type II errors (relatives are not tested when one of them does match)—a lenient standard for invoking familial searches will produce many Type I errors; a restrictive standard will raise the number of Type II errors.

Paoletti and colleagues [25] have published the only sophisticated discussion of standards for familial searching and the trade-offs between Type I and Type II errors.

They presented formulae for assessing the "closeness" of a match based on both the number and rarity of matching alleles, and showed how kinship analysis can be used to assess the relative likelihood of finding a particular "near match" if the source of the evidentiary sample is a relative of the person who nearly matched rather than an unrelated person. They argued that the standards of "closeness" that states have used in the past have been ill-defined and ad hoc.

One of the most interesting aspects of the Paoletti et al. article is its finding that the rate of Type I and Type II errors depends not just on the closeness of the match between profiles but also on the strength of other evidence against the people being tested. If the relatives being tested are part of a relatively small pool of possible suspects, then the probability of *both* Type I and Type II errors is lower than if there is less reason *a priori* to suspect them. This conclusion indicates that, regardless of the standard used to invoke it, familial searching will generally be far less effective (more Type I *and* Type II errors) when it is used in connection with broad, suspectless searches of databases. In fact, if the pool of possible suspects is large (many thousands) familial searching may become nearly pointless because the standards needed to keep Type I errors at workable levels will be so high that there will be unacceptable levels of Type II errors.

Familial searching may increase the number of people falsely incriminated by coincidental matches because it increases the effective size of the population subject to genetic monitoring. With familial searching, the government can access (for purposes of comparison) not just the people in the database but also their relatives, hence the size of the population that can potentially be reached by the testing regime is multiplied. While this strategy increases the probability of catching the guilty, it also increases the

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likelihood of finding people who happen by coincidence to match the guilty person, if such people exist in the population. Consider, again, a partial DNA profile from a crime scene that occurs with a frequency of 1 in 10 million. Although the guilty person will have this profile, it is likely that about 30 other Americans will also have it. The larger the effective size of the database, the greater will be the likelihood that one of those innocent people will be identified.

Explaining Cold Hits to a Jury

People have been prosecuted based on cold hits to partial profiles. Earlier this year, for example, a man named John Puckett was convicted of murdering a San Francisco woman in 1972.[26] The key evidence against him (uncovered in a recent search of the state offender database) was that his DNA profile matched a partial evidentiary profile found on the dead victim. The estimated frequency of the matching characteristics was 1 in 1.1 million, hence one would expect to find more than 250 people in the United States with a matching profile. In the absence of other persuasive evidence of the defendant's guilt, the probability of a false incrimination in a case like this would appear to be high. According to press accounts, the only evidence of Puckett's guilt was the DNA match, the fact that he had lived in San Francisco and been old enough to commit the crime in 1972, and the fact that he had pleaded guilty to two rapes and a sexual assault in 1977 (although he had been free and had a clean record since 1988).[27,28]

There has been considerable debate over the manner in which DNA evidence should be presented to juries in cold hit cases. Two reports of the National Research Council took the position that the random match probabilities presented in connection

with a cold hit should be adjusted to take into account the greater likelihood of finding a coincidental match when searching a database. A 1992 NRC report suggested that once a cold hit is obtained the government test additional genetic loci and then, if they match, present statistics based only on these new matching loci.[29] A 1996 NRC report suggested presenting what it called a "database match probability," which reflects the probability of finding a match, by coincidence in the database.[30] The database match probability is determined by multiplying the estimated frequency of the matching DNA profile by the number of different samples in the database. In the Puckett case the cold hit occurred during the search of a California offender database, which contained 338,000 samples, hence the database match probability was approximately 1 in 3.[28]

Statisticians with a Bayesian perspective have criticized both of the NRC proposals.[31,32] They favor the use of likelihood ratios to characterize the strength of DNA evidence. (The likelihood ratio they favor is generally the reciprocal of the random match probability). Although they recognize that the probability of a coincidental match in a case like Puckett's may be quite high, they contend that this risk arises from the weakness of the other evidence in such cases and not due to any weakness in the DNA evidence *per se*. In fact, they argue that DNA evidence is stronger in a cold hit case than the same DNA match would be in a confirmation case (where the government compared the evidence to a single suspect) because the search of the database not only matches the suspect but also rules out other people in the database. They would favor telling the jury in the Puckett case that the DNA profile found on the victim was 1.1 million times more probable if the DNA came from Puckett than if it came from another random individual.

It is unclear whether jurors appreciate the risk of false incrimination in cases like Puckett's. It is also unclear how their evaluations of such cases are influenced by the nature of the statistics that are presented in connection with the DNA evidence. Defendants in cold-hit cases often face a difficult dilemma. In order to explain to the jury that the incriminating DNA match arose from a database search (in which the government had thousands or millions of opportunities to find a matching profile), the defendant must admit that his profile was in the database, which in many states entails admitting to being a felon, a fact that might otherwise be inadmissible. Courts in some cold-hit cases have, at the urging of defense counsel, opted to leave the jury in the dark about the database search in order to avoid the implication of a criminal record. Jurors are told about the DNA match, but are not told how the match was discovered. The danger of this strategy is that jurors may underestimate the probability of a false incrimination because they assume the authorities must have had good reason to test the defendant's DNA in the first place. In other words, jurors may mistakenly assume the DNA test compared the crime scene sample to the DNA of a single individual who was already the focus of suspicion (a circumstance under which the risk of a coincidental false incrimination is extremely low) and not realize that the defendant was identified through a cold hit (a circumstance under which the risk of a coincidental false incrimination is much higher).

A key factor in the conviction of John Puckett might well have been the decision of the trial judge, over the objection of defense counsel, to exclude any mention of the fact that the DNA match was discovered in a database search.[33] Jurors were told about the DNA match, but not that it arose from a cold hit. The judge excluded testimony by an expert called by the defendant to explain the statistical implications of a cold hit. The

judge also excluded any mention of a database match probability. During their deliberations, the jurors sent a note to the judge asking for information on how Puckett had been identified as a suspect. The judge told the jury that that information was irrelevant to their decision and should not be considered.[28,33]

Needless to say, a trial procedure of this nature raises concerns about fairness. The jury may well have assumed (incorrectly) that Puckett became a suspect as a result of evidence that was later ruled inadmissible and that the DNA test was conducted for confirmation. Under those assumed circumstances, the probability of getting a DNA match by coincidence is only 1 in 1.1 million, because only a single person (Puckett) was compared to the evidentiary sample. So the jurors could reasonably have dismissed the theory of a coincidental match as farfetched and implausible. But this would have been a mistake because, as already discussed, the theory of a coincidental match is *very* plausible given that the probability of a coincidental match to *someone* in the database was approximately 1 in 3.

I am not arguing that a DNA match found through a database search constitutes weaker evidence than the same DNA match found in a confirmation case. I agree with the Bayesian scholars [31,32] that the likelihood ratio one would assign to the DNA evidence would be roughly the same in both cases. My argument is that jurors' evaluations of *the case as a whole* may be inaccurate if they are not told the match was found through a database search. I am suggesting that jurors will assume (incorrectly) that the DNA evidence confirms other evidence that made the defendant the subject of police suspicions and hence will underestimate the likelihood that the defendant could

have been incriminated by coincidence. This is a process that, in my view, puts innocent

people who happen to be included in a database at risk of false conviction.

Only a few appellate courts have considered how DNA evidence should be

presented to juries in cold hit cases. In the District of Columbia and in California

criminal defendants have argued that there is no generally accepted method for

computing statistics in cold hit cases and hence that DNA evidence should be

inadmissible in such cases. (Both jurisdictions follow the *Frye* standard, under which

scientific evidence is admissible only if the method used to produce it is generally

accepted in the relevant scientific community). This argument was soundly rejected by

both the highest court in the District of Columbia [34] and, quite recently, by the

California Supreme Court. [35] Both courts approved the presentation of statistics on the

frequency of the matching profiles in connection with cold hits. The California Supreme

Court's rationale, which may have had some weaknesses,[3] was explained as follows:

> The fact that the match ultimately came about by means of a database search does
> not deprive the rarity statistic of all relevance. It remains relevant for the jury to
> learn how rare this particular DNA profile is within the relevant populations and
> hence how likely it is that someone other than defendant was the source of the
> crime scene evidence. [36]

In a footnote, the California Supreme Court suggested that a "database match probability

statistic might *also* be admissible."[37] However, there has been no definitive appellate

ruling on the admissibility of any statistical characterization other than the frequency of

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[3] *The quoted passage is a bit disconcerting because it suggests the justices may have been influenced by the prosecutor's fallacy. As noted above, DNA evidence cannot, by itself, tell us "how likely it is that someone other than the defendant was the source of the crime scene evidence." The use of the word "hence" in the quoted passage suggests a more direct connection between the frequency of the matching profile and the probability the defendant was the source of the evidence than actually exists. Of course, DNA evidence is relevant to the probability the defendant is the source, when considered in conjunction with other evidence, so perhaps this is just a careless use of language by the court.*

the matching profile and a number of trial judges have decided to admit *only* frequency statistics in cold hit cases.

The Accuracy of Frequency Estimates

Thus far I have been assuming that the statistical estimates computed by forensic laboratories are accurate, but there is still some uncertainty about that. And this uncertainty must also be considered when evaluating the risk of false identifications through coincidental matches. To generate a number like 1 in 2 quadrillion from statistical databases that each consist of a few hundred profiles requires an extrapolation based on assumptions about the statistical independence of various markers. A key issue is whether population structure—the tendency of people to mate with those who are genetically similar to themselves within population subgroups—might make the true probability of coincidental matches higher than theoretical estimates. The 1996 National Research Council (NRC) report on DNA evidence recognized the potential importance of population structure, but concluded based on 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, when computing match probabilities.[38] But not all population geneticists are convinced that the problem has been adequately addressed.

An important source of uncertainty is the relatively small size of available statistical databases, which 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 state offender databases used for criminal

identification. For example, Professor Bruce Weir published an analysis of a government database from the state of Victoria, Australia, which contained fifteen thousand profiles.[12] 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.[39] 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 upon for computing profile frequencies should be tested empirically using national database system: "Instead of saying we predict there will be a match, let's open it up and look."[40]

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."[41] Requests for access to anonymized (de-identified) 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.[39, 40] The FBI has reportedly 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 [40].

The lingering debate over population structure resurfaced recently when the Arizona Department of Public Safety reported, in response to a court order, that a search of its state offender database consisting of 65,493 profiles at the 13 CODIS loci had

produced a large number of near matches—that is profiles that are identical for all but a few alleles. One hundred twenty-two pairs of people matched at 9 out of 13 loci; 20 pairs matched at 10 loci; 1 pair matched at 11 loci, and 1 pair matched at 12 loci.[39] The probability that two people will *nearly* match (e.g. that they will match at any 9 of 13 loci) is far higher than the probability that they will exactly match at all 9 of 9 loci specified in advance, let alone 13 of 13 loci. Nevertheless, the large number of near matches in Arizona surprised a lot of people. It has been common for experts to testify that a nine-locus match is tantamount to a unique identification. The discovery of a single 9-of-13 locus match between different people in the Arizona database in 2001 was thought sufficiently noteworthy to report at a scientific meeting.[42] Hence, the report of so many additional near matches at nine or more (of 13) loci attracted considerable attention.

Subsequent studies have sought to determine whether the Arizona findings can be reconciled with the fundamental assumptions about statistical independence that laboratories rely upon when computing profile frequencies. The results so far have been mixed and the research has generally been hindered by the investigators' lack of access to the complete set of profiles in the database and lack of information about the composition of the database. Forensic scientist Steven Myers has argued that the Arizona findings do not fundamentally challenge the assumptions of statistical independence.[43] He has argued that the findings can be explained by a modest degree of population structure coupled with the presence of a large number of close relatives, particularly siblings, in the database.

Population geneticist Laurence Mueller criticized Myers' analysis based on a more elaborate statistical study in which he attempted to create models that could explain the Arizona findings in a manner consistent with the hypothesis of statistical independence.[39] Although Mueller's analysis could not rule out the hypothesis of statistical independence, his best models assumed both a substantial degree of population structure and that siblings constitute 3-9% of people in the database. Even under these best assumptions (which may or may not correspond to reality), the model predicted that the probability of findings as many near matches as appeared in Arizona was relatively low (although not statistically insignificant). Hence, Mueller called for additional study of the Arizona database and of databases from other states, saying: "Perhaps the most important quality control issue in forensic DNA typing is determining the adequacy of the methods for computing profile frequencies."[39]

At the request of criminal defendants, judges in Illinois and Maryland have ordered Arizona-style searches for matching profiles in the Illinois and Maryland state databases.[40] Unfortunately, the results of these searches are covered by protective orders and have been disclosed only to the parties in litigation. The Los Angeles Times recently reported that, like the Arizona search, these searches found a surprising number of profiles that almost matched.[40] In Illinois there were reportedly 903 pairs of profiles that matched at nine or more loci in a database of about 220,000. In Maryland there were said to be 32 such profiles in a database of less than 30,000. Three of the Maryland profiles matched were said to match at 13 of 13 loci. These results are difficult to evaluate, however, due to the protective order. The only publicly available information about these studies is a sketchy news report.

The continuing uncertainty about the accuracy of statistical estimates is not a neutral factor when weighing the chances of a false incrimination due to coincidence. Some people mistakenly assume that statistical uncertainty "cancels out"—i.e., that the estimates may be too low but on the other hand they 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.[44] The extreme estimates produced by forensic laboratories depend on the assumption of perfect knowledge about the frequency of DNA profiles, and to the extent our knowledge is uncertain, the estimates should be considerably less extreme. Hence, Balding declares that "ignoring this uncertainty is always unfavourable to defendants."[44]

Erroneous Matches

When DNA evidence was first introduced, a number of experts testified that false positives are impossible in forensic DNA testing. According to Jonathan Koehler, these experts engaged in "a sinister semantic game" in which they denied that a DNA test could be wrong by distinguishing error by *the test itself* from error by the people administering and interpreting the test (which they labeled "human error").[1] Claims that the *tests themselves* are error-free have contributed to the rhetoric of infallibility that has surrounded DNA testing.[3] Whether such claims are sinister or not, they are misleading because humans are necessarily involved in conducting DNA tests. When assessing the risk of false incriminations, it does not matter whether false positives are due to human or technical failure; what matters is how often (and under what circumstances) such errors occur and how easily they can be detected.

False positives have occurred in proficiency tests and actual cases.[45,46] Among the first 200 people exonerated by post-conviction DNA testing were two men (Timothy Durham and Josiah Sutton) who were convicted in the first place due partly to DNA testing errors. In both cases a combination of technical problems in the laboratory and careless or mistaken interpretation of the test results produced misleading DNA evidence that helped send innocent men to prison for many years.[47] False DNA matches have come to light in a number of other cases as well.[45,46]

False Cold Hits Due to Cross-Contamination of Samples

One cause of false DNA matches is cross-contamination of samples. Accidental transfer of cellular material or DNA from one sample to another is a common problem in laboratories and it can lead to false reports of a DNA match between samples that originated from different people. An interesting illustration is the case of Brian Kelly, a former police officer who was convicted of rape in Scotland in 1989. The victim knew Kelly well and did not believe that he was the rapist, but evidence that semen left by the rapist matched Kelly's DNA profile was sufficient to persuade the jury to convict. After conviction, Kelly, who adamantly maintained his innocence, asked a number of experts, including most prominently Dr. Simon Ford from the United States, to review the case. The experts discovered that the laboratory had run Kelly's reference sample in a lane immediately adjacent to the semen stain on an analytical gel, a dangerous practice given the potential for lane-to-lane DNA contamination, which could have accidentally put Kelly's DNA in the semen sample. In 2004, the Scottish Criminal Cases Review Commission referred the case to Scotland's High Court of Justiciary. The High Court reviewed scientific evidence about the danger of cross-contamination of DNA samples in

circumstances like those in the Kelly case, and found it to be "evidence which is of such significance that the fact that it was not heard by the jury constituted a miscarriage of justice."[48] Kelly's conviction was therefore quashed.

Accidental cross-contamination of DNA samples has caused a number of false "cold hits." For example, the Washington State Patrol laboratory accidentally contaminated samples from a rape case with DNA from the reference sample of a juvenile felon. The juvenile was identified through a database search but could not have been involved in the rape because he was only a child when the rape occurred. According to the lab's Contamination/Extraneous DNA Log, "it was determined that the felon's sample was being used as a training sample by another analyst" when the rape case was being analyzed.[46]

Another false cold hit occurred when a DNA analyst in the Orange County, California, Sheriff-Coroner's crime lab accidentally cross-contaminated samples from two rape cases that were being processed at the same time.[46] Similar errors, leading to false database matches have been reported in Broward County, Florida, in New Zealand [49] and in Western Australia.[50]

One of the best-known false cold hits occurred in a high-profile Australian case involving the murder of a toddler named Jaidyn Leskie.[51] The toddler disappeared in 1997 under bizarre and mysterious circumstances while in the care of the boyfriend of the toddler's mother. The toddler's body was found in a reservoir six months later, with a crushed skull, and the boyfriend was charged with murder. But the case was clouded by the discovery of DNA from an unknown woman in what appeared to be bloodstains on the toddler's clothing. In late 1998, the boyfriend was acquitted.

In 2003, the unknown DNA was matched, via a database cold hit, to a young "mentally challenged" woman who lived hundreds of miles away and who, by all accounts, had never left her own village. Police could find no way to link the young woman to the toddler's murder and at first dismissed the cold hit as an "adventitious" (coincidental) match. It was a seven-locus match and the estimated frequency of the matching profile was 1 in 227 million.[52]

When the case became the subject of a Coronial investigation, I was asked to assist counsel for the Victorian State Coroner in reviewing the laboratory records. This review established that DNA from the young woman had been processed through the same laboratory at about the same time as the toddler's clothing. The young woman had allegedly been the victim of a sexual assault involving a condom. Her DNA, which was extracted from the outside of the condom, had been in close proximity in the laboratory to extracts from the toddler's clothing. Although laboratory personnel maintained that accidental transfer of samples between cases is impossible, I was able to document dozens of cases in which cross-contamination of samples had occurred under similar circumstances in other laboratories, and therefore suspected that accidental contamination explained the match with the young woman.[52]

In order to test the alternative theory of a coincidental match, the Coroner had the matching samples tested at additional genetic loci. If the DNA on the toddler came from another person, and the seven-locus match to the young woman was coincidental, then one would expect testing at additional loci to exclude the young woman. But the additional testing showed that the woman also matched at six additional loci. Furthermore, re-examination of the data produced in the first test revealed low-level

matching alleles at two additional loci. Altogether there were fifteen matching loci with an estimated frequency of less than 1 in 100 trillion, which made the theory of a coincidental match seem far less plausible than the alternative theory of cross-contamination.[53] The Victorian State Coroner issued a formal finding in 2006 that the evidence linking the young woman to the toddler was a false match caused by cross-contamination in the laboratory.[51]

The facts of some recent cases in the United States have also raised suspicions about false cold hits due to contamination across cases. For example, in 2002, while investigating the 1969 murder of University of Michigan law student Jane Mixer, the Michigan State Police Crime Laboratory in Lansing found DNA of two men on her clothing. The profiles were searched through a database and matched two Michigan men, Gary Leiterman and John Ruelas. Police immediately suspected that Leiterman and Ruelas had been involved in the murder, but there was a problem—Ruelas was only four years old when Mixer was killed and had been living with his parents in another city. According to news account, police could find no link between young Ruelas and Mixer.[54] That did not deter Washtenaw County Assistant Prosecutor Steven Hiller who charged Leiterman with the murder. Hiller "created a scenario placing a young Ruelas at the [murder] scene as a chronic noise-bleeder whose blood dropped on Mixer."[55] Although creative, this explanation seems rather farfetched. There was no evidence that Leiterman had ever had contact with young Ruelas or his family and they lived in different parts of the state. A more likely scenario is that this "cold hit" occurred through the same type of laboratory error as in the Leskie case. Examination of laboratory records revealed that known samples of DNA *from both Leiterman and Ruelas* were

being processed in the Michigan State lab *on the same day* as the old samples from the

Mixer murder.[56] Both men were being tested in connection with other cases unrelated

to the Mixer murder. Although the Michigan State laboratory maintains that cross-

contamination of samples across cases was impossible, it seems a very strange and

unlikely coincidence that two men who, according to the prosecutor, were present when

Mixer was murdered in 1969 just happened to have their DNA tested (for other cases) on

the very same day as samples from the Mixer case were tested. Leiterman was

nevertheless convicted of Mixer's murder in 2005.

A similar incident in New Jersey led to a different outcome. During a cold case

investigation of the 1968 rape/murder of a 13-year-old girl named Jane Durrua, a

laboratory discovered male DNA on the girl's underwear. In early 2004, a database

search revealed that the male profile matched a man named Jerry Lee Belamy. Belamy

was charged with the 1968 murder. Fortunately for him, however, the forensic scientists

who had made this "cold hit" were invited, in late 2004, to appear on a television

program about the case. While preparing for their TV appearance, they went back over

their laboratory notes and made a disturbing discovery. The analyst who extracted the

male DNA from the victim's underwear had, on the same day, been working on another

case that included samples from several individuals—including Jerry Lee Belamy.[57,58]

There was no direct evidence that cross-contamination of samples had occurred, but it

seemed a very unlikely coincidence that Bellamy just happened to be involved in two

different criminal cases, years apart, that were processed by the same analyst at the same

time. The theory that the "cold hit" had been produced by cross-contamination of

samples between the two cases was sufficiently plausible to persuade the district attorney

to dismiss the murder charges against Bellamy. One can only wonder what would have happened to Bellamy had the forensic scientists not been invited to make the television appearance.

Very recently, yet another false cold hit came to light in Victoria, Australia. [59] On August 6, 2008, the government dropped charges against Russell Gesah, who was about to stand trial for the 1984 murder of a woman and her nine-year-old daughter. Gesah had been incriminated in the murders when a DNA sample allegedly from the murder scene was matched to his DNA profile through a cold hit. On the eve of trial, it was discovered that "an unrelated exhibit containing DNA from Mr. Gesah was tested on the same day and in the same place as material from the [murder] scene…" [59] According to an officer who worked at the Victoria Police Forensic Services Centre, "crime scene samples, including bloodied clothing, were left on sinks and open shelves" in a manner that could have allowed items from different cases to be cross-contaminated. [60] In light of the problem, a deputy police commissioner announced that the police force would re-examine DNA evidence in over 7000 previous cases looking for other such opportunities for cross-contamination.[59]

False Cold Hits Due to Mislabeling of Samples

A second potential cause of false DNA matches is mislabeling of samples. Sample labeling problems are known to have caused false DNA incriminations in cases in Nevada, California, and Pennsylvania.[45,46] These cases came to light during the judicial process, and before conviction, but only due to 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.[61] 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.[62] For example, he said that analysts' own DNA, from blood samples used as analytical controls, often was mixed up with (or found its way into) casework samples, creating false matches: "[Q]uite often my (colleague) would walk down the aisle and say, 'I've just committed another rape on the Gold Coast.'"[62] The analyst said that while many such errors were caught, sample limitations made it impossible to resample or retest in some questionable cases. He claimed that he was haunted by concerns about the reliability of the DNA evidence he had presented in court.

The best way to detect labeling errors is to obtain new samples from the original sources and retest them, but this safeguard is not always available. Evidence at crime scenes is typically cleaned up (and thereby destroyed) once samples are taken, and the original samples are sometime exhausted during the initial round of testing. Retesting is rarely done, even when samples are available. Routine duplicate testing by forensic laboratories is another possible safeguard, but it too is rarely done.

False Cold Hits Due to Misinterpretation of Test Results

A third potential cause of false DNA matches is misinterpretation of test results. Laboratories sometimes mistype (i.e., assign an incorrect STR 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 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.[63] A male DNA profile was developed from a swab of the victim's breast. The profile, which consisted of "eight STR markers" 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. 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."[64]

Interpretation of DNA mixtures can be challenging under the best of circumstances, but is particularly difficult when the quantity of DNA is limited, as was true in the Sacramento case. Under these conditions STR tests often fail to detect all of the contributors' alleles (a phenomenon known as "allelic drop-out") and can sometimes detect spurious or false alleles (a phenomenon known as "allelic drop-in").[11] 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.[65]

A few laboratories (most notably the Wetherby Laboratory of the British Forensic Science Service) have developed special procedures for typing samples containing low quantities of DNA. These LCN (low-copy number) procedures have a heightened risk of allelic drop-in and drop-out.[11] LCN practitioners attempt to deal with the unreliability of the basic data by testing samples in duplicate, and sometimes in triplicate, and then inferring which results are reliable (i.e., which alleles are true alleles and which are spurious) based on the consistency of the results across replications. However, the reliability of this method has been questioned. In one case I examined, the laboratory typed a sample three times and produced three different profiles (due presumably to drop-out and drop-in of alleles). The analyst then constructed a fourth profile, called a "consensus profile" based on commonalities in the first three. In my view, this consensus profile was at best a good guess at the true profile. It could easily have been wrong. Nevertheless, the consensus profile was searched against a national database and produced a cold hit, which led to a criminal prosecution. I worry that the DNA typing procedure in such cases adds an element of random error to the generation of STR profiles. If the resulting profiles were compared to a single person who was already a suspect, I would have little fear that random alteration of the evidentiary profile would produce a false match. But when these "random" profiles are compared to millions of people in a database, the probability of finding an innocent person who matches may well be significant.

One of the LCN-DNA profiles in the Omagh bombing case was matched, through a database search, to a 14-year-old English schoolboy from Nottingham.[66] The police could find no link between the schoolboy and the evidence—a car bomb planted in Lisburn, Northern Ireland—on which his DNA profile was supposedly found. Unless the boy has a secret life as a bomb-building terrorist that police failed to detect, this appears to be yet another false cold hit. Perhaps the match could be due to incidental transfer of the tiny quantities of DNA detected by the test. Professor Dan Krane, who testified for the defense in the Omagh case, speculated that the boy might have shaken hands with someone who later shook the hand of the bomb maker. In my view a more likely explanation is that this was a coincidental match that followed mistyping of a difficult evidentiary sample.

Even straightforward typing of reference samples sometimes results in mistaken profiles. One such error came to light in Missouri in 2005 when a 13-locus evidentiary profile from a homicide case was searched against CODIS. There was no exact match but officials identified an individual in the Missouri state database who matched the evidentiary profile at 12 of the 13 loci (and on 25 of 26 alleles). This individual was retested and a state laboratory determined that his profile had initially been mistyped at the non-matching locus, and hence that the two profiles actually matched across all 13 loci.[67]

There is evidence that a number of similar errors occurred when Australian laboratories produced the STR profiles in the state database of Victoria Australia. (The profiles in that database were provided to me, in anonymized (de-identified) form, in connection with the Coronial investigation in the Leskie case, and I have made them

available to other experts for examination and study). A review of that database, which contains about 15,000 samples, found a large number of duplicate 9-locus profiles. The duplications were expected because it was possible for the profile of a given individual to be entered into the database on more than one occasion. What was not expected, and indicated a potential problem of mistyping, was the discovery of sixteen 9-locus profiles that matched on every allele but one—a result that cannot be explained by the presence of relatives in the database but is perfectly consistent with the kind of typing error that occurred in the Missouri case. This finding suggests that the error rate, when typing simple reference samples for the database, was slightly higher than 1 in 1000. The error rate when typing more difficult evidentiary samples, such as those in the Sacramento case, or in LCN cases, would likely be much higher.

When typing errors occur they tend to produce profiles that are similar but not identical to the correct profile. Because relatives tend to have similar profiles due to common descent, typing errors are far more likely to incriminate a relative of the true contributor, such as a brother, than a random person. Familial searching may increase this risk by making it easier for authorities to find and test relatives of a mistyped individual. Suppose, for example, that a murderer left blood at a crime scene and the blood was mistyped with respect to a few alleles. If the murderer's profile was in the database, it would not be matched to the crime scene, due to the mistyped alleles, but the close fit between the two profiles could well prompt testing of a number of close relatives of the murderer, who would be uncommonly likely to match the mistyped evidence due to their genetic relationship with him.

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.[68,69] Each new method for stopping crime or catching criminals is followed by the development of counter-measures 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 so on, which has led to the develop of additional protective devices (steering wheel bars, locator beacons), which eventually proved vulnerable to further criminal countermeasures. The history of safe-cracking has been a virtual arms race between safe manufacturers, looking to build ever-safer boxes, and criminals finding more advanced ways to break in.[70] It would hardly be surprising, therefore, if criminals sought ways to avoid being identified by DNA tests.

Police officials have expressed concern about that very issue.[71] Between 1995 and 2006, a period when DNA testing was becoming more common, the clearance rate for rape cases reportedly declined by 10 percent.[72] When asked to explain this trend, a number of police officials suggested that criminals have become more sophisticated about evading detection.[72]   While there is no good empirical evidence to prove the claim,[73] a number of police officials have suggested that television shows like "CSI" can serve as tutorials on getting away with crime.[74]

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

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plant it on a woman who then falsely claimed to have been raped.[71] 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, a glass

the person drank from 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 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.[10]

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 won't occur or haven't occurred already. Consequently, this risk is one that must be weighed against the benefits of database expansion.

In the future, more sophisticated criminal counter-measures 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 PCR *amplicons.* (Amplicons are short fragments of DNA copied from the DNA in a biological sample).[75] She used a standard test kit of the type employed by forensic DNA laboratories, and a procedure known as 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 was 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, and sometimes 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.[75]

Kary Mullis, who invented 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 it himself, he predicted that someone would do so within the next ten years. As far as I know, Mullis' prediction has yet to come true, but it may only be 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.

The Need for Transparency

Do innocent people really have *nothing to fear* from inclusion in government DNA databases? It should now be clear to readers that this claim is overstated. If your profile is in a DNA database you face higher risk than other citizens of being falsely linked to a crime. You are at higher risk of false incriminations by coincidental DNA matches, by laboratory error, and by intentional planting of DNA. There can be no doubt

that database inclusion increases these risks, the only real question is how much. In order to assess these risks, and weigh them against the benefits of database expansion, we need more information.

Some of the most important information for risk assessment is hidden from public view under a shroud of governmental secrecy. For example, the government's refusal to allow independent experts to examine the (de-identified) DNA profiles in offender databases is a substantial factor in continuing uncertainty about the accuracy of frequency estimates (and hence the probability of coincidental matches). I believe there is no persuasive justification for the government's insistence on maintaining the secrecy of database profiles, so long as the identity of the contributors is not disclosed. The government's refusal to open those profiles to independent scientific study is a significant civil liberties issue.

Several government databases containing anonymous offender profiles have been disclosed to outside experts and circulated within the scientific community.[39] To my knowledge, no problems of any kind resulted from these disclosures. I have a DNA database from Victoria, Australia on the hard drive of my computer as I write. I have examined the database myself and shared the database with other experts who conducted their own analyses. I have presented results of those analyses at scientific meetings in Australia as well as the United States. I am at a loss to imagine how my use and distribution of this database could do any harm. So why is there such secrecy about the profiles in databases in the US and UK? I think there is no good reason.

Release of anonymized (de-identified) STR profiles is unlikely to lead to genetic discrimination. The profiles have limited value for predicting anything meaningful about

a person (such as health or medical status). Although STR profiles are weakly predictive of race and ethnicity, and may have some weak correlations with other individual characteristics,[76] Professor David Kaye has argued persuasively that their predictive value is negligible relative to other information that would be readily available from other sources.[77] Based on this assessment, Kaye declared that "scenarios for the misuse by the government, insurers, or employers of the STR-identification profiles in NDIS and other law enforcement databases border on science fiction."[77]

Even if STR profiles did contain information that someone might use as the basis for discrimination, it is difficult to see how discrimination could occur so long as the profiles are not identified. You cannot discriminate against someone if you don't know who they are.

I have asked a number of experts, including government officials who have been resisting disclosure of database profiles, to explain the government's interest in keeping the profiles secret. What possible harm to anyone could arise from such a disclosure? How might disclosure lead to a bad outcome? The only answer I have heard that seems remotely plausible is that disclosure might create a way to determine whether a given individual has a criminal record. For example, a potential employer could surreptitiously collect the DNA of applicants, have it typed, and then search the applicants' profiles against the anonymized profiles in an offender database looking for matches.

That scenario seems unlikely given the ability of employers to determine more rapidly and cheaply from public records whether an applicant has a criminal record. The only possible value of genetic testing to the employer would be identification of former offenders who have misrepresented their identities. Even then, the value would likely be

limited. Suppose, for example, that an employer determined that a job applicant's profile matches a de-identified profile in NDIS. The employer might suspect the applicant was a convicted offender, but would not know for sure because NDIS now includes profiles from a number of states that include arrestees in their databases. Nor would the employer know the nature of the offense (or arrest) or where or when it occurred.

Nevertheless, it is conceivable that such a scenario could occur, and could cost the applicant a job he would otherwise have gotten. This obviously harms the applicant, but it would not be a case of genetic discrimination. The decision not to hire would have nothing to do with the applicant's genetic characteristics; it would be based on the applicant's having an undisclosed criminal record, which does not strike me as a particularly egregious violation of civil liberties. The only liberty at stake is the ability of a person with a criminal record to hide that fact from others. If that is the only privacy interest that the government seeks to protect, then the government's interest in non-disclosure seems pretty weak.

Disclosure of anonymized (de-identified) profiles would help clarify the frequency of DNA profiles and hence the probability of coincidental matches. It would also have the benefit of opening the government's DNA databank operations to external scrutiny that could identify potential problems with their accuracy and reliability, such as the unreliable typing of duplicated samples in the database of Victoria, Australia (discussed above). So long as the profiles are identified only by number and cannot be associated with any particular individual, I see no convincing ethical or social reason for keeping them secret.

It would also be helpful for the government to provide additional information about the operation of databases. In order to assess the risk of coincidental matches we need to know how often police search partial DNA profiles through the database. Data on the range and distribution of profile frequencies, for the profiles actually searched against the database in a given year, would give important clues as to how often searches of partial profiles could be expected to lead to coincidental matches—information vital for assessing the likelihood that an innocent person in the database might have "something to fear." It would also be helpful to know how often database searches lead to multiple "hits." Information about this topic has been provided in Annual Reports on the NDNAD in the UK [13] but is not available in the US.

A third very important type of information that should be made public concerns the frequency of cases in which a database search incriminates the wrong person. In 2004 forensic scientist Keith Inman and mathematician Charles Brenner made the interesting suggestion that the rate of false positives in database searches could be estimated by looking at the number of cases in which a cold hit incriminates a person with an iron-clad alibi, such as a person who was in prison when the crime was committed.[78] Although their assumptions and methods were questionable [79], their basic argument is valid and important. To assess the risk of false database matches in the future, we need to know how many there have been in the past.

To assess the risk of erroneous matches in a rigorous manner it will be necessary to know 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 and disconfirmed by subsequent evidence. This information is relevant to an issue of

significant public importance—the overall rate of error in databank searches.

Consequently, I believe the government should systematically collect and report this

information. Those who argue that there is little or nothing to fear should be the first to

support efforts to create a transparent environment in which such claims can be evaluated

and put to the test.

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