

affinal method produces generally accepted and valid estimates of random-match probabilities.³⁸

As a result of the large databases, however, this seemingly settled issue is being revisited. Investigative reporters are asking, “How reliable is DNA in identifying suspects?”³⁹ Radio talk show hosts are discussing “disturbing doubts about DNA.”⁴⁰ One law professor is demanding “an immediate congressional investigation.”⁴¹ More circumspectly, another simply states that “recent evidence calls into question the accuracy of . . . match probabilities.”⁴² A defendant charged with robbery, carjacking, and related firearms violations in Maryland produced expert opinion that FBI “statements or inferences of uniqueness [might] be fundamentally incorrect.”⁴³ But are the new doubts justified? The next part traces the finding that prompted the current outcry and uses a well known result in probability theory to show that the concern, while appropriate, is exaggerated.

II. THE IMPLICATIONS OF PARTIAL MATCHES IN DATABASE TRAWLS

A. *The Arizona Experience*

The commotion began after staff from the Arizona Department of Public Safety’s DNA laboratory posted an announcement of “A Nine STR Locus Match Between Two Apparently Unrelated Individuals” at an annual scientific meeting on DNA identification methods in Phoenix in 2001.⁴⁴ It is not clear from published accounts how this nine-locus match—between a white and a black man with felony convictions—was discovered.⁴⁵ The database records consisted of a list of the alleles at thirteen distinct loci. When the same thirteen loci can be typed in a crime-scene sample, a mere nine-locus match will not generate a suspect. In fact, the discrepancies in the full profile at the other four loci will

³⁸ See KAYE, *THE DOUBLE HELIX*, *supra* note 27, at 139.

³⁹ Felch & Dolan, *supra* note 17.

⁴⁰ Airtalk, *How Reliable is DNA Testing?*, Southern California Public Radio, July 23, 2008, available by contacting Southern California Public Radio at <http://www.scpr.org/contact>.

⁴¹ Turley, *supra* note 20.

⁴² Murphy, *supra* note 16, at 781.

⁴³ *United States v. Davis*, 602 F. Supp. 2d 658, 681 (D.Md. 2009) (quoting Laurence Mueller, but rejecting this argument).

⁴⁴ See Kathryn Troyer et al., Lab Analysts, Arizona Department of Public Safety, *A Nine STR Locus Match Between Two Apparent Unrelated Individuals Using AmpFISTR Profiler Plus™ and Cofiler™*, PROCEEDINGS OF THE PROMEGA 12TH INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION (2001).

⁴⁵ According to Murphy, *supra* note 16, at 782, “an alert analyst happened to observe” it. Smith, *supra* note 18, states that Troyer was “doing a routine check of the state’s criminal offender database.” The director of the state crime laboratory did not respond to my request for clarification. Probably, the finding resulted from an expanded version of a standard check to see, by comparing all the profiles in the database, whether there were any duplicates.

exclude a suspect as a possible source of crime-scene DNA. But even partial matches at nine loci are almost never encountered in case work. Indeed, according to one report, the RMP for the matching nine-locus genotype in Arizona was “1 in 754 million in Caucasians, 1 in 561 billion in African Americans, and 1 in 113 trillion in Southwest Hispanics.”⁴⁶ The discovery of such a match in the state database surely seemed anomalous.

In 2005, Bicka Barlow, a public defender in San Francisco, contacted Kathryn Troyer, the DNA analyst who came across the partial match in the Arizona database.⁴⁷ Barlow, herself a “molecular biologist turned lawyer,”⁴⁸ was defending a man in a California case in which the state had only typed nine loci.⁴⁹ Troyer told Barlow that she had found more nine-locus matches.⁵⁰ Barlow asked Troyer to send her more information.⁵¹ Todd Griffith, the head of the Arizona Department of Public Safety lab, interceded.⁵² He notified Barlow that no further information would be released. Barlow applied to an Arizona court for a subpoena.⁵³ At a hearing in Phoenix, Troyer stated that she had found “approximately 90” nine-locus, partial matches. Barlow was astounded. “‘I almost fell over when I heard that,’ Barlow says now, with a laugh. ‘I was thinking she had 10 matches, or 20. That would have been huge, right?’”⁵⁴ The Arizona lab produced no testimony to counter Barlow’s representation to the Arizona judge that the 90 matches meant that “the FBI’s population-rarity statistics are ‘only an estimate, and the estimate is wrong.’”⁵⁵ The court ordered the lab to produce a summary of the numbers of partial hits at nine or more loci among all pairs of people in the Arizona convicted-offender database. The report stated that 122 pairs matched at nine loci (and did not match at the other four loci); another 20 pairs matched at ten loci (and did not match at the remaining three loci).⁵⁶

⁴⁶ Murphy, *supra* note 16, at 782. The figure of 1 in 113 billion is mentioned in other accounts. See, e.g., Charles Brenner, ARIZONA DNA DATABASE MATCHES, Jan. 8, 2007, <http://dna-view.com/ArizonaMatch.htm>.

⁴⁷ See Smith, *supra* note 18.

⁴⁸ *Id.*

⁴⁹ See Murphy, *supra* note 16, at 782.

⁵⁰ See Smith, *supra* note 18.

⁵¹ See *id.*

⁵² See *id.*

⁵³ See *id.*

⁵⁴ *Id.*

⁵⁵ *Id.*

⁵⁶ The crux of the report, as described by Ungvarsky, *supra* note 16 at 12, is that the offender database “profiles of . . . 65,493 persons . . . had 122 pairs of people who matched at 9 out of the 13 loci, 20 that matched at 10 loci, 1 that matched at 11 loci, and 1 that matched at 12 loci. The last two matches were confirmed to be between pairs of siblings.” See also Bruce Budowle et al., *Partial Matches in Heterogeneous Offender Databases Do Not Call into Question the Validity of Random Match Probability Calculations*, 123 INT’L J. LEGAL MED. 59, 61 (2009).

Lawyers, and at least one mathematician, have found this number to be “remarkable”⁵⁷ and “startling.”⁵⁸ If the RMP for a nine-locus match is anything like “one in 754 million for whites, and one in 561 million for blacks,”⁵⁹ how can it be that a database as small as “a mere 65,493 entries”⁶⁰ produces even one such match? “Scary isn’t it?” asked Devlin.⁶¹

B. *The Combinatorial Explosion: All-pairs Trawls and the Birthday Problem*

This scenario is only scary if we conflate the size of the database with the number of comparisons being made to find a match.⁶² Three distinct situations for DNA matches can arise, and no end of confusion results if they are not disentangled. They are pictured in Figure 1.

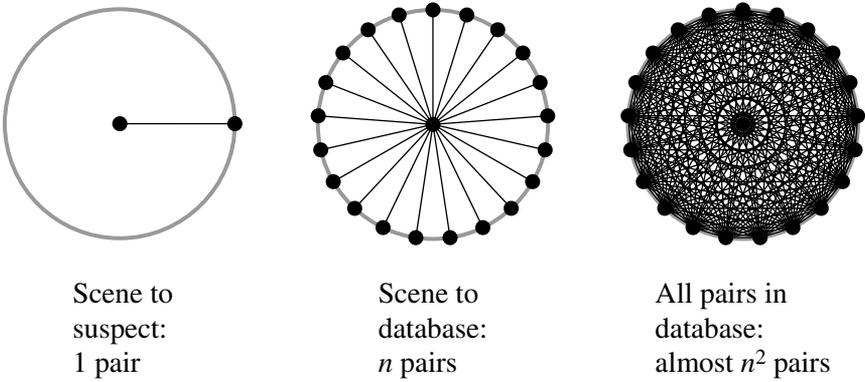


Figure 1. Comparisons in a confirmation case, an ordinary database trawl, and an all-pairs database trawl. Each line represents a comparison. There is 1 comparison in the first situation, n in the second, and about half of n^2 in the third.

First, a confirmation case involves a one-to-one search. The crime-scene profile is compared to the suspect’s profile. This is shown by the single line from the crime-scene sample to the suspect in the left-hand panel of Figure 1. The probability of a match when an unrelated individual is the source of the crime-scene DNA is some number p . This is the random-match probability. Second, a database trawl is a one-to- n search for a match to the crime-scene profile among the n profiles in the

⁵⁷ Ungvarsky, *supra* note 16 at 12.
⁵⁸ Devlin, *supra* note 12.
⁵⁹ Smith, *supra* note 18. Professor Murphy provides different numbers. See Murphy, *supra* note 16, at 782 (“Under the statistical models then in place, a person picked at random would match that nine loci profile at a rate of 1 in 754 million in Caucasians, 1 in 561 billion in African Americans, and 1 in 113 trillion in Southwest Hispanics.”).
⁶⁰ Devlin, *supra* note 12.
⁶¹ *Id.*
⁶² See Brenner, *supra* note 46.

database. Because there are n independent comparisons, as shown by the lines radiating from the crime-scene sample at the center of the circle of database samples in the middle panel, these trawls can be expected to produce approximately np matches when no one in the database is the source and no one is related to each other or to the source. Finally, in a trawl through all possible pairs in a database, every profile in the database is compared with every other profile. Instead of the n comparisons to a single crime-scene profile in the simple database trawl, the all-pairs trawl entails nearly n^2 comparisons. This combinatorial explosion, shown by the crisscrossing lines in Figure 1, creates a vastly greater number of opportunities for a match among profiles. Hence, the database need not be so huge before one can expect many matches that have very small random-match probabilities. One-to-one comparisons (the testing of a known suspect) and one-to- n searches (for a cold hit) are markedly different from large n -to- n comparisons (the all-pairs trawls), although commentary confusing the latter two types of searches is all too common.⁶³

All-pairs trawling—an artificial form of searching that is not used in criminal investigations—is analogous to the famous “birthday problem.”⁶⁴ The problem is to determine the minimum number of people in a room such that the odds favor there being at least two of them who were born on the same day of the same month.⁶⁵ In its simplest form, the birthday problem assumes that equal numbers of people are born every day of the year. Since the random-match probability for a specified birthday is about $1/365$, most people think that more than 180-some people must be in the room.⁶⁶ Indeed, one might think that for a match to be likely, the number should be larger still. After all, the chance of a match between two randomly selected individuals having a given birthday (say, January 1) is a miniscule $1/365 \times 1/365 = 1/133,225$.

But a precise calculation shows that it takes only 23 people before it is more likely than not that at least two people in the room share a birthday.⁶⁷ The actual number is this small because the matching birthday can be any one of the 365 days in the year and because the number of

⁶³ See, e.g., Humes, *supra* note 18, at 20 (misreporting that “the birthday problem” caused the “the odds of a coincidental match” in an ordinary cold-hit case to go from 1 in 1.1 million to “a whopping 1 in 3”).

⁶⁴ See, e.g., BRUCE BUDOWLE ET AL., CLARIFICATION OF STATISTICAL ISSUES RELATED TO THE OPERATION OF CODIS, PRESENTATION TO THE 17TH INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION 6 (2006), <http://www.promega.com/GENETICIDPROC/ussymp17proc/oralpresentations/budowle.pdf> [hereinafter CLARIFICATION] (using the “birthday problem” to illustrate the high probability of DNA profile matches).

⁶⁵ See *id.*

⁶⁶ See *id.*

⁶⁷ See, e.g., Persi Diaconis & Frederick Mosteller, *Methods for Studying Coincidences*, 84 J. AM. STAT. ASS’N 853, 857 (1989).

comparisons among birthdays scales as n^2 with an increasing number n of people in the room.⁶⁸

Thus, all-pairs trawling in databases makes it much less surprising to come across partial (or even full) matches among unrelated people than in ordinary casework.⁶⁹ Just think about how many distinct pairs can be formed, and then compared, with the “mere 65,493 entries”⁷⁰ in the Arizona database. For example, number each individual 1 through 65,493. Number 1 can be paired with number 2, 3, and so on. That is 65,492 pairs right there. Number 2 can be paired with number 3, 4, and so on. That is another 65,491 pairs. The exact formula for the number of distinct pairs of n items is $n(n-1)/2$.⁷¹ For $n = 65,493$ items, the number of distinct pairs therefore is $65,493 \times 65,492/2 = 2,144,633,778$. But that is not all. For each pair, there is only one way to match all thirteen loci, but there are many more ways to get a nine-locus partial match. The profiles in the pair might match at the first nine loci and not match at the next four; they might not match at the first four but then match at the next nine; and so it goes for the $(13!)/(9!)(4!) = 715$ distinct combinations of nine items out of thirteen. With no particular set of nine loci that need to match, we perform $715 \times 2,144,633,778$ comparisons, which gives us more than 1.53×10^{12} opportunities to find some nine-locus matches. If the chance of any nine-locus match for any pair were “one in 754 million,”⁷² then the expected number of nine-locus matches would be not just one. It would not even be 90, as Troyer mentioned, or 122, as the court-ordered report stated.⁷³ It would be $(1.53 \times 10^{12}) / (7.54 \times 10^8) = 2,034$ nine-locus matches. It seems as if random-match probabilities are even smaller than the theoretical estimates.

⁶⁸ See *id.*

⁶⁹ The more cynical view, attributed to Erin Murphy, a “graduate” of the District of Columbia Public Defender’s Office, and now Acting Professor of Law at the University of California at Berkeley, is that the forensic science community is nefariously engaging in “goal-post shifting on a grand scale.” Smith, *supra* note 18. “The story before Arizona was that a nine-locus match was, like, a one-in-a-trillion thing,” [Murphy] says. “Now the story is, we expected that all along.” *Id.* The real story is that DNA analysts, who are not necessarily skilled in probability and statistics, failed to distinguish between ordinary casework and all-pairs searching within a database. The failure of forensic analysts to apply appropriate statistical procedures is all too common. See, e.g., NATIONAL RESEARCH COUNCIL OF THE NATIONAL ACADEMIES, COMMITTEE ON SCIENTIFIC ASSESSMENT OF BULLET LEAD ELEMENTAL COMPOSITION COMPARISON, FORENSIC ANALYSIS: WEIGHING BULLET LEAD EVIDENCE 31–35 (National Academies Press 2004) (criticizing the FBI’s “chaining method” for matching bullet fragments); Kaye, “False, But Highly Persuasive”, *supra* note 12 (discussing errors in the computation and presentation of DNA random-match probabilities).

⁷⁰ Devlin, *supra* note 12.

⁷¹ The first member of a pair is any one of the n items. The second member is any of the $n-1$ remaining items. That gives $n(n-1)$ pairs. But these include pairs such as (1, 50) and (50, 1), so we divide by two to get the total number of distinct pairs.

⁷² Smith, *supra* note 18.

⁷³ See *id.*

But that conclusion cannot rest on these particular numbers. The theoretical random-match probability is not 1 in 754 million. That estimate pertained to Caucasians with the genotype seen in the first nine-locus match back in 2001. Each profile has its own random-match probability in each population group. A detailed study would need more than the summary statistics to ascertain whether the observed numbers of partial matches exceed those predicted by the basic product rule for unrelated individuals. To account for the vast number of possible pairings, we could refer to the individual profiles to compute the different RMP for each pair of profiles and derive an expected number of partial matches. Or, we could use a more efficient procedure that merely requires the number of loci at which all the pairs match and the number of loci at which they partially match.⁷⁴ In principle, more detailed studies with individual-level data on profiles and relatedness (or suitably detailed counts) might suggest that the theoretical RMPs are just fine, are too high (benefitting defendants), or are too low.⁷⁵

III. THE FBI'S PURISM AND STATISTICAL RESEARCH WITH OFFENDER DATABASES

The FBI opposes statistical studies of offender databases that might undercut the theoretical RMPs that were the subject of a decade of litigation and scores of academic papers. Its arguments range from the purist to the practical. At a Promega conference five years after the Arizona report was posted, the leader of the FBI's scientific work on DNA evi-

⁷⁴ See B.S. Weir, *Matching and Partially-matching DNA Profiles*, 49 J. FORENSIC SCI. 1009 (2004) [hereinafter Weir, *Matching and Partially-matching DNA Profiles*]. The phrase "partial match" can be confusing. A match at every allele at 9 out of 13 loci, for example, is a partial match in the sense there is a full match at nine loci and something less than a full match at the other four loci. But how much less? Without additional specification, a nine-locus partial match is consistent with various possible numbers of "partial matches" at the four incompletely matching loci. Let "9/4" mean that nine loci are fully matching and that the pair of profiles contain exactly one matching allele at each of the other four loci. The total partial match thus consists of nine fully matching loci and four partly matching ones. Next down on the scale of nine-locus partial matches is a "9/3" match, that is, a full match at nine loci, partial matches (for exactly one of the two alleles) at another three loci, and a complete mismatch at the remaining locus. A "9/0" represents the weakest nine-locus partial match, being a full match at nine loci and a full mismatch at the other four loci. This notation is borrowed from James M. Curran et al., *Empirical Testing of Estimated DNA Frequencies*, 1 FORENSIC SCI. INT'L: GENETICS 267, 268 (2007). The most informative comparison of expected to observed numbers of partial matches is possible only when all degrees x/y of partial matching have been counted. See Weir, *supra*.

⁷⁵ The family relationships of the individuals whose profiles are in a database are potentially important. Assuming that everyone is unrelated can result in underestimates of the expected numbers of matches. More partial matches would be likely because close relatives will match more often than will the unrelated individuals to whom the theoretical RMPs apply. Therefore, further analysis would be required to interpret an excess of partial matches as a defect in the theory for computing RMPs. See *infra* Part III.