Database-driven investigations
The promise—and peril—of using forensics to solve “no-suspect” cases

Andrea Roth
Stanford Law School

Anyone who reads the popular press is familiar with backlogs in DNA and other forensic testing (Moore, 2008). The forensic science community seems to understand the danger of such backlogs, which “can result in prolonged incarceration for innocent persons wrongly charged,” “delayed investigation of those who are not yet charged,” and “can contribute to the release of guilty suspects who go on to commit further crimes” (National Research Council, 2009: 40). Less understood are the reasons such backlogs exist. The mystery is, in large part, a function of poor data; the National Academy of Sciences’s groundbreaking 2009 report on the state of forensic science noted that “backlog data are not entirely reliable” because of the lack of uniformity in how laboratories count submissions, tests, and outcomes (National Research Council, 2009: 62). One might assume that the problem simply is related to funding and that efforts such as President George W. Bush’s $1 billion “DNA Initiative” in 2003 eventually would ameliorate the backlog issue (National Research Council, 2009).

Strom and Hickman’s (2010, this issue) startling empirical piece on forensic laboratory processing offers two central insights that challenge existing assumptions about the backlog problem and will surely be critical to any successful effort at reform. The first is that DNA typing and other forensic sciences can and should be used not only as confirmatory evidence in cases already proceeding to trial but as tools of investigation in “no-suspect” cases by comparing evidence profiles with profiles in offender databases. The second is that laboratory backlogs are a direct result not only of a lack of resources but also of a culture in which forensic scientists—and perhaps even prosecutors—do not fully grasp the first point. Rather, as Strom and Hickman revealed through their 2008 data, current laboratory bureaucracy and law-enforcement politics tend to prioritize open cases, however minor the crime, that already have trial dates at the expense of unsolved homicides and rapes. One necessary component of any long-term solution, then, is
a paradigm change among laboratories, police agencies, and prosecutors toward more frequent use of forensic testing at the investigative stage before a suspect is identified.

A large-scale cultural shift toward forensics-based investigation of no-suspect cases surely will save lives, as well as time and resources, across the long term. But database-driven investigation of no-suspect cases raises critical ethical, scientific, and jurisprudential questions that the scientific and legal communities must acknowledge and resolve. I briefly explore some of those policy issues here and offer concrete suggestions for how to proceed.

**Avoiding Complacency and Confirmatory Bias in Subsequent Investigation**

When a criminal suspect initially is identified through traditional, nonforensic means, the fear exists—voiced by many—that confirmatory forensic testing might be biased if the examiner knows the context of the case and the identity of the existing suspect (Krane et al., 2008; Risinger, 2007). For example, a DNA examiner who knows an existing suspect’s profile might be more likely to view a comparison with the evidence sample profile as an “inclusion” by interpreting what might be an artifact of the testing process as a true and matching allele or by interpreting a true but nonmatching allele as merely an artifact (Thompson, 2009: 260–261).

Although Strom and Hickman (2010) rightly noted that early forensic analyses in no-suspect cases do not suffer from this particular type of post hoc confirmatory bias, a related problem does exist in reverse. In cases in which a suspect initially is identified through a “cold hit,” or database match, investigators must be conscious of how knowledge of the match might lead them to view innocuous facts as inculpatory evidence against the suspect. For example, in the notorious Brandon Mayfield case, in which an Oregon attorney was accused falsely of participating in the 2004 Madrid train bombings based solely on a cold hit from the Federal Bureau of Investigation’s (FBI) fingerprint database, investigators found no other evidence linking him to the crime but viewed Mayfield’s conversion to Islam, as well as the absence of records showing that Mayfield had left the country, as suspicious (Cole and Lynch, 2006). In the hands of an investigator ignorant of the forensic testing results, the latter fact might seem exculpatory.

Others have expressed concern that the use of forensic science to identify suspects in the first instance will supplant traditional investigatory techniques because database searches are quicker and cheaper than gumshoe detective work (Cole and Lynch, 2006; McCartney, 2006), an observation somewhat at odds with Strom and Hickman’s (2010) findings that forensic testing is often sidelined until shortly before trial when other inculpatory evidence already has been collected. Although finding suspects through database hits is a laudably objective and efficient method of identification, the virtues of common sense, objectivity, and persistence in nonforensic investigation will become more, not less, critical to prosecute the guilty effectively and to protect those whose database profile matches might be erroneous or coincidental.
The Need to Ensure Reliability of Database Matches and Match Statistics

The more we rely on forensic science to resolve no-suspect cases, the more we must ensure that reported database matches are themselves reliable and their probative value properly understood. Law enforcement must ensure that the testing of offender samples is contamination-free and that the recording of database entries is error-free. Numerous errors in DNA databases have been reported, some of which have led to erroneous database matches (Geddes, 2010; Thompson, 2008), whereas other false DNA cold hits have been blamed on contamination at the time the suspect’s sample was tested (Cole and Lynch, 2006; Thompson, 2006).

An increased reliance on database matches to resolve no-suspect cases likely will lead to more prosecutions in which the entirety, or near-entirety, of the state’s case is a database match (Roth, 2010). The older a no-suspect case is, the less likely it is that the government will present fact witnesses to corroborate forensic testing results. Such “pure cold hit” cases will require judges not only to consider whether DNA evidence alone is sufficient evidence of guilt (Song, Patil, Murphy, and Slatkin, 2009) but also to ensure that fact-finders understand the probative value of a database match and that the state’s match statistics are reliable. The statistical significance of a database match is a function of the “random match probability” (RMP)—the probability that a person randomly selected from the population would match the profile—and the size of the likely suspect population (Kaye, 2009a). Take, for example, People v. Puckett (pending, No. A121368, Cal. Ct. App.), a San Francisco rape/murder case in which the only evidence against the suspect—a now elderly man identified 30 years after the crime—was a prior sex conviction and a DNA database match with an RMP of 1 in 1.1 million (Humes, 2009). Although the 1.1 million figure might sound damning to lay persons, who often mistake the RMP for the chance the suspect is not the source of the DNA, consider that approximately 2 million prime-aged men were in the Bay Area at the time of the crime, which means that one would expect potential suspects other than Puckett to match the profile (Kaye, 2009a). Absent direction from judges and experts, juries might not grasp the limited probative value of an uncorroborated database match in cases in which the RMP is relatively high or the suspect population is large.

Although “pure” cold hit cases such as Puckett are still relatively rare, their numbers are growing (Cole and Lynch, 2006; Murphy, 2007; Song et al., 2009). And although most such cases will have RMPs with denominators much larger than 1.1 million, cases involving degraded samples and mixtures, like Puckett itself, might require judges to adopt a numerical threshold for determining when the match statistics make out a legally sufficient case for guilt (Roth, 2010).

Moreover, some statisticians and population geneticists have argued that infinitesimally small RMPs, with denominators in the quintillions or higher, are likely the product of inaccurate assumptions about independence of loci or population substructure (Devlin, 2006; Weir, 2001). Analyses of Arizona, Illinois, and Maryland offender databases have suggested that matches at 9 or more of the 13 loci used in most forensic typing are much more common than originally
believed, and at least one biologist has concluded that these results are incompatible with current independence assumptions (Mueller, 2008).

One obvious and critical step laboratories should take to test the reliability of its RMP estimates is to give academic researchers access to anonymized profiles in offender databases. As Thompson (2008) noted, “the relatively small size of available statistical databases . . . makes it impossible to perform sensitive tests of the statistical independence of markers across multiple loci.” Although the FBI and local law-enforcement agencies as of this writing have refused to allow such access (Geddes, 2010; Kaye, 2009b), several scientists, scholars, lawyers, and journalists have called for law enforcement to end its resistance in the name of justice and good science (Kaye, 2009b; Krane et al., 2009; Murphy 2009; Editorial, New Scientist, 2010).

The foregoing discussion of the reliability of match statistics might seem at first glance irrelevant to the identification of suspects through fingerprint database searches. But fingerprint cases raise an even more fundamental issue—the validity of the forensic science community’s position that claims of individualization in latent print analysis are justified without the need for reporting match probabilities. Forensic examiners are not permitted by their professional organizations to testify that a known print and a recovered latent print have a particular probability of coming from a common source (Cole, 2009). Rather, they testify that two impressions necessarily come from the same source, with 100% certainty, because of the number of consistent points of comparison and the fact that fingerprints are “unique” (Cole, 2009: 239). Presumably, the uniqueness assumption led Strom and Hickman (2010) to describe latent print analysis as an “individualizing” forensic science. Yet scholars have questioned the scientific basis for such claims and have called for friction ridge analysts to develop population-data-based rarity estimates and to substitute probabilistic conclusions for claims of individualization (Cole, 2009; National Research Council, 2009).

Expansion of Forensic DNA Databases
The trend toward database-driven investigations of no-suspect cases also might place pressure on lawmakers to expand existing offender databases and to consider calls for universal citizen databases. Even now, the categories of offenders who must place samples in DNA databases are ever-expanding. State and federal DNA databases have grown to include not only convicted felons but also misdemeanants, juveniles, noncitizen detainees, and even arrestees (Gabel, 2010; 42 U.S.C. § 14132[(a)(1)(C) (as amended Jan. 5, 2006)]. Moreover, respected voices in the policy discourse, such as James Hodge, director of the Center for Law and Public Health at Johns Hopkins University, already have suggested the creation of universal databases in which all citizens place their DNA samples (Doherty, 2006). Michigan’s Commission on Genetic Privacy similarly has suggested that DNA samples be stored for all newborns (McCartney, 2006).

Comprehensive citizen databases arguably would address the civil rights concern raised by some that current offender databases contain a disproportionate number of persons of color (Kaye and Smith, 2004; Levine, Small, Gettman, and Reinarman, 2008). But universal data-
bases also could exacerbate racial disparities in arrests if the government someday could profile citizens on the basis of certain “suspicious” biomarkers (McCartney, 2006: 147). Moreover, the more expansive DNA databases become, the more likely investigators will chance upon a coincidental or erroneous match and falsely accuse someone based solely on his genetic profile (Thompson, 2008). Then again, if databases were truly universal, a suspect might be less likely to be accused falsely based on a coincidental match because any other profile matches in the population also would be revealed. Others fear that the government cannot be trusted with using citizens’ genetic information solely for forensic identification purposes, and that universal databases will create a “surveillance society” (Editorial, Nature, 2008).

One answer to the privacy dilemma would be to ensure, at a minimum, that the DNA samples of arrestees—who still are cloaked in the presumption of innocence and whose charges have not yet been subject to public scrutiny by grand or petit jury—are not retained by the state unless the case leads to conviction. In 2008, the European Court of Human Rights ruled that the United Kingdom could not retain the DNA samples of two men who were arrested but whose cases ended in acquittal and dismissal, respectively (Annas, 2009). Although a person’s 13-loci forensic DNA profile—ostensibly consisting of “junk” DNA—might contain little sensitive genetic information that we know of, the same cannot be said of a sample of the person’s DNA.

**Familial Searching**
As database searching takes a central role in criminal investigation, policy makers also will have to contend with the ethics of “familial searching.” The term refers to the practice of searching offender databases not only for complete profile matches but also for partial matches (e.g., 9 of 13 loci). Although the partially matching offender himself is excluded as a suspect, the similarity between his profile and the evidence sample arguably suggests that one of his close relatives might be the perpetrator (Gabel, 2010). Some jurisdictions have begun in earnest to use familial searching in criminal investigation with a handful of highly publicized results (Epstein, 2009). Although the technique holds promise for solving some otherwise unresolvable no-suspect cases, the process is controversial from a civil liberties standpoint because it subjects family members to police scrutiny based solely on the misdeeds of their relatives and is sure to affect minorities disproportionately (Mnookin, 2007). Assuming courts continue to uphold the practice’s legality, states at least should require that the DNA sample of a family member be destroyed when he is cleared of wrongdoing.

**Due Process Issues with Resurrecting Older No-Suspect Cases through Forensic Testing**
A final legal issue raised by resolving no-suspect cases through forensic testing is the potential unfairness of bringing a criminal prosecution years after the alleged crime. Older “cold hit” cases “raise justice-related concerns, especially since mounting a defense to a crime that occurred in the past is becomes increasingly difficult as time progresses” (Song et al., 2009: 22). Such
justice concerns with old cases are the reason statutes of limitations exist. But in more and more no-suspect cases with only a genetic profile to go on, prosecutors have begun to secure so-called “John Doe” indictments against the person(s) matching the genetic profile recovered from the evidence sample (Garrett, 2008). Although some argue that this practice allows prosecutors to perform an effective end-run around statutes of limitations, several states explicitly have amended their laws to allow such indictments (Garrett, 2008). Indeed, the federal Justice for All Act has extended the use of John Doe indictments to all felonies prosecuted under federal law (Powell, 2008).

Although the “John Doe” practice inherently might not offend due process, Congress and state legislatures should adopt standards requiring courts to consider the potential prejudice of pretrial delay on a case-by-case basis in deciding whether to allow a prosecution to proceed (Powell, 2008). Another potential and seemingly critical safeguard would be to appoint counsel for the “John Doe” target. This solution would allow counsel to investigate and document the crime scene, attempt to interview the government’s witnesses, and raise possible jurisdictional or other legal defenses to the indictment in a timely manner. If a human suspect matching the profile then is apprehended years later, the prejudice from pretrial delay at least has been minimized.

**Conclusion**

The investigation and potential resolution of no-suspect cases through forensic testing is a laudable goal, and police, prosecutors, and forensic examiners should heed Strom and Hickman’s (2010) call for uniformity and for a shift toward prioritizing testing in no-suspect rape and homicide cases. This priority shift necessarily will require increased reliance on forensic DNA and fingerprint databases to identify suspects in the first instance. As long as policy makers responsibly address the legal, ethical, and scientific issues uniquely raised by database-driven investigation, the promises of forensic testing in solving cold cases will outweigh the perils.

**References**


**Cases Cited**
*People v. Puckett*, No. A121368 (Cal. Ct. App.).

**Statutes Cited**

**Andrea Roth** is a teaching fellow at Stanford Law School. For 9 years, she was a public defender in Washington, DC, and litigated issues relating to DNA admissibility and access to forensic testing. She has written and lectured throughout the country on DNA and other forensic science issues. Her latest article, “Safety in numbers?: Deciding when DNA alone is enough to convict,” is forthcoming in the *NYU Law Review*. She is a 1998 graduate of Yale Law School.