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The Problem Child: Forensic DNA Databases, Familial Search, and A Call for Reform

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“It would be foolish to contend that the degree of privacy secured to citizens by the Fourth Amendment has been entirely unaffected by the advance of technology.”

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INTRODUCTION

The FBI’s Combined DNA Index System (CODIS) and its component databases are expanding rapidly. Originally profiling only certain classes of convicted violent felons, CODIS now includes all federal arrestees, convicts, and foreign detainees, as well as convicts from every state and arrestees from many. This expansion is driven by the desire to solve more crimes with forensic DNA evidence, which has proven a potent investigative tool.

This expansion has largely been blessed by courts, although some question remains as to the ultimate Fourth Amendment treatment of including DNA from arrestees.

The most controversial expansion, however—and one not yet examined by any court—comes in the form of familial DNA searching, a technology that permits indirect identification of blood relatives through their genetic similarity to a profiled offender. FBI labs have rejected this “problem child” of CODIS, but in response to strong state lobbying, the Bureau now permits states to perform familial searches at will. Two states, California and Colorado, have authorized familial DNA search regimes.

Familial DNA search is worrisome for several reasons: It overextends CODIS both legally and technically, improperly subjects individuals to scrutiny solely on account of their relatives’ misdeeds, and greatly aggravates the racial inequality already present in the offender database.

This paper summarizes the scientific and legal underpinnings of U.S. forensic DNA databases, and argues for several key changes to database policy.

Section I presents scientific background sufficient to understand what DNA profiles are, what they are not, and how DNA identification functions. This section also explains the principles underlying familial DNA search, and discusses DNA profiling in terms of genetic privacy.
Section II details the statutory authorization and subsequent expansion of CODIS and its component databases, at both federal and state levels. It also discusses authorization for collecting DNA from arrestees, and for familial DNA search.

Section III summarizes current legal treatment of DNA profiling, including the status of DNA collection as a Fourth Amendment search, past legal challenges to CODIS, and the arguments courts employ when upholding DNA collection. It then reports three ongoing cases concerning sampling of arrestees, and presents a legal analysis of familial search using established Fourth Amendment principles.

The final three subsections identify two key problems with current CODIS policies—DNA sample retention and familial DNA search—and propose specific reforms to tackle these concerns.

Section IV addresses privacy concerns stemming from DNA sample retention, and argues that forensic laboratories should retain only numerical DNA profiles, not full biological samples from profiled offenders.

Section V sets forth the troubling implications of familial DNA search, including technical and legal overextension of CODIS, improper singling out of offenders’ family members, and gross aggravation of existing racial inequality in offender databases. This Section argues for an immediate end to familial DNA searching, but notes also the difficulty in prohibiting this technique given current Fourth Amendment jurisprudence.

Section VI presents a separate approach to neutralize the intolerable symptoms of familial search: Expanding CODIS into a universal, population-wide, sample-free database.

This Section argues for a universal database for five reasons: (1) Universal coverage comports with genetic privacy concerns because CODIS-style DNA profiles offer virtually no possibility for misuse; (2) universal coverage will eliminate problems stemming from incomplete coverage, as well as (3) aborting familial search and the aggravated racial inequality it brings; (4) including all citizens will properly subject
CODIS to increased political oversight; and (5) a universal database is potent tool for law enforcement, permitting first-time offenders to be identified and more innocents exculpated, while at the same time removing stigma associated with inclusion. This Section closes with a legal analysis of this proposal, arguing that universal coverage may be possible now—and if not, suggesting avenues by which such coverage could legally be achieved.

I. **SCIENTIFIC FOUNDATIONS OF FORENSIC DNA**

Every human on earth—barring identical twins—carries unique genetic material, encoded in DNA and called the genome. Although the vast majority of the human genome is common to all people, about 0.5% differs between any two individuals. This tiny fraction of divergent genetic material makes each human different, and also makes forensic DNA identification possible. This section provides a primer on the science underlying DNA profiling, as well as highlighting genomic privacy concerns.

**DNA, the Genome, and STRs**

This subsection presents a brief introduction to the science behind DNA profiling, including genomic organization, a brief overview of repeated DNA sequences and their usefulness in forensic identification, and how DNA profiles are computed from 13 genetic markers.

**Genomic Organization**

A human being consists of roughly 50-100 trillion cells, virtually all of which carry a full diploid copy of that individual’s complete genetic information, or genome. This genome in turn consists of some 3 billion nucleotides of deoxyribonucleic acid.
DNA—the four component nucleotides of which are chemical bases commonly represented by the letters A, C, G and T—arranged into 23 long strands, called chromosomes. There are 22 autosomal chromosomes (numbered 1 through 22) and one sex chromosome; the latter can take two forms (X or Y). A normal human cell carries two copies of each autosomal chromosome, and two copies of the sex chromosome, making 46 chromosomes in total; the normal sex chromosome arrangement is XX in females, and XY in males. The human genome, then, is a duplicate set of long chemical strands, each copy of can be envisioned as a single concatenated text string of about 3 billion A, C, G and T characters. To the unaided observer, the order of these characters appears largely random.

Every living thing on Earth carries its genetic material in strands of DNA, although chromosomal number and arrangements differ between species. These long strings composed of just four chemical bases encode a stunning diversity of life. An individual’s precise genetic DNA sequence, or genotype, helps determine its appearance, or phenotype. Two individuals of a given species – say, two humans, or two hamsters – will share nearly identical genomes, with small differences in sequence

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3 Each chromosomal strand is itself a long DNA double helix, coiled around a protein scaffold. Each double helix consists of two complementary strands of DNA base-paired together: that is, A pairs with T, and G pairs with C. Because the two strands are complementary, the sequence of one dictates the sequence of the other, and as such, scientists need only report the sequence of one of the strands.

4 Some cells differ in their DNA complement. For instance, mature red blood cells do not have a nucleus, and thus do not carry genomic DNA. Sex cells (sperm and egg cells) each carry only a half complement, namely a single copy of each autosomal chromosome and a single X or Y.

5 Some types of viruses carry their genetic information as ribonucleic acid (RNA), a chemical compound very similar to DNA. However, a virus is not considered free-living, since it must infect a host cell and hijack its machinery to reproduce.

6 The genome of a rosebush, for instance, is very different from that of a whale, both in sequence length, chromosomal number and arrangement, and sequence content. However, both genomes consist of long strings of these same four nucleotides. It is possible to compute similarity scores between any two species based on their DNA, and thereby to deduce their evolutionary distance and relatedness. This practice is called phylogenetics.

7 Genotype is important, but not all-determining. The standard rubric taught to biology undergraduates is that genotype + environment = phenotype. Environmental conditions (which includes, among many other things, availability of nutrients at given points in the developmental process) can influence biological development as well. This is readily observable in identical twins, or more recently, in cloned animals: these individuals, despite being genetically identical to one another, nonetheless exhibit some slight morphological differences.
contributing to observable morphological differences between individuals. In two humans selected at random, the sequence of nucleotides will be 99.5% identical.\(^8\)

This near-identity can cause some confusion when discussing the human genome. The draft human genome, sequenced and widely publicized in 2001,\(^9\) was in actual fact a mixture of several individuals’ genomes called a reference genome. Researchers at that time were interested in elucidating the sequence of the vast majority of DNA shared by all humans. In this context, sequencing the “human genome” was a monumental achievement that continues to shed light on the genetic and biological underpinnings of our species.

More recently, attention has turned to the relatively small amount of genetic material at which individuals differ.\(^10\) This roughly 0.5% of divergent sequence corresponds to about 15 million nucleotides of DNA. Some of this sequence likely accounts for commonly observed differences such as height, eye color, skin pigmentation and so forth; other sequence may correlate with unseen differences among individuals, such as predisposition to various forms of disease; and still other divergent DNA sequence has no biologically meaningful effect, and may therefore be useful as a marker to differentiate individuals from one another without disclosing sensitive genetic information. It is this latter type of sequence that is measured in CODIS profiles to uniquely identify an individual.

**Short Tandem Repeats (STRs)**


10 See, e.g., the Personal Genome Project, [http://www.personalgenomes.org/](http://www.personalgenomes.org/) (last visited July 3, 2009). This project, led by Dr. George Church of Harvard Medical School, aims to sequence the genomes of a large number of individuals, enabling comparisons between them.
To appreciate the way in which such DNA markers are used for identification, it is necessary to understand in general terms the organization of the human genome. Each of our 3 billion nucleotides can be classified as either coding DNA or non-coding DNA. Coding DNA corresponds roughly to genes, which in general usually means discrete DNA sequences that are “read” to produce functional molecules such as proteins. Coding DNA accounts for less than 2% of the human genome. The other 98% is non-coding DNA, which was at one time called “junk DNA” due to its apparent lack of function.

A large number of repeated DNA sequences exist, chiefly within these non-coding regions. Stretches of repeated DNA can be classified according to the length of the repeated sequence block (for instance, a string of 5 nucleotides “CATGC” could be repeated several dozen times, yielding “CATGCCATGCCATGC…”).

One such class of repeats is called short tandem repeats (STRs), and is characterized by a block of 1 to 6 nucleotides repeated anywhere from 5 to 100 times. Individuals may differ in the number of times any given sequence block is repeated in their DNA.

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12 See ENCODE Project Consortium, *Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project*, 447 NATURE 799 (Jun. 14, 2007). Estimates of the number of genes in humans varies and is frequently revised as new discoveries are made; at the time of this writing, there are 21,370 known protein-coding genes and a further 5,732 RNA-coding genes in human, although the predicted number of actual genes ranges as high as 50,000. See Ensembl genome browser 54 – H. sapiens – Assembly and Genebuild, http://www.ensembl.org/Homo_sapiens/Info/StatsTable (last visited July 12, 2009).

13 More recently, however, this term has fallen out of favor as scientists have begun to uncover novel functions in these vast non-coding regions. See, e.g., W. Wayt Gibbs, *The Unseen Genome: Gems Among the Junk*, SCIENTIFIC AMERICAN 29 (Nov. 2003).

With very rare exceptions, an individual will carry two alleles per STR locus, one at each chromosomal copy. These alleles can be the same (homozygous) or different (heterozygous).

STRs offer a convenient way to differentiate between individuals through markers that are, biologically speaking, essentially meaningless. At a given STR locus, one individual may have five copies of the repeated unit, whereas others might have three, four, or six copies. Each different number of repeats is called a different “allele” of the STR. Thus, at any one STR site, two randomly selected humans may share the same alleles (number of repeats), or their alleles may differ.

Because many thousands of STRs exist in the human genome, and because many display this sort of limited, integer-based allelic variation, it is possible to genetically “fingerprint” any individual by characterizing the number of repeats at their various STR loci.

To uniquely pinpoint an individual, however, it is not necessary to examine all STR loci in the genome, or anywhere close to that number. In the UK, forensic DNA labs characterize just 10 STR loci, and in the US, the FBI uses a set of 13. Even a small set of loci carries tremendous resolving power, and indeed has accounted for virtually all forensic DNA identification up to this point.

Law enforcement agencies began identifying suspects via DNA forensics considerably before the announcement of the draft human genome sequence in 2001. This is because the process for amplifying and characterizing STRs is straightforward,

17 Locus (plural: loci) commonly refers to a specific span or region of DNA sequence.
20 See *infra* notes 71-74 and accompanying text.
has been common practice for several decades, does not depend upon knowing the full genome sequence, and in fact involves no DNA sequencing at all.

Once an STR is selected for analysis, differentiating individuals based upon their number of repeats at that site amounts to taking DNA samples from each person concerned, amplifying the repeated region via PCR, then assessing its length in each sample via electrophoresis. The result will be a numerical measure of sequence length, corresponding to the number of nucleotides present in the repeated region, and therefore proportional to the number of times the sequence block is repeated. For instance, if a given person has 6 copies of the repeat ATGG at a certain locus, then the total length of the repeated region at that locus will be 24 nucleotides (6x4); an individual with 7 copies would return a value of 28, and so on. Factoring out the length of the repeated block, the process yields an even simpler numerical value: the number of repeats present at each site (in these examples, 6 and 7).

DNA profiles, then, are conceptually similar to a genomic abacus, counting up repeated sequence units at various specific locations to arrive at a final numerical tally.

**CODIS Alleles Differ in Prevalence, Mutation Rate**

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21 Polymerase Chain Reaction. This technique, which revolutionized molecular biology in the early 1980s, involves amplifying a specific region of DNA by several million-fold through thermal cycling, and the use of short molecules of DNA called primers that flank the region to be amplified. Today, the technique is readily performed by machines in the lab, and allows quick and easy amplification of STRs, along with many other regions of interest.

22 Electrophoresis is a well-established laboratory technique that separates charged molecules (such as DNA or denatured proteins) by size and shape, by drawing them through a gel matrix with an electric charge. Linear DNA molecules of various lengths migrate at known rates in an electric field, and as such, after staining the gel to reveal how far each band of DNA has travelled, the nucleotide length of a DNA sample can be discerned without the need for DNA sequencing.
The 13 STR loci selected for use in CODIS\(^\text{23}\) are not created equal: An individual is more likely to match a stranger at certain of these loci than at others, and even at a single locus, some alleles (numbers of repeats) are more prevalent in the general population than others.

At each CODIS STR locus, only a finite number of alleles exist at an appreciable frequency within the population: This number of alleles ranges from 6 to 21, depending on the locus.\(^\text{24}\) A locus with only 6 possible alleles, or genetic states, means that two individuals are much more likely to match randomly at that locus—that is, to share the same number of repeats by chance—than they are to match at a locus with, say, 21 possible alleles. (In the former case, each person occupies one of only six states; in the latter, one of 21.)

Moreover, even within the finite set of possible alleles at a given locus, each allele is not equally prevalent within the population. For instance, it may be much more common to see five repeats at a given STR locus than it is to see three, or eight, in the population at large.\(^\text{25}\) (If this were so, an individual with five repeats would match many more people at that locus by chance, simply by virtue of carrying a more common allele.)

To complicate things still further, the CODIS loci and their alleles mutate at different rates. (Mutation at STRs generally causes insertion or deletion of repeats, and

\(^{23}\) The 13 CODIS STR markers are: D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, THO1, TPOX, and CSF1PO. Also included is the amelogenin (AMEL) sex determining polymorphism.

\(^{24}\) See Budowle et al., supra note 34, at 62 (Table 1, recounting the number of alleles that occur with a frequency greater than 0.01); Bruce Budowle, B. Shea, et al., CODIS STR loci data from 41 sample populations, 46 J. FORENSIC SCI. 453 (2001). Professor Greely refers to a range of 7-23 alleles at STR loci, but does not reference this figure. See Greely, supra note 83 at 250. In actuality, because the human population continues to reproduce and our DNA accrues new mutations, there is no single definitive answer to the total number of alleles at any STR locus; a new allele can arise in the population at any time. Hence, Budowle’s approach— including only those alleles that have achieved some prevalence in the population—seems the most sensible, and yields the figures reported here.

\(^{25}\) See, e.g., Thomas M. Reid, Michael L. Baird et al., Use of sibling pairs to determine the familial searching efficiency of forensic databases, 2 Forensic Sci. Int’l: Genetics 340, 340 (2008) (discussing the ‘kinship matching’ approach, which takes into account the population frequency of matching alleles to compute relatedness).
therefore, changes one allele into another). Initially, a single standard mutation rate\(^{26}\) was assumed to apply all STR loci, but more recently mutation rates have been shown to vary between loci.\(^{27}\) Also, it has now become evident that even within a single STR locus, certain alleles are more prone to mutation than others.\(^{28}\)

**Identifying Individuals using CODIS STRs**

The 13 CODIS STRs are spread across 12 of the 22 autosomal chromosomes.\(^{29}\) A DNA profile\(^{30}\) therefore contains 26 two-digit numerical scores,\(^{31}\) corresponding to the nucleotide lengths at 13 different STR loci on both chromosomal copies (26 alleles total).\(^{32}\) This 52-digit profile (a two-digit measurement per STR, times two chromosomal copies, times 13 STRs) is an individual’s genetic fingerprint.

“Fingerprinting” an individual by measuring these 26 alleles\(^{33}\) generates surprisingly complex combinations, sufficient for highly reliable statistical matches between searched profiles and the CODIS database.

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\(^{26}\) Here, mutation rate refers to the rate of spontaneous change in repeat number at a given STR locus. This change occurs between generations. This standard mutation rate (\(\mu\)) was initially assumed to be ~0.001, or one in one thousand. That is, it was assumed that 1/1000 children would inherit through mutation a different number of repeats than either parent had at any one locus. The new number of repeats was usually +/- 1 repeat; spontaneous insertions or deletions of more than one repeat are less common. Note that in most cases, gain or loss of a single repeat through mutation will yield an allele already present in the population – just not present in the parents.


\(^{29}\) For an inventory of these STRs, see supra note 23.

\(^{30}\) An actual CODIS database record contains other pieces of information in addition to this 13-STR profile, see infra note 84, and related text.


\(^{32}\) Recall that each individual carries two copies of each autosomal chromosome, and two sex chromosomes. If a given STR locus is located on chromosome 8, for instance, then the individual will have two loci to examine: one on each copy of chromosome 8. These two alleles need not be, and often are not, the same.

\(^{33}\) Given a DNA sample, crime labs can now amplify all CODIS loci at once with a single kit, averaging $20 per sample. See, e.g., Promega® PowerPlex 16 system, http://www.promega.com/catalog/catalogproducts.aspx?categoryname=productleaf_1428, (last visited
The statistics underlying pairwise matches of DNA profiles to CODIS have been thoroughly discussed elsewhere and lie beyond the scope of this paper, but in brief, it suffices to note that CODIS returns highly significant matches using just these 13 loci.

On average, two randomly selected individuals are likely to share no more than 8-9 alleles out of 26 total; cousins will share 11; parents and their children will share at least half, with 16 being most common, and siblings will share 17 alleles on average. Identical twins, of course, share all 26 alleles.

The chance of two unrelated people matching all 26 alleles (i.e., matching both at all 13 STR loci) is infinitesimal, with the odds usually estimated as upwards of one in several billion, up to one in a quadrillion.

**CODIS Ignores Allelic Prevalence and Distribution Patterns**

April 28, 2010 (allowing users to “[a]mplify all 13 CODIS STR loci in one reaction” and listing the price for a 100 reaction kit at $2069).

34 See, e.g., Bruce Budowle, F. Samuel Baechtel & Ranajit Chakraborty, *Partial matches in heterogeneous offender databases do not call into question the validity of random match probability calculations*, 123 INT. J. LEGAL MED. 59, 62 (2009); Yun S. Song, et al., *Average Probability that a “Cold Hit” in a DNA Database Search Results in an Erroneous Attribution*, 54 J. FORENSIC SCI. 22 (2008) (providing a formula to calculate the average probability that another person exists in the population whose profile matches the crime-scene sample but who is not in the database).

35 Paoletti, supra note 15, at 3 (listing hypothetical shared allele counts among 13 CODIS loci as 8.59 between random individuals, 10.95 between cousins, and 16.94 between siblings). Barring mutation, normal parent-child pairs must share at least 13/26 alleles, in a distinctive pattern (at least one shared allele per locus); on average, they will share 15.7 alleles. Siblings can theoretically share anywhere from 0-26 alleles, but on average will share 16.7. 13 of these come from a 50% chance of each sib inheriting the same allele from a parent; additional alleles come from 1) parents possibly having 2 copies of an allele (i.e. being homozygous at that locus), or 2) parents sharing an allele. For an average pair of Caucasian siblings at 13 STR loci, there is 1 locus with no shared alleles, 7 loci with one shared allele, and 5 loci with both alleles shared. See Greely, supra note 83 at 250, 252.

36 Greely, supra note 83 at 250 (giving the odds as “one in several hundred billion”); Department of Energy, Human Genome Project Information: DNA Forensics, at http://www.ornl.gov/sci/techresources/Human_Genome/elsi/forensics.shtml (last accessed July 16, 2009) (giving the odds as “one in a billion”); Jason Felch & Maura Dolan, *FBI resists scrutiny of ‘matches’*, L.A. TIMES (Jul. 20, 2008), available at http://articles.latimes.com/2008/jul/20/local/me-dna20 (last accessed May 4, 2010) (giving odds as “1 in 100 billion” and “as remote as 1 in 1 quadrillion”). A precise answer is difficult to produce due to the relatively high incidence of monozygotic (identical) twins, triplets and so on in human populations, and the omnipresent chance of encountering outliers even within a relatively small population.
CODIS achieves these highly significant matches despite not using STR-based DNA profiles to their full resolving potential. Specifically, CODIS ignores two useful genetic factors: allele frequency, and allelic distribution patterns.  

First, CODIS does not currently take into account the relative rarity of each allele in the population. Thus, a hit based on two profiles matching at the most common allele is treated the same as a hit based on two profiles matching at a very rare allele, even though in the latter case, the two samples are more likely to come from the same source—or in the case of familial DNA search, to come from actual relatives.  

Second, CODIS does not report allelic distribution patterns. When comparing DNA profiles from parents and children, a common pattern is for one of each pair of alleles to match—that is, not only will at least 13 of 26 alleles match, but they will do so in a distinctive pattern: matching at least one allele of every pair. The odds of matching 13/26 alleles in general is roughly 3%; however, the odds of matching 13/26 alleles in this particular pattern (one of every pair) is less than 1 in 2000. Hence, parents and children share a particular inheritance pattern than that CODIS could spot—but does not.

CODIS remains capable of producing matches with a very high statistical significance, even without taking these factors into account. However, its inability to

37 CODIS also does not exploit chromosomal linkage. Two of the 13 CODIS loci are located on chromosome 5 (these loci are D5S818 and CSF1PO; see National Institutes of Standards and Technology, supra note 72) and each individual has two separate copies of chromosome 5. If two DNA profiles match, CODIS is not set up to report whether the same two alleles co-localize to the same physical chromosome in each sample. Granted, this analysis may be of limited use when the odds of a match at all 13 loci are so long. However, this analysis would be highly valuable for partial match or familial searching, because parents and children share different allelic conservation patterns than siblings—and neither group normally matches at all 13 loci. Of course, at increasing distances between markers on the same chromosome, normal DNA recombination during sexual reproduction effectively de-links even such ‘linked’ markers.

38 Steinberger & Sims, Familial Searching in California, supra note 46, at 31.

39 To be fair, this is presumably because when CODIS was launched, allelic population distributions were not well known. Of course, even currently accepted allelic distributions are taken from the database as it now stands; these distributions could shift dramatically if suddenly all Americans were profiled and added to the database.

40 CODIS could conceivably assign a scaled score according to the relative rarity of the alleles constituting each match or mismatch between profiles.

41 See Greely, supra note 83 at 252.
process allele frequency and allelic distribution are a major hindrance to familial DNA searching, the topic of the next subsection.

**Identifying Close Relatives with CODIS STRs**

Close relatives share a substantial fraction of their DNA, and along with it, a substantial fraction of their STR-based DNA profiles. This principle can be exploited in so-called familial DNA searches to match forensic DNA profiles against a CODIS profile belonging to a relative of the profiled offender. This section sets forth the genetic underpinnings of Mendelian inheritance, and the partial profile matching techniques that make such searches possible.

**Inheritance of STRs and Family Relatedness**

In each normal somatic cell, a person carries 46 chromosomes: 2 copies of each of the 22 autosomal chromosomes, and 2 copies of the sex chromosome. Within each chromosome pair, one copy is inherited from the mother and the other from the father.42

The same principles that Gregor Mendel elucidated through his study of pea plants43 also apply to human reproduction. Namely, human alleles display segregation (each sperm or egg receives one chromosome from each parent) and independent

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42 To illustrate this, consider the sex chromosomes. Because women are XX, all of a woman’s egg cells should carry one X chromosome: When partitioning the chromosomes, the mother has only X to give. The sex of the child, then, is up to the father (XY); half of his sperm should carry X and the other half should carry Y. Women received an X from their mother and an X from their father; men received an X from their mother and a Y from their father. This also explains why at a population level, nearly half of all babies born are boys, and half are girls.

43 Gregor Mendel is widely considered to be the father of genetics. Crossing and breeding pea plants in the mid-19th century, Mendel showed that certain traits (such as flower color or plant height) are passed on as discrete entities, and do not appear blended in offspring. See Mendel, J.G. 1866. *Versuche über Pflanzenhybriden. Verhandlungen des naturforschenden Vereines in Brünn 4 ABHANDLUNGEN*, 3–47. Cited by Robert C. Olby (1997) on [http://www.mendelweb.org/MWolby.html](http://www.mendelweb.org/MWolby.html) (last visited Mar. 16, 2009).
assortment (which of the two chromosomes a given sperm or egg receives—i.e., whether it is maternal or paternal in origin—is random). 44

STR alleles are inherited. Barring mutation, if an individual has \( n \) copies of a given repeat at a particular STR locus, those \( n \) copies were inherited from a parent, and the same number \( n \) may be passed on to a child. STR alleles do mutate (that is, the number of repeats may change) at a higher rate than other, non-repetitive DNA, 45 although mutation is not so frequent as to seriously impact the basic inheritance patterns described here.

To illustrate inheritance in the STR context, consider the example of a particular STR locus on an autosomal chromosome. A father carries 2 copies of this chromosome, so the STR of interest occurs twice, once on each copy: imagine the father carries two alleles, with 4 and 6 repeats. His wife, the child’s mother, carries 3 and 3. What might their child carry?

From the father, the child will receive a single chromosome carrying either 4 or 6 repeats; from the mother, the child will receive a single chromosome necessarily carrying 3 repeats. Thus, 50% of the children should have 4 and 3, and 50% should have 6 and 3 at this locus. If an impostor child arrives who is found to have 1 and 3 repeats at this locus, we can be reasonably certain that he arose from a different father. Thus, along with blood type analysis and other methods, STR analysis is useful in paternity testing—as well as determining biological relatedness in general.

**Partial Matches and Familial DNA Searching**

Familial DNA search exploits the fact that close relatives share a substantial fraction of their DNA. Matching a DNA sample to a close relative profiled in CODIS is relatively simple, and in principle involves only changing the threshold on the database

44 Note here that “maternal” refers to the parent of the sperm donor, or the grandmother of any child the sperm eventually produces. When the individual in question generates sperm cells, each sperm receives one chromosome from each pair—either the maternal or paternal copy.

45 See Jia & Chu, supra note 14.
search. Whereas a typical exact hit requires a high-stringency search—that is, all 26 alleles at all 13 CODIS markers must match—searches can also be performed at lower stringencies, thereby reporting pairs of profiles that match only at some fraction of the alleles.\footnote{46 For a general overview of this technique, see Frederick R. Bieber \textit{et al.}, \textit{Human Genetics: Finding Criminals Through DNA of Their Relatives}, 312 \textit{Science} 1315 (2006); David R. Paoletti \textit{et al.}, \textit{Assessing the Implications for Close Relatives in the Event of Similar But Nonmatching DNA Profiles}, 46 \textit{Jurimetrics} J. 161 (2006); Eva Steinberger & Gary Sims, \textit{Finding Criminals Through the DNA of their Relatives – Familial Searching of the California Offender DNA Database}, 31 Prosecutor’s Brief 28, 30 (2008) (hereafter Steinberger & Sims, \textit{Familial Searching in California}).}

Low stringency (or “partial match”) searches arose as a tool to deal with degraded DNA samples, where some alleles may be missing or improperly recorded;\footnote{47 Steinberger & Sims, \textit{Familial Searching in California}, supra note 46, at 29.} they are also useful when the forensic sample contains a mixture of DNA from multiple individuals.\footnote{48 \textit{Id.}}

Because first-degree relatives match, on average, at half their alleles or more, a low stringency search of a crime-scene profile against CODIS can also return any close relatives of the offender who might be profiled in the database.

When partial matches are returned in the course of normal CODIS queries (i.e., when searching for an exact match) they are referred to as “partial matches” or “candidate matches”\footnote{49 Interview with Michael T. Bourke, Ph.D., Connecticut CODIS State Administrator (Storrs, CT; Oct. 5, 2010).},\footnote{50 Steinberger & Sims, \textit{Familial Searching in California}, supra note 46, at 29.} when deliberately sought, the technique is referred to as familial searching.\footnote{50 Steinberger & Sims, \textit{Familial Searching in California}, supra note 46, at 29.}

Although familial DNA searching sounds simple, even elegant, in practice it is complicated by several issues.

\textbf{Known Issues with Familial DNA Searching in CODIS}

Due chiefly to its inability to process allele frequency and allelic distribution data, partial match searches of CODIS are crippled by an “unmanageable” number of false
positive results.\textsuperscript{51} A single low-stringency search may return many thousands of partial matches,\textsuperscript{52} the bulk of which match only by chance—meaning the matching profiles do not actually belong to close relatives of the search target.\textsuperscript{53}

A candidate partial match result may be a true parent-child or sib-sib relative, but more often is likely to belong to a random individual with no meaningful genetic relationship to the queried individual.\textsuperscript{54} Even expanding the number of CODIS loci from 13 to 15 would not permit true sib-pairs to be distinguished with confidence from false matches.\textsuperscript{55}

Because of these CODIS limitations, familial search is feasible only with specialized search software\textsuperscript{56}—for instance, a program that measures allele sharing.

\textsuperscript{51} Steinberger & Sims, Familial Searching in California, supra note 46, at 31.

\textsuperscript{52} The odds of matching 13 of 26 alleles is 3\% in the general population. See infra note 41 and related discussion. Matching 3\% of the ~7 million records in CODIS today would return 210,000 matches.

\textsuperscript{53} Such partial matching profiles may be statistically interesting, but they are useless for lead generation: after all, the motivation underlying familial DNA search—identifying a relative of the offender, and then using this lead to reach the offender—does not work if the resulting “match” is unrelated to the offender, but simply happens to match at a number of loci.

\textsuperscript{54} Such searches will still return a large number of false positives, even if allelic rarity is considered. This was neatly illustrated by a 2008 research study. Using a mock offender database containing 12,292 profiles, Reid and coworkers sought through two methods to identify known (true) sibling pairs and exclude false positive matches. This study tests both profile matching based on shared alleles and kinship matching, which also takes into account the population frequency of the shared alleles. While both methods were effective at (eventually) identifying true sib pairs, they both produced an unacceptably high number of false positives alongside the true match. Thus, siblings are always easy to identify in partial-match-stringency searches; in other words, a partial search of an offender database will likely return siblings, if any exist, as well as other unrelated individuals who nonetheless share similar DNA profiles at the CODIS loci. See Thomas M. Reid, Michael L. Baird \textit{et al., Use of sibling pairs to determine the familial searching efficiency of forensic databases}, 2 \textit{FORENSIC SCI. INT’L: GENETICS} 340 (2008).

\textsuperscript{55} See Chang E. Pu & Adrian Linacre, \textit{Systematic evaluation of sensitivity and specificity of sibship determination by using 15 STR loci}, 15 \textit{J. FORENSIC & LEGAL MED.} 329 (2008). (Even using 15 STR loci does not permit all true sib pairs to be distinguished from non-sib-pairs. The best approach for distinguishing them, absent parental DNA, is a combination of “combined sibship index” and “two-allele-sharing locus” measures.)

\textsuperscript{56} See Pu & Linacre, supra note 55. See also Dolan & Felch, supra note 110 (quoting Lance Gima, California’s top forensic scientist, who stated that although familial searching would provide new leads to police, “the search for relatives would be a longshot because many unrelated people share genetic markers. He said he hoped the state's decision would spur technology to improve the accuracy of such searches.”).
patterns, as well as the rarity of each allele—and by following up candidate matches with further analysis such as Y-STR typing.57

**Genetic Privacy: DNA Samples versus DNA Profiles**

May 21, 2008 saw the enactment of the Genetic Information Nondiscrimination Act (GINA), a new law designed to prevent improper use of genetic information in the areas of employment and health insurance.58 In its final form, GINA enjoyed overwhelming support, passing the Senate 95-059 and House of Representatives 414-1.60 This success has been credited to mounting public fear over once-unknown genetic information becoming available to and misused by employers, insurers and others.61

Flatly stated, this fear is well founded. The human genome is an information-rich data warehouse that poses a considerable privacy threat for two reasons.

First, human genomic DNA—the full genome, as found in a DNA sample such as a blood sample, hair sample or cheek swab—encodes the biological blueprint necessary

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57 Steinberger & Sims, *Familial Searching in California*, supra note 46, at 31. Y-STR typing involves profiling a different set of STRs, all located on the Y-chromosome. The normal male genotype consists of one Y chromosome and one X chromosome, with the Y chromosome inherited directly from the father. Any siblings would inherit the same Y haplotype. A match between profiles at all Y-STRs provides strong support for the profiles belonging to true blood relatives, whereas differences in Y-STRs readily eliminates false positives. Note that normal females do not carry a Y chromosome, so this particular technique is useful only as a follow up to male-male profile matches.


61 See Steven Greenhouse, *Law Seeks to Ban Misuse of Genetic Testing*, N.Y. TIMES (Nov. 15, 2009) at B5 (stating that “[GINA] was passed by Congress last year because many Americans feared that if they had a genetic test, their employers or health insurers would discriminate against them, perhaps by firing them or denying coverage[,]” and citing survey results).
to create an individual person. As such, it can divulge a vast amount of sensitive biological information, from outwardly observable characteristics to health information such as genetic predispositions to disease. Moreover, because of the high degree of DNA commonality between relatives, an individual’s genome also carries substantial information about blood relatives, particularly close kin like parents, children and siblings.

Second, we routinely shed DNA samples—in shed skin cells, in hair, in saliva on soda cans and cigarette butts, and so on.62 This reality is sure to pose challenging legal questions in coming years, as DNA sequencing becomes ever less expensive and time-consuming, and thus available to an ever broader audience.63

CODIS-style DNA profiles, by contrast, are useless from a health privacy perspective.64 The 13 CODIS STRs were specifically chosen from stretches of non-coding DNA not “associated with any known physical or medical characteristics.”65 The CODIS DNA profile is simply a collection of numbers characterizing the varying length

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62 See, e.g., Kincade, 379 F.3d at 873 (Kozinski, J., dissenting) (“[W]e can’t go anywhere or do much of anything without leaving a bread-crumb trail of identifying DNA matter.”)


64 See DNA-Sample Collection and Biological Evidence Preservation in the Federal Jurisdiction, Final Rule, 73 FED. REG. 74932-74943 (Dec. 10, 2008) (to be codified at 28 C.F.R. pt.28), at 74938 (stating that “the DNA profiles retained in the system are sanitized genetic fingerprints that can be used to identify an individual uniquely, but do not disclose an individual’s traits, disorders, or dispositions”) (internal quotation marks omitted) (hereinafter DNA Collection in the Federal Jurisdiction).

65 U.S. v. Kincade, 379 F.3d 813, 818 (9th Cir. 2004) (en banc), cert. denied, 544 U.S. 924 (2005), (citing H.R.Rep. No. 106-900(I) at *27). See also Solomon Moore, In a Lab, an Ever-Growing Database of DNA Profiles, THE NEW YORK TIMES (May 11, 2009) (“By collecting such “junk DNA,” [as the CODIS markers,] which have no known genetic characteristics, police agencies can argue that they are not violating privacy rights. “There is nothing that would reveal any medical or physical characteristics at all,” said Jennifer C. Luttman, who runs the offender-DNA collection program.”).
of repeated DNA at a handful of STR sites: A form of stochastic variation that has no known connection to meaningful biological function.

As Arizona State Professor David H. Kaye has noted, only four ways exist through which “genetic loci could possess predictive or diagnostic value with regard to diseases,” and “none of these mechanisms can be exploited to produce a valid and useful disease-screening test” with CODIS loci, either now or in future. Forensic DNA scientists prefer STR loci precisely because they do not convey meaningful phenotypic information.

Profiling a small number of loci also forecloses potential abuses through data mining. Neither a geneticist nor a data-mining expert would be particularly surprised to learn that personal information can be extracted from STR profiles given a sufficiently large data set. For instance, recent scientific work has shown that by profiling 500,000 loci (as opposed to the FBI’s 13), it is possible to pinpoint an European individual’s birthplace to within a few hundred kilometers. By limiting the number of profiled loci to the minimum necessary to ensure match accuracy, CODIS avoids such concerns.

As with whole-genome sequencing, new technologies also promise to speed and cheapen the processing of CODIS-type STR profiles. Indeed, DNA profiles may soon be

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66 Kaye, Let’s Bury the Junk, supra note 16 at 72. The four mechanisms through which a locus could have predictive or diagnostic value are “(1) mutations at the locus itself,” which would mean that individuals with differing CODIS alleles display some meaningful biological difference, something known to be untrue; “(2) physical linkage of this locus to a locus at which a disease-causing mutation is present,” a situation which is unlikely to present itself because STRs in general have a high mutation rate, which would effectively destroy useful linkage in the general population; “(3) population structure,” which is unlikely to be useful, since even if STR profiles could be correlated efficiently to race, for instance, predicting disease propensity based on race alone is weak and inefficient; and the fact that “(4) trisomies” or abnormal chromosome number conditions, such as Down’s Syndrome, might be detectable with STRs, which is unlikely to be useful since the condition is likely to be known already via other means. Id. at 72-78.

67 Interview with Dr. Carll Ladd, Ph.D., head of DNA forensics, Connecticut State Crime Lab, 278 Colony St., Meriden CT (Fri. Mar. 27, 2009).

68 John Novembre, Toby Johnson et al., Genes mirror geography within Europe, 456 Nature 98 (Nov. 6, 2008) (analyzing some 500,000 variable markers among 3,000 European individuals and generating with “surprising accuracy” a map of their origins).
processed in minutes via hand-held devices. But even if this were to occur, and even if such devices were to become publicly available, even a rapid hand-held CODIS processor used indiscriminately on shed DNA samples is unlikely to reveal any sensitive health information about the individuals who left them. As should by now be clear, distilling a CODIS profile from genomic DNA ignores potentially sensitive health information. The profiles cannot reveal what they do not contain.

A full treatment of the privacy implications of the fascinating and fast-approaching future of inexpensive routine personal genome sequencing is beyond the scope of this paper. However, it is valuable to note that whereas DNA profiles are harmless from a health privacy perspective, DNA samples—containing the entire genome—certainly are not.

**Summary: The Genome, As Seen By CODIS**

The human genome is a vast chemical information repository, which scientists have chosen to represent with an equally vast character string composed of just four different letters. The fanfare surrounding the 2001 release of the draft human genome sequence centered on the fact that researchers had uncovered the common genetic blueprint of all humans. However, to a forensic DNA scientist wishing to differentiate

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69 Such devices have been promised for some time. See, e.g., Jack Kelly, DNA Takes the Stand, INVENTION & TECHNOLOGY MAGAZINE Vol. 22 Iss. 2 (Fall 2006), available at http://www.americanheritage.com/articles/magazine/it/2006/2/2006.2_44.shtml (last visited April 16, 2010) (stating that “[w]ithin a few years, police will be able to analyze evidence and produce a profile in minutes using hand-held devices right at the scene of a crime. By tapping into a computerized database, they may be able to implicate a specific individual almost immediately”); Lori Pilger, Cold Cases Reopened, LINCOLN JOURNAL-STAR (Oct. 28, 2006), available at http://journalstar.com/news/article_508dfb09-0f91-575c-9f28-1680262582b0.html (last visited April 16, 2010) (noting that “within five years, [a police investigator] suspects investigators could be doing DNA analysis in the field, feeding drops of blood at a crime scene into a hand-held device that spits out a preliminary DNA profile. The technology is there, he said . . . .”) (emphasis added).

70 Due in part to the increased mutation rate at STR loci, this applies equally to applying data mining techniques to the profiles. For more information, see the discussion of the four potential ways CODIS loci might reveal health information in Kaye, Let’s Bury the Junk, supra note 16 at 72-78.
between individuals, our shared DNA blueprint is of very little use. Instead, forensic analysts pay attention to the small fraction of genomic sequence at which individual humans consistently differ. Within this small set, they focus on short repeated sequences with no apparent biological or medical meaning. Having settled on a group of just 13 STRs, technicians measure the length of each repeated region, and proceed to identify individual humans by just 26 integer numbers—corresponding to the number of repeated sequences, on both chromosomal copies, at these 13 STR sites.

Thus, DNA profiles—these sets of 26 numbers—are incapable of disclosing sensitive health information or disease propensities, even if these records were not anonymously stored, and even if they were somehow released. By comparison, a DNA sample—for instance a blood or saliva sample containing the entire genome—most certainly can disclose sensitive information and poses a far more meaningful risk to personal privacy, not least because humans shed copies of their full genomic DNA with abandon, and with surprising regularity.

II. DNA DATABASES: ORIGIN, EXPANSION AND ORGANIZATION

The seeds of forensic DNA identification were sown in 1980, when American geneticists Ray White and Arlene Wyman identified a variable-length polymorphism in humans, called an RFLP.\(^1\) True forensic DNA typing began in 1985, when UK scientist Sir Alec Jeffreys first proposed the use of such polymorphisms to identify individuals in criminal cases.\(^2\) This technique was soon adopted in America, and by 1988 it had already

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\(^1\) Restriction Fragment Length Polymorphism, which means that DNA cleavage by restriction enzymes—at sites flanking what would today be called an STR—yielded fragments of variable length in different individuals. See Arlene R. Wyman & Ray White, *A Highly Polymorphic Locus in Human DNA*, 77 Proc. Nat’l Acad. Sci., 6754 (1980).

appeared in a Florida appellate case. The adoption of PCR techniques enabled swift and accurate characterization of newly discovered STRs.

Although DNA typing began as a means to perform an identity test on a pair of human genetic samples—normally, one taken from a crime scene and the other from a suspected offender—law enforcement agencies soon became interested in storing profiles in computer databases for later comparison. This section surveys the organization of CODIS, and the statutory basis for its creation and subsequent expansion.

**How CODIS is Organized**

The FBI database system, CODIS, supports three tiered databases: the National DNA Index System (NDIS) maintained by the FBI, a collection of State DNA Index Systems (SDIS) maintained by each state, and the Local DNA Index Systems (LDIS) administered by local police departments or sheriffs’ offices. Local labs can upload their LDIS records to their respective state databases, which in turn contribute their own records to NDIS. NDIS, the highest tier, therefore contains all federal profiles (deposited directly to NDIS by the FBI) as well as all contributed state material. Federal, state and local member labs can search NDIS directly via CODIS; in addition, CODIS conducts an automated weekly search on all DNA profiles in NDIS.

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73 Murphy, supra note 72, at 731 (citing Andrews v. State, 533 So. 2d 841 (Fla. Dist. Ct. App. 1988)).
74 For a brief discussion of PCR, see supra note 21.
75 CODIS actually refers to the software the FBI uses to administer the database; however, it has come to be used as a shorthand to refer to the database system itself. See Murphy, supra note 72, at 739 n74.
77 Id.
78 Request for specific searches go to the custodian of the national DNA database. See Rosen, supra note 31.
79 DNA.gov: Combined DNA Index System (CODIS), [http://www.dna.gov/dna-databases/codis/](http://www.dna.gov/dna-databases/codis/) (last accessed July 12, 2009). See also Rosen, supra note 31 ("Every Monday at 9 a.m., the national database automatically conducts two searches, looking for matches between the DNA of convicted offenders and..."
After a DNA sample is collected, in the case of Federal offenders the sample is sent to the FBI, which analyzes the sample and includes the resulting profile directly in NDIS. Local and state agencies process their own samples, and can upload DNA profiles to LDIS and SDIS databases according to their own laws and regulations; however, certain parameters must be met in order to upload locally computed profiles to NDIS. This is important, because NDIS relies to a large extent on state submissions for DNA samples from felons: of the more than 1 million felonies committed in the U.S. each year, less than 10% of these are federal crimes.

A CODIS-searchable NDIS record consists of a 13-STR locus DNA profile, the sex of the individual (typically determined by a length polymorphism in the amelogenin gene), along with an identifier for the associated stored DNA sample, and the identifier of the laboratory responsible for the record. CODIS stores DNA profiles anonymously – that is, names and other identifying information corresponding to each profile are stored separately at the state level (or at the FBI, for federal offenses), and cannot be searched through CODIS. In the event of a profile match, associated identifying information for the relevant matching record can be requested.
CODIS originally stored only two types of profiles: (1) offender profiles, which are samples taken from criminals convicted of qualifying offenses; and (2) forensic profiles, drawn from crime-scene samples (blood, semen, saliva and other biological material containing useful DNA).86 A match between two forensic profiles suggests that a common offender has committed crimes at different scenes, whereas a match between a forensic profile and an offender profile may suggest a suspect for a previously unsolved crime.87 Recently, CODIS has expanded to include the Arrestee Index, the Unidentified Human Remains Index, and the Missing Persons Index, and the Missing Persons Reference Index.88

As of April 2010, the CODIS database contains almost 8 million offender profiles and more than 300,000 forensic profiles, making it the largest such database in the world.89

**Statutory Authorization and Subsequent Expansion**

CODIS grew out of an early technical working group sponsored by the FBI in the late 1980s.90 Following an initial pilot project,91 the DNA Identification Act of 1994

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86 See Murphy, *supra* note 72, at 738; DNA.gov: Combined DNA Index System (CODIS), http://www.dna.gov/dna-databases/codis/ (last accessed July 12, 2009).
87 See Murphy, *supra* note 72, at 738.
“(DNA Act”) created CODIS and provided funding to law enforcement for DNA collection.\(^92\) CODIS officially launched in 1998.\(^93\)

**Federal Coverage: “Qualifying” Offenses, to All Felons, to Arrestees**

The DNA Analysis Backlog Elimination Act of 2000 limited compulsory DNA collection by federal agencies to those convicted of “qualifying” federal, military and D.C. offenses, which included selected felonies such as murder, kidnapping and some sex crimes.\(^94\)

A series of statutory changes in the ensuing decade have greatly expanded DNA database coverage. The USA PATRIOT Act of 2001 added terrorism-related crimes,\(^95\) and the Justice for All Act of 2004 expanded qualifying federal offenses still further to include all felonies and some misdemeanors.\(^96\)

In the most substantial regulatory shift to date, the DNA Fingerprinting Act of 2005 authorized the collection of DNA from all federal arrestees—regardless of offense\(^97\)—and from federal detainees, including non-U.S. persons.\(^98\) This policy was implemented by the DOJ in December 2008, and took effect in January 2009.\(^99\)
In 2009, the FBI began collecting DNA samples from individuals awaiting trial. The FBI expects that this move will sharply increase database growth, from 80,000 new entries added per year to 1.2 million new entries per year by 2012.

In just over a decade since its launch, CODIS has expanded from profiling only certain “qualifying” federal felony offenses to profiling all federal felonies, and now all federal offenses, including arrestees not yet convicted of any crime.

State Coverage Mirrors Federal Expansion

All 50 states have enacted laws authorizing DNA collection from criminals, and all state DNA databases participate in CODIS. Mirroring the aforementioned changes in federal law, the notion of specific “qualifying offenses” at the state level has largely vanished: As of February 2010, 47 states now require that all convicted felons provide a DNA sample to that state’s database.

California, which presides over the largest state DNA database in the country—with profiles from nearly 1.5 million convicts—announced its inclusion of arrestee profiles beginning in January 2009, a move expected to double its annual database

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99 DNA Collection in the Federal Jurisdiction, supra note 64, at 74,935.
101 Id.
102 See, e.g., Conn. Gen. Stat. 54-102g(f) (providing that “[t]he identification characteristics of the profile resulting from the DNA analysis shall be stored and maintained by the division in a DNA data bank . . .”)
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growth. Colorado is slated to follow suit, including arrestee DNA beginning September 2010. At least 21 states now require DNA collection from certain arrestees, with some states preserving the notion of “qualifying offenses” in this area.

CODIS and Familial Search

Because of the special inheritance patterns that link close biological relatives, certain law enforcement agencies have sought to expand their use of the CODIS database system to track down offenders’ kin using familial DNA search. This development has received national media coverage, as well as some early treatment in law reviews. Thus subsection summarizes the regulatory background and current authorization for familial DNA search in the United States.

105 See Rosen, supra note 31.
107 See State Laws of DNA Data Banks, supra note 103 (listing states: “Alabama, Alaska, Arizona, Arkansas, California, Colorado, Florida, Kansas, Louisiana, Maryland, Michigan, Minnesota, Missouri, New Mexico, North Dakota, South Carolina, South Dakota, Tennessee, Texas Vermont and Virginia.”)
108 For a description of this approach, see Section I, supra notes 38-57 and accompanying text.
**One District Attorney’s Crusade, and the Road to Approval**

In the U.K., law enforcement agencies have performed deliberate familial DNA searches since 2004, and have solved at least 18 cases in this way. For example, the so-called “shoe rapist,” who eluded authorities for decades, was ultimately identified via his sister’s DNA obtained on a drunk-driving arrest; in another case, a drunken man dropped a brick from an overpass, killing a truck driver; a familial DNA search of the database turned up his brother and led to a confession.

Until 2006, the FBI neither conducted familial searches itself, nor permitted states to use CODIS for familial searching—on the dual theories that CODIS software was ill-suited to fulfill such requests, and that such an authorization might draw

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113 The shoe rapist attacked women in the U.K. and thereafter stole their high heels. The perpetrator’s sister was arrested on DUI charges some 20 years after these crimes, and her DNA sample was automatically searched against cold case records. A close match was returned that led police to her brother. “When he was arrested, his DNA was a perfect match and police found more than 100 stiletto heels hidden under a trap door.” See Ellen Nakashima, From DNA of Family, a Tool to Make Arrests, WASHINGTON POST (Apr. 21, 2008), available at http://www.washingtonpost.com/wp-dyn/content/article/2008/04/20/AR2008042002388.html.


115 Note that it is not always necessary to conduct familial DNA searches of a database in order to use family DNA. In Kansas, the BTK Killer was snared in part by his daughter's DNA, recovered from a pap smear sample at her college. Late in the BTK investigation, police had a suspect, and also had crime scene DNA samples. However, rather than try to recover a DNA sample from their suspect, they accessed his college-aged daughter’s pap smear sample, on file with a health clinic, and found a partial match. The killer’s full confession negated the need to introduce this DNA evidence at trial, however. See Nakashima, supra note 113. In Louisiana, a rapist was caught by a chance partial DNA match with another rapist’s victim in another county, who turned out to be his own sister. Id. Neither case involved an open-ended database search to find the relative in question, but both nonetheless highlight the potential investigative value of familial DNA.

116 For a full discussion of why this is so, see Section I, supra note 37 and accompanying text.
unwanted public attention at a time when database expansion to include arrestees was planned.\textsuperscript{117}

Although state and local crime labs could carry out partial match searches at their discretion, FBI administrators did not permit identifying information—which resides largely in state and local CODIS databases, and is necessary to associate a CODIS profile with an individual person—to be transferred between states in response to such requests.\textsuperscript{118} Thus, a state crime lab could conduct a family search, but if it matched a record out-of-state, there was no way to pursue the lead.

Denver District Attorney Mitchell R. Morrissey has been instrumental in obtaining approval for familial DNA searching in the U.S.\textsuperscript{119} Pursuing a Colorado rapist in 2005, Morrissey discovered three partial matches in CODIS; each uploaded by a different state.\textsuperscript{120} Frustrated by the FBI policy against sharing family search results, Morrissey contacted senior FBI directors in June 2006 to complain, and in response the FBI instituted an interim policy permitting states to perform deliberate partial match searches.\textsuperscript{121}

Even with FBI approval, however, individual states could decide whether to release the names of partial matches to out-of-state inquiries. California, the holdout on Morrissey’s list, eventually buckled to pressure and not only granted Morrissey access to

\textsuperscript{117} Then-CODIS Director Callaghan is quoted in several news reports as having responded with this concern. See, e.g., Dolan & Felch, supra note 110 (“The FBI feared that racing ahead to familial searching could prompt a backlash and endanger database expansion”).

\textsuperscript{118} Although CODIS at the time prohibited deliberate trolling for partial matches, the system did permit low-stringency searches designed to match at least 10 of 13 CODIS markers (that is, 20 of 26 alleles) – this functionality was included mainly to uncover matches to degraded DNA samples, although it occasionally would return partial matches to complete profiles. See Seth Axelrad, \textit{State Regulations on Low Stringency / Familial Searches of DNA Databases}, American Society of Law, Medicine & Ethics, available at \url{http://www.aslme.org/dna_04/reports/axelrad1.pdf} (last accessed July 9, 2009).

\textsuperscript{119} See Maura Dolan & Jason Felch, \textit{Tracing a Crime Suspect Through a Relative}, L.A. TIMES (Nov. 25, 2008) (“The FBI and California law enforcement officials long resisted the approach, fearful of inciting legal opposition and a public backlash. They yielded only after aggressive lobbying by prosecutors, who pointed to some dramatic successes . . . It took a dogged three-year campaign by a Colorado prosecutor to bring down the barriers to familial searching in the United States.”); Denver D.A.’s office, DNA Resource, \url{http://www.denverda.org/DNA/DNA_INDEX.htm} (last accessed July 17, 2009).

\textsuperscript{120} Dolan & Felch, supra note 119.

\textsuperscript{121} Id.
his long-sought suspect, but in a surprising turn, instituted a full-fledged familial DNA search policy of its own.122

In the end, District Attorney Morrissey’s pursuit of three partial matches resulted in watershed reform and the approval of state familial search in CODIS, but all three leads turned out to be duds—random partial matches from unrelated individuals.123

**Familial DNA Search: Current Authorization**

Two states—California124 and Colorado125—now explicitly authorize and conduct familial DNA searches.126 A 2009 survey by Natalie Ram revealed a patchwork of laws and regulations in the remaining states.127

California’s policy limits familial searches to “major violent crimes where there is a serious risk to public safety and all other investigative leads have been exhausted,”128 and does not include the arrestee index.129

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123 Dolan & Felch, supra note 110.
124 See California Familial Search Policy, supra note 122.
125 See Colorado Familial Search Policy, supra note 106.
128 Steinberger & Sims, Familial Searching in California, supra note 46, at 29. California has several other restrictions in place on familial searching. See Ram, Familial Search Survey Data, supra note 127 (listing restrictions as requiring: “(1) single-source profiles; (2) additional confirmatory testing; (3) at
The Colorado policy is far broader, permitting “routine familial search” by state authorities, as well as following up on routine partial matches and responding to special requests from law enforcement, with no mention of excluding arrestee profiles.\(^{130}\)

Maryland is currently the only state to have banned familial DNA searching by statute—or indeed, to have explicitly addressed familial search by statute at all\(^{131}\)—having enacted a statute in 2008 prohibiting any “search of the statewide DNA data base for the purpose of identification of an offender in connection with a crime for which the offender may be a biological relative of the individual from whom the DNA sample was acquired.”\(^{132}\)

With the exception of California, Colorado and Maryland, state policies on deliberate familial search (and the use of “fortuitous” partial matches) are, broadly speaking, uneven. Most states have neither explicit legislative endorsement nor prohibition of familial search or partial match use,\(^{133}\) effectively leaving both to the discretion of the crime lab.\(^{134}\)


\(^{130}\) See Colorado Familial Search Policy, supra note 106, at 1.

\(^{131}\) See Ram, Familial Search Survey Summary, supra note 127 (reporting that “Only one state thus far has enacted a statute related to partial match reporting and familial searching specifically . . . . [although] [f]our states have written prohibitions of both partial matching reporting and familial searching—all four of which appear in lab manuals.”)

\(^{132}\) MD Code, Public Safety, § 2-506(d).

\(^{133}\) See Natalie Ram, DNA Confidential: State Law Enforcement Policies for Genetic Databases Lack Transparency, SCIENCE PROGRESS, http://www.scienceprogress.org/2009/11/dna-confidential/ (Nov. 2, 2009) (reporting results of the first comprehensive survey of state familial search and partial match reporting policies, and stating that “[m]ost states . . . have refrained from prescribing rules governing partial match reporting or familial searching in statute, regulation, or well-publicized memoranda.”) (hereinafter, Ram, DNA Confidential).

\(^{134}\) Interview with Dr. Carl Ladd, supra note 67. Dr. Ladd stated that while no regulation prohibits his lab from conducting partial stringency searches, it is currently unclear whether to do so, whether to report any inadvertently obtained partial matches, and more importantly, how courts would deal with the use of such evidence. See also, E-mail from Natalie Ram, personal communication (Mar. 17, 2010) (on file with author) (summarizing the results of comprehensive survey and stating that “in at least a dozen states, including Connecticut, Florida, and Oregon, partial match policies appear only in internal laboratory manuals, which are not easily accessible. Louisiana, Montana, North Carolina, and South Carolina have turned over partial match information without any written policy at all.”)
For instance, Nebraska permits familial searching on a case-by-case basis (though this policy appears only in a laboratory manual), whereas West Virginia and North Dakota both have draft policies that, if enacted, would permit familial searching;\textsuperscript{135} Massachusetts and New York broadly authorize familial DNA searches via statute, but neither state regularly conducts them.\textsuperscript{136} At least thirteen states—although they do not perform deliberate familial searches—do permit the use of “fortuitous” partial matches that occur during routine searches.\textsuperscript{137}

As previously mentioned, the FBI permits states to conduct familial DNA searches under an interim policy, but does not openly conduct familial searches itself. The FBI held a symposium in March 2007 to consider reform of this policy, but has to date elected not to perform familial searches,\textsuperscript{138} since the Bureau would be “more comfortable with congressional authorization” before doing so.\textsuperscript{139}

\section*{Sample Retention and Record Expungement}

CODIS is organized such that law enforcement agencies store not only electronic DNA profiles in databases, but participating crime labs also preserve the physical DNA

\textsuperscript{135} See Ram, Familial Search Survey Data, supra note 127.

\textsuperscript{136} In the case of Massachusetts, Mass. Regs. Code ch. 515, § 2.14 states, “the laboratory or other authorized agency may, at its discretion, request that a search be performed using fewer loci if there are scientific reasons which support using fewer than four loci in a particular case, including but not limited to . . . the possible involvement of relatives.” But see Ram, Familial Search Survey Data, supra note 127, reporting that “[Massachusetts] state CODIS administrator reports that neither familial searching nor partial match reporting are conducted because no additional policy is in place to regulate such practices.”

In the case of New York, N.Y. Comp. Codes R. & Regs. ch. 9, § 6192.3 states, “the laboratory may, at its discretion, request that a casework search be performed using fewer loci if there is an investigative need and sufficient scientific reasons which support using fewer than four loci in a particular case.” New York has now implemented a rule permitting partial matches to be used, though still not authorizing deliberate familial search. See Jeremy W. Peters, New Rule Allows Use of Partial DNA Matches, N.Y. TIMES, Jan. 24, 2010, at A12; see also Press Release, New York State Division of Criminal Justice Services, Forensic Science Commission Approves Regulations Governing “Partial-Match” DNA (Dec. 13, 2009), http://www.criminaljustice.state.ny.us/pio/press_releases/2009-12-13_pressrelease.html (last accessed Apr. 30, 2010).

\textsuperscript{137} See Ram, Familial Search Survey Data, supra note 127.

\textsuperscript{138} See Rosen, supra note 31.

\textsuperscript{139} Nakashima, supra note 113.
samples from every profiled individual. DNA samples can be taken from various tissues and fluids, but when taken from offenders are generally blood samples or buccal (cheek) swabs.\(^{140}\)

Preserving biological DNA samples is mandated by federal law requiring the government to preserve biological evidence in federal criminal cases.\(^{141}\) This statutory requirement extends only during imprisonment, however, and therefore DNA samples need not be retained following release.\(^{142}\) However, the FBI and most states continue to do so\(^{143}\) on a quality-control rationale.\(^{144}\) Only Wisconsin requires that DNA samples be destroyed after profiling;\(^{145}\) by contrast, Arizona requires that samples be retained for at

\(^{140}\) The DNA Act defines a DNA sample as “a tissue, fluid, or other bodily sample of an individual on which a DNA analysis can be carried out.” 42 U.S.C. § 14135a(c)(1); see also California Penal Code § 296.1(a)(1)(A), stating that “[e]ach adult person arrested for a felony offense as specified . . . shall provide . . . buccal swab samples”; see also Kincade, 379 F.3d at 846 (Reinhardt, J., dissenting) (noting that “that the FBI has required all participating CODIS laboratories to construct DNA profiles by obtaining blood samples”).


\(^{142}\) See DNA Collection in the Federal Jurisdiction, supra note 64 (Dec. 10, 2008) (stating that “this limitation of scope is explicit in the statute, which requires preservation of biological evidence only in relation to a defendant who is under a sentence of imprisonment. 18 U.S.C. 3600A(a); see 70 FR 21952 (explaining in preamble to interim rule that this statutory language does not cover convicts released under supervision)” (internal quotation marks omitted).

\(^{143}\) See Federal Bureau of Investigation – Laboratory Services – Standards for Forensic DNA Testing Labs, http://www.fbi.gov/hq/lab/codis/forensic.htm (last visited April 17, 2010), at §7.2 (stating that “[w]here possible, the laboratory shall retain or return a portion of the evidence sample or extract”). Samples are also retained indefinitely in nearly every state. See Seth Axelrad, Survey of State DNA Database Statutes, AM. SOC. OF LAW, MED. & ETHICS, http://www.aslme.org/dna_04/grid/guide.pdf (last visited April 17, 2010).

\(^{144}\) See Helen Wallace & Tania Simoncelli, Expanding Databases, Declining Liberties, 19 GENEWATCH 1 (Jan.-Feb. 2006), available at http://www.councilforresponsiblegenetics.org/GeneWatch/GeneWatchPage.aspx?pageId=191 (last accessed April 17, 2010) (stating that “In the US, samples are also retained indefinitely, except in some states that require purging of DNA records upon reversals or convictions . . . . Law enforcement authorities in both the UK and the US have argued that sample retention is necessary for ‘quality assurance purposes.’ But re-testing the same sample clearly cannot correct for many sorts of errors, such as sample mix-ups. In fact, in both the UK and the US, testing of a fresh DNA sample from the suspect is always required before the DNA evidence is admissible. Thus the stored samples do nothing to prevent future miscarriages of justice’’); M. Dawn Herkenham, Retention of Offender DNA Samples Necessary to Ensure and Monitor Quality of Forensic DNA Efforts: Appropriate Safeguards Exist to Protect the DNA Samples from Misuse, 34 J.L. MED. & ETHICS 380, 381 (2006).

\(^{145}\) See Wis. Stat. Ann. § 165.77(3) (providing that “laboratories shall destroy specimens obtained under this subsection after analysis has been completed and the applicable court proceedings have concluded.”)
minimum thirty-five years.\textsuperscript{146} Most state DNA statutes are silent on the issue, but in practice retain DNA samples indefinitely.\textsuperscript{147}

The FBI must expunge the DNA profile of anyone whose conviction is overturned, or who was arrested and whose charges were later dismissed.\textsuperscript{148} As a condition of access, states participating in CODIS must also agree to expunge such records.\textsuperscript{149} However, these provisions do not address retention of DNA profiles or DNA samples from those who have successfully completed their sentences.\textsuperscript{150} Thus, convict DNA samples are currently retained indefinitely, along with DNA profiles. Arrestee DNA samples are also retained,\textsuperscript{151} and the process for their expungement can be complex.\textsuperscript{152}

The CODIS statutory framework sets forth criminal and financial penalties for the misuse or sharing of DNA samples and profiles, including a fine of up to $250,000, or imprisonment not exceeding one year.\textsuperscript{153} Most states also have explicitly criminalized

\begin{footnotesize}
\begin{enumerate}
\item See Natalie A. Bennett, \textit{A Privacy Review of DNA Databases}, 4 \textit{I/S: J.L. & POL’Y FOR INFO. SOC’Y} 821, at 830.
\item See Kriesel, 508 F.3d at 952 (“once they have [an individual’s] DNA, police at any level of government with a general criminal investigative interest . . . can tap into that DNA without any consent, suspicion, or warrant, long after his period of supervised release ends.”).
\item Haskell v. Brown, 677 F.Supp.2d 1187, 1191, (N.D.Cal. 2009) (In California, “[a]rrestee DNA profiles are entered into a special Arrestee Index. The DNA samples themselves are retained at the lab.”)
\item See, e.g., \textit{Id.} at 1191-92 (In California, “the process for expunging an individual's sample and profile is rather lengthy. Where no charges are filed, the case is dismissed, or the arrestee is found not guilty or factually innocent, the arrestee must still wait until the statute of limitations has run before applying for expungement. Depending on the felony for which he or she was arrested, this is a minimum of three years. After requesting relief and notifying the DOJ, former arrestees must then wait an additional 180 days before a court can authorize expungement. Then, the court's order, either granting or denying expungement, is nonappealable. Moreover, expungement can be prevented if there is “an objection by the Department of Justice or the prosecuting attorney. The government . . . has apparently not [yet] expunged any arrestee samples.”) (citations omitted, internal quotation marks omitted).
\item “A person who knowingly discloses a sample or result described in subsection (a) of this section in any manner to any person not authorized to receive it, or obtains or uses, without authorization, such sample or result, shall be fined not more than $250,000, or imprisoned for a period of not more than one year. Each instance of disclosure, obtaining, or use shall constitute a separate offense under this subsection.” 42 U.S.C. § 14135e(c), as amended by the 2004 Justice for All Act, H.R.5107. See also 42 U.S.C. 14132, 14133(b)-(c), 14135e.
\end{enumerate}
\end{footnotesize}
misuse or disclosure of DNA information.\textsuperscript{154} To date, no charges have been brought against any DOJ employee for violating the DNA Act.\textsuperscript{155}

As an interesting side note, the U.K. has been much more aggressive in retaining profiles in its own national DNA database—even in cases of acquittal—although its policies must soon change in this regard.\textsuperscript{156}

**III. LEGAL TREATMENT OF DNA DATABASES**

Virtually all courts that have heard the issue have upheld compulsory DNA collection against Fourth Amendment challenges. The Supreme Court has yet to hear a case specifically concerning DNA collection for CODIS, but Circuit courts have unanimously upheld the 2004 version of the DNA collection laws—that is, the version authorizing collection from convicts.\textsuperscript{157} DNA collection from arrestees has found support in federal district courts, and at the time of writing is pending before two circuit courts.

This Section sets forth the legal landscape in which law enforcement DNA collection and databasing operates in the United States.

\textsuperscript{154} See Herkenham, \textit{supra} note 144, at 383.

\textsuperscript{155} Haskell, 677 F.Supp.2d at 1191.

\textsuperscript{156} Britain has aggressively expanded its own DNA database, NDNAD. For example, NDNAD includes DNA from arrestees charged with even minor crimes, and its policies provide no means of expungement, even in the case of acquittal. As a result, as of March 2008 “857,000 people in the British database, or about one-fifth, [had] no current criminal record.” Solomon Moore, \textit{F.B.I. and States vastly expand DNA databases}, \textit{THE NEW YORK TIMES}, (April 18, 2009). In December 2008 the European Court of Human Rights in Strasbourg unanimously decided that the indefinite retention of DNA samples and profiles, even when people are not charged or found not guilty of an alleged crime, breached Article 8 of the European Convention on Human Rights. \textit{S. and Marper v. The United Kingdom}, 30562/04 [2008] ECHR 1581 (4 December 2008). As of this writing the U.K. has yet to enact regulatory changes in response to this ruling. This has led to enhanced criticism from commentators, including Sir Alec Jeffreys, the founder of forensic DNA analysis. See James Sturcke, \textit{DNA Pioneer Alec Jeffreys: Drop Innocent From Database}, \textit{THE GUARDIAN} (London) (Apr. 15 2009).

\textsuperscript{157} \textit{U.S. v. Weikert}, 504 F.3d 1 (1st Cir. 2007); \textit{U.S. v. Amerson}, 483 F.3d 73 (2d Cir. 2007); \textit{U.S. v. Kriesel}, 508 F.3d 941 (9th Cir. 2007); \textit{U.S. v. Banks}, 490 F.3d 1178 (10th Cir. 2007); \textit{Wilson v. Collins}, 517 F.3d 421 (6th Cir. 2006); \textit{U.S. v. Hook}, 471 F.3d 766 (7th Cir. 2006); \textit{U.S. v. Kraklio}, 451 F.3d 922 (8th Cir. 2006); \textit{U.S. v. Castillo-Lagos}, 147 Fed. App’x. 71 (11th Cir. 2005).
DNA Collection is a Fourth Amendment Search

The Fourth Amendment is the main grounds by which DNA collection is contested; for instance, courts have roundly rejected Fifth Amendment substantive due process challenges,158 as well as other challenges to the constitutionality of DNA collection.159

The Fourth Amendment protects the rights of the people to be secure against “unreasonable searches and seizures.”160 Thus, to challenge a government action under the Fourth Amendment, courts must determine whether the accused action constitutes a search or seizure, and if so, whether that search or seizure is reasonable.

Following the Supreme Court’s 1989 decision in Skinner v. Railway Labor Executives’ Association161—which held that random drug testing for employees constitutes a search “even if there is no actual surgical intrusion”162—it has become “settled law” that compulsory DNA collection constitutes a search under the Fourth Amendment.163 As such, in order to be constitutionally permissible, DNA collection must constitute a reasonable search.

158 See Rise v. Oregon, 59 F.3d 1556, 1563 (9th Cir. 1995) (holding that the extraction of blood from an individual in a medically acceptable manner – despite the individual’s lack of opportunity to object – does not implicate the Due Process Clause); see also, U.S. v. Hugs, 384 F.3d 762, 768-69 (9th Cir. 2004) (DNA testing as a condition of supervised release is not unconstitutionally vague and so meets procedural due process requirements); Johnson v. Quander, 370 F.Supp.2d 79, 89-93 (Dist.DC. 2005) (DNA Act does not violate substantive or procedural due process under the Fifth Amendment), aff’d, 440 F.3d 489, 503 (D.C.Cir. 2006) (Fifth Amendment challenge to DNA Act is “without merit and do[es] not warrant separate discussion”).


160 U.S. Const. Amend IV. (“The right of the people to be secure in their persons, houses, papers, and effects, against unreasonable searches and seizures, shall not be violated, and no Warrants shall issue, but upon probable cause, supported by Oath or affirmation, and particularly describing the place to be searched, and the persons or things to be seized.”).


162 Id. at 616-17.

163 See, e.g., U.S. v. Amerson, 483 F.3d 73, 77 (2d. Cir. 2007) (“It is settled law that DNA indexing statutes, because they authorize both a physical intrusion to obtain a tissue sample and a chemical analysis to obtain private physiological information about a person, are subject to the strictures of the Fourth Amendment. The extraction and analysis of plaintiffs’ blood for DNA-indexing purposes constitutes a search . . . .”) (citations omitted, internal quotation marks omitted); see also Kincaide, 379 F.3d at 821 n.15 (“The compulsory extraction of blood for DNA profiling unquestionably implicates the right to personal security embodied in the Fourth Amendment, and thus constitutes a search within the meaning
Assessing Reasonableness of the DNA Collection Search

Standards for evaluating reasonableness differ according to the circumstances of the search. The normal and most stringent—the probable cause standard—applies to traditional law enforcement activities such as arrests or searches of residences, and must generally be provided in the form of a warrant. A somewhat lower standard, reasonable suspicion, governs Terry stops and other less intrusive searches. Lastly, in so-called “suspicionless” searches, several search regimes exist free of the need for a warrant or probable cause: these are (1) searches at “exempted areas” such as border crossings, (2) “administrative” searches for routine regulatory purposes, and (3) “special needs” searches or other law-enforcement searches not subject to warrant or probable cause. DNA collection has traditionally been classified as a category (3) suspicionless search.

For this type of search, courts have generally assessed reasonableness of DNA statutes by applying one of two tests: either a “special needs” analysis, or a “totality of the circumstances” test.

The Special Needs Test

of the Constitution.”) (citing Skinner 489 U.S. at 616 (“We have long recognized that a compelled intrusion into the body for blood to be analyzed for alcohol content must be deemed a Fourth Amendment search.”));

164 U.S. Const., Amend IV (“. . . no Warrants shall issue, but upon probable cause . . . .”); see also Payton v. New York, 445 U.S. 573, 586 (1980) (“It is a basic principle of Fourth Amendment law that searches and seizures inside a home without a warrant are presumptively unreasonable.”) (Internal quotation marks omitted); see also United States v. United States Dist. Ct., 407 U.S. 297, 315-16 (1972).

165 See Terry v. Ohio, 392 U.S. 1 (1968) (holding that a seemingly random pat-down for weapons by police was permissible under the Fourth Amendment if grounded in “specific reasonable inferences.”).

166 See Alabama v. White, 496 U.S. 325, 330 (1990) (stating that “[r]easonable suspicion is a less demanding standard than probable cause”).

167 See, e.g., Kincade, 379 F.3d at 822 (citing United States v. Ramsey, 431 U.S. 606, 616 (1977) (“[S]earches made at the border, pursuant to the longstanding right of the sovereign to protect itself by stopping and examining persons and property crossing into this country, are reasonable simply by virtue of the fact that they occur at the border.”)).

168 Id. at 823 (citing Camara v. Mun. Ct. of S.F., 387 U.S. 523, 535-539 (1967) (authorizing municipal “area inspections” designed to monitor compliance with building safety codes)).

169 Id. at 823-4.
A warrantless search that serves “special needs” beyond normal law enforcement may qualify for a special balancing test, and thereby avoid the blanket presumption of unreasonableness for warrantless searches.

The term “special needs” dates from a 1985 concurrence by Justice Blackmun in *New Jersey v. T.L.O.*, a case in which the Supreme Court upheld the warrantless search of a high school student.170 As the doctrine now stands, if a search involves special needs beyond the ordinary need for law enforcement, this triggers a balancing test: the reasonableness of the search can then be determined by a simple balancing of the government interest in conducting the search against the individual’s privacy interest.171

The special need allegedly served by DNA collection is the government’s need to gather evidence to aid in the investigation and prosecution of future crimes.172

This is complicated by the fact that the special needs doctrine has “produced a tradition of ad hoc reasoning that makes it difficult to draw the line between law enforcement and special needs.”173 The Supreme Court has stated that the special needs exemption does not apply to searches that serve the “general interest of crime control.”174 Qualifying searches can occur either where true special needs make more stringent

170 469 U.S. 325, 351 (1985) (Blackmun, J., concurring) (advocating that “only in those exceptional circumstances in which special needs, beyond the normal need for law enforcement, make the warrant and probable cause requirement impracticable, is a court entitled to substitute its balancing of interests for that of the Framers”) (emphasis added, internal quotation marks omitted).

171 See, e.g., *National Treasury Employees Union v. Von Raab*, 489 U.S. 656, 665-6 (1989) (stating that “where a Fourth Amendment intrusion serves special governmental needs, beyond the normal need for law enforcement, it is necessary to balance the individual’s privacy expectations against the Government’s interests to determine whether it is impractical to require a warrant or some level of individualized suspicion in the particular context.”)

172 See *Nicholas v. Goord*, 430 F.3d 652, 658 (2d. Cir. 2005), cert. denied, 127 S. Ct. 384 (U.S. Oct. 10, 2006); *Kincade*, 379 F.3d at 855 (“The government maintained from the outset of this litigation that the purpose of the searches authorized by the DNA Act is to help law enforcement solve unresolved and future cases.” (Renhardt, J., dissenting, internal quotation marks omitted)). See also *Monteleoni*, *supra* note 159 at 263-4 nn.90-92.

173 *Bennett*, *supra* note 147, at 845, n.143. See also *Kincade*, 379 F.3d at 824 (“Almost as soon as the “special needs” rationale was articulated, however, the Court applied special needs analysis in what seemed—at least on the surface—to be a clear law enforcement context” (citing *Griffin v. Wisconsin*, 483 U.S. 868 (1987))).

analyses impracticable, or alternately where justified by some routine administrative purpose.175

The Second and Seventh Circuits, as well as several federal district courts and state Supreme Courts, have specifically applied special needs analysis to DNA collection for the purposes of establishing and maintaining DNA databases.176 By holding that DNA collection serves a special need, these searches avoid the presumption of unreasonableness, and proceed to the balancing test—where “these circuits have uniformly found that the state’s interest outweighs the individual’s, and they have upheld the criminal DNA database statutes as a result.”177

The Totality of the Circumstances Test

The second—and for DNA collection, more popular178—theory supporting suspicionless searches is the more general “totality of the circumstances” test, which turns upon a diminished privacy interest on the part of the search target.179 In this test, a simple balancing approach is applied, weighing the target’s privacy interest180 against the state’s interest in conducting the search—however, unlike the special needs test, the only

176 Nicholas, 430 F.3d at 655; Green v. Berge, 354 F.3d 675, 677-78 (7th Cir. 2004) (citing Shelton v. Gudmanson, 934 F. Supp. 1048, 1050-51 (W.D. Wis. 1996)). The Tenth Circuit previously applied a special needs test to DNA collection, see U.S. v. Kimler, 335 F.3d 1132, 1146 (10th Cir. 2003), but switched to the totality of the circumstances test in 2007, see Banks v. U.S., 490 F.3d at 1184 (“Thus, while we do not eliminate the possibility that the Act satisfies the special-needs test, we [apply] the totality-of-the-circumstances test here.”); see also Kincade, 379 F.3d at 830-31 (citing cases).
177 Monteleoni, supra note 159, at 263.
178 A key problem with applying the special needs test in this context is distinguishing DNA collection from ordinary law enforcement. As one law review author opines, “courts’ reliance on the special needs exception to justify forcible DNA testing schemes sets a dangerous precedent . . . accepting the reasoning of [such] cases would so broaden the special needs exception that Fourth Amendment protection ‘would approach the evaporation point.’” Julie Rikelman, Justifying Forcible DNA Testing Schemes Under the Special Needs Exception to the Fourth Amendment: A Dangerous Precedent, 59 Baylor L. Rev. 41, 57 (2007) (quoting Chimel v. California, 395 U.S. 752, 765 (1969)).
179 This test has also been termed the “general balancing test” and the “diminished privacy interest rationale.” See Monteleoni, supra note 159, at 267 n.109-110.
180 As Monteleoni points out, courts typically refer to a diminished privacy interest as a diminished or reduced reasonable expectation of privacy, but this terminology is misleading since it is based on a judicial conclusion rather than the actual subjective expectation of an individual. Monteleoni, supra note 159, at 267-8 n.110.
specific trigger required to invoke this balancing test is the target’s diminished privacy interest itself.\textsuperscript{181} Then, “the reasonableness of a search is determined by assessing, on the one hand, the degree to which it intrudes upon an individual’s privacy and, on the other, the degree to which it is needed for the promotion of legitimate governmental interests.”\textsuperscript{182} Thus, the individual’s diminished privacy interest not only serves as a gateway to this balancing analysis, but also tends to tip its outcome in the state’s favor.

The totality of the circumstances test originated in \textit{U.S. v. Knights}, a 2001 Supreme Court case that upheld the warrantless search of a probationer’s residence based on reasonable suspicion.\textsuperscript{183} The \textit{Knights} court found that because probation served two purposes—only one of which constitutes a special need—it could not apply the special needs rationale,\textsuperscript{184} and as such applied a more general balancing test.\textsuperscript{185} \textit{Knights} left open the question of “whether a condition of release can so diminish or eliminate a released prisoner’s reasonable expectation of privacy that a suspicionless search by a law enforcement officer would not offend the Fourth Amendment.”\textsuperscript{186} Therefore, the \textit{Knights} court did not explicitly state that the probationer’s diminished privacy interest itself always triggered this balancing test, but did mention that it was a “salient circumstance” in this instance.\textsuperscript{187}

\textsuperscript{181} See \textit{Kincade}, 379 F.3d at 832.


\textsuperscript{183} 534 U.S. 112 (2001). The Ninth Circuit extended this doctrine to suspicionless searches in \textit{Kincade}, discussed below.

\textsuperscript{184} The dual purposes of probation are rehabilitation, and the prevention of future crime. Only the former is a special need, meaning that the prevention of future crime is not sufficiently distinguishable from normal law enforcement motives to constitute a special need. \textit{Id.} at 120-121.

\textsuperscript{185} The possibility of which had been left open by the Supreme Court in \textit{Griffin}, 483 U.S. 868. See \textit{Kincade}, 379 F.3d at 827 (Describing \textit{Knights}: “[r]ather than analyze the warrantless search of Knights's apartment within the special needs framework, the [Knights] Court instead opted to “consider the question left open by \textit{Griffin} in assessing the constitutionality of the search of Knights's apartment [as something other than special needs].” (citing \textit{Knights}, 534 U.S. at 118)).

\textsuperscript{186} \textit{Samson v. California}, 547 U.S. 843, 847 (U.S. 2006) (citing \textit{Knights}, 534 U.S. at 120 n.6 (“We do not decide whether the probation condition so diminished, or completely eliminated, Knights' reasonable expectation of privacy ... that a search by a law enforcement officer without any individualized suspicion would have satisfied the reasonableness requirement of the Fourth Amendment”)).

\textsuperscript{187} \textit{Knights}, 534 U.S. at 118.
In 2004, the Ninth Circuit, sitting en banc, relied on *Knights* to uphold the DNA Act in *United States v. Kincade.*188 In so doing, the plurality implicitly answered the question left open by *Knights*, finding that conditional releasees’ diminished privacy interests alone were sufficient to trigger the “totality of the circumstances” balancing test, even absent individualized suspicion or a special need. Over a heated dissent by Judge Reinhardt, with whom Judges Pregerson, Kozinski and Wardlaw joined,189 the plurality held that “[i]n light of conditional releasees’ substantially diminished expectations of privacy, the minimal intrusion occasioned by blood sampling, and the overwhelming societal interests so clearly furthered by the collection of DNA information from convicted offenders,” “compulsory DNA profiling of qualified federal offenders is reasonable under the totality of the circumstances.”190

Two years later, the Supreme Court legitimized the *Kincade* interpretation with its decision in *Samson v. California,* which upheld suspicionless searches of California parolees through a totality of the circumstances rationale.191 Although *Samson* did not involve DNA collection, the decision nonetheless cemented the idea that the balancing test could be invoked, without first identifying a special need, on the grounds of the subject’s diminished privacy interest.

Circuit courts promptly set about applying *Samson* to DNA collection, thereby reaffirming the totality of the circumstances approach.192

In all, the First, Third, Fourth, Fifth, Eighth, Ninth, Tenth and Eleventh Circuits, as well as several state courts, have now applied the totality of the circumstances test to

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188 379 F.3d 813 (2004).
189 *Id.* at 842.
190 *Id.* at 839 (emphasis added).
191 547 U.S. 843, 847 (2006) (“Answering [the question left open in *Knights*] in the affirmative today, we affirm the judgment of the California Court of Appeal.”)
192 See, e.g., *U.S. v. Kriesel,* 508 F.3d 941, 946 (9th Cir. 2007) (“In light of *Samson v. California,* we continue to ground our analysis in the totality of circumstances test.”); *Weikert,* 504 F.3d at 3 (“We interpret the Supreme Court’s decision in *Samson v. California* to require that we join the majority of the circuits in applying a totality of the circumstances approach to the issues in this case, rather than the special needs analysis . . . .”) (Citation omitted, internal quotation marks omitted).
uphold searches pursuant to federal and state DNA database statutes, thereby applying (and also deciding) a balancing test based upon the diminished privacy expectation of the individual whose DNA is to be sampled.193

Surviving Fourth Amendment Challenges, on Either Theory

In sum, in the majority of Fourth Amendment challenges to DNA database statutes, courts have directly applied a totality of the circumstances analysis without first establishing that a special needs situation applied.194

By contrast, even in the wake of Samson, the Second and Seventh Circuits have continued to rely upon special needs reasoning in upholding DNA collection.195

At first glance, this distinction between special needs and general reasonableness approaches appears moot, since the outcome of either approach has been to uphold DNA collection. The Sixth Circuit has suggested that DNA collection from parolees and those on probation could be upheld regardless which test is applied;196 the plurality in Kincade made a similar statement,197 as did the Tenth Circuit.198 However, the distinctions

193 See Kriesel, 508 F.3d at 946; Weikert, 504 F.3d at 3; Banks v. U.S., 490 F.3d 1178, 1183 (10th Cir. 2007); U.S. v. Kraklio, 451 F.3d 922, 924 (8th Cir. 2006); U.S. v. Castillo-Lagos, 147 Fed.Appx. 71 (11th Cir. 2005). See also Monteleoni, supra note 159, at 267 n.109 (citing cases); Kincade, 379 F.3d at 831 (citing cases).
194 See supra note 193.
195 Amerson, 483 F.3d at 73, 78-79 (where the Second Circuit in 2007 read Samson narrowly and declined to directly apply the general balancing test to a case involving DNA collection from people on probation); U.S. v. Hook, 471 F.3d 766, 772-74 (7th Cir. 2006).
196 See Wilson, 517 F.3d at 427, n. 4 (“Even if we were to apply the more stringent special-needs test, there is no reason to believe the ultimate result would be different.”). See also U.S. v. Conley, 453 F.3d 674, 677-81 (6th Cir. 2006).
197 379 F.3d at 832 (“While not precluding the possibility that the federal DNA Act could satisfy a special needs analysis, we today . . . hold that . . . a totality of the circumstances analysis to uphold compulsory DNA profiling of convicted offenders both comports with the Supreme Court's recent precedents and resolves this appeal in concert with the requirements of the Fourth Amendment.”) (emphasis added); Judge Gould, concurring in Kincade, stated his preference for upholding the DNA Act under a special needs theory. See Kincade, 379 F.3d at 840 (Gould, J., concurring).
198 See Banks v. U.S., 490 F.3d at 1184 (10th Cir. 2007) (“Thus, while we do not eliminate the possibility that the Act satisfies the special-needs test, we [apply] the totality-of-the-circumstances test here.”)

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between these approaches will become apparent at the margin, as further expansions—arrestees, and familial search—are considered.

Including Arrestee DNA

The aforementioned cases have dealt exclusively with taking DNA from convicted criminals, parolees or individuals on supervised release. But perhaps the most dramatic and immediate shift in DNA database policy has been the recent move to include those arrested for, but not yet convicted of, a crime.199

State court response to such expansion has so far been mixed. In 2006, the Minnesota Court of Appeals struck down a state law that authorized DNA collection from arrestees on Fourth Amendment grounds;200 in 2007 the Virginia Court of Appeals reached the opposite result, upholding DNA collection upon arrest on the theory that it is similar to fingerprinting.201

Although Federal circuit courts had previously upheld DNA collection from convicts, parolees and individuals on probation,202 until summer 2009 no federal court had extended this approval to arrestees in a Fourth Amendment challenge. Indeed, in U.S. v. Kriesel (2007), the Ninth Circuit explicitly stated that its approval of DNA collection in that case did not extend to arrestees.203 In 2009, however, three federal court cases

199 See supra notes 97-108, and accompanying text.
200 In the Matter of the Welfare of C.T.L., 722 N.W.2d 484 (Ct. App. Minn. 2006) (Minnesota Court of Appeals invalidated a statute that authorized DNA collection after a judicial finding of probable cause that arrestee had committed a crime).
201 Anderson v. Commonwealth, 274 Va. 469 (VA Sup. Ct., 2007) (holding that the taking of defendant's DNA sample upon arrest was analogous to fingerprinting upon arrest, was not an unlawful search under the Fourth Amendment, and that no additional finding of individualized suspicion was required to do so).
202 See supra notes 176-177, 188-193, and accompanying text.
203 U.S. v. Kriesel, 508 F.3d 941, 948-49 (9th Cir. 2007) (This 2007 Ninth Circuit decision emphasized “that our ruling today does not cover DNA collection from arrestees or non-citizens detained in the custody of the United States, who are required to submit to DNA collection by the 2006 version of the DNA Act”). See also, United States v. Purdy, No. 8:05CR204, 2005 WL 3465721 at *7 (D.Neb. Dec. 19, 2005) (holding that DNA sampling of arrestees is unconstitutional, in part because “[t]he probable cause that supports an arrest is not necessarily probable cause for a DNA search.”).
addressed the issue with differing results, and each is currently on appeal in its respective circuit.


On May 27, 2009, in a case of first impression for the federal courts, the U.S. District Court for the Eastern District of California applied the totality of the circumstances test in *United States v. Pool* to uphold mandatory DNA collection from individuals arrested upon probable cause for felony criminal charges. In its decision, the court tied authorization for sampling to a pre-existing finding of judicial probable cause, and inventoried the various ways in which a defendant’s liberty is routinely restricted after such a finding and before trial. Moreover, the court noted that after such a finding, individuals have a “diminished expectation of privacy in [their] own identity,” and that DNA identification as a law enforcement tool is simply a “technological progression” from traditional fingerprints and photographs, both of which are “part of the routine booking process upon arrest.” Given this, the court stated “the decision to impose the DNA testing requirement on pre-trial detainees or releasees seems clearly warranted, if not compelling.”

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204 *U.S. v. Pool*, CR S-09-0015 EJG GGH (E.D.Cal., May 27, 2009) (hereinafter *U.S. v. Pool*). In its 20 page opinion, the court holds that after a judicial or grand jury determination of probable cause has been made for felony criminal charges against a defendant, no Fourth Amendment or other Constitutional violation is caused by a universal requirement that a charged defendant undergo a “swab test,” or blood test when necessary, for the purposes of DNA analysis to be used solely for criminal law enforcement identification purposes.

205 *Id.* at *13 (The court’s holding “does not authorize DNA sampling after citation or arrest for infractions or misdemeanors, as in these cases there will be no judicial finding of probable cause soon after the arrest or citation, or no grand jury finding before or after the arrest. It does not authorize police officials to perform DNA sampling prior to a judicial finding of probable cause . . . . [I]t is the finding of probable cause on criminal charges which allows the court to set release conditions similar to those of probation and parole, which is the underpinning of the court’s holding in this case.”) (emphasis in original, citation omitted).

206 *Id.* at *7-8.

207 *Id.* at *8 (citing *Napolitano v. U.S.*., 340 F.2d 313, 314 (1st Cir. 1963)).

208 *Id.* at *8.
Appeals for the Ninth Circuit, where it was argued and submitted on Dec. 7, 2009.209


In a striking departure from the *U.S. v. Pool* analysis, on November 6, 2009, the U.S. District Court for the Western District of Pennsylvania held unconstitutional the revised federal DNA Act authorizing sample collection from arrestees.210 In *United States v. Mitchell*, the court granted plaintiff’s motion in opposition of pretrial DNA collection on the grounds that such collection violated the Fourth Amendment.211 The court rejected the special needs analysis212 and applied the more common totality of the circumstances test,213 but found that although

> [t]he Court agrees that [an arrestee] has a diminished expectation of privacy in his identity[,] . . . to compare the fingerprinting process and the resulting identification information obtained therefrom with DNA profiling is pure folly. Such oversimplification ignores the complex, comprehensive, inherently private information contained in a DNA sample. DNA samples may reveal private information regarding familial lineage and predisposition to over four thousand types of genetic conditions and diseases; they may also identify genetic markers for traits including aggression, sexual orientation, substance addiction, and criminal tendencies.”214

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209 This magistrate opinion was adopted by District Judge Garcia, see *U.S.v. Pool*, No. CR S-09-0015, 2009 WL 2152029 (E.D.Cal. July 15, 2009), and is currently on appeal to the Ninth Circuit. See PACER case record for Ninth Circuit case no. 09-10303, *USA v. Jerry Pool* (last accessed April 27, 2010).
211 *Id.* at *13.
212 *Id.* at *7* (declining to apply special needs analysis because “[a] DNA profile generates investigatory evidence that is primarily used by law enforcement officials for general law enforcement purposes.”)
213 *Id.* at *7-10.
214 *Id.* at *10* (emphasis added).
The court also stated that “the search in this instance is one that reveals the most intimate details of an individual's genetic condition, implicating compelling and fundamental interests in human dignity and privacy.”

Thus, on the logic that DNA samples can disclose far more than mere identity, the court “strongly disagree[d]” with Pool and found instead that the balancing of interests disfavors DNA collection from arrestees.

Like Pool, this case is ongoing: Notice of appeal was filed on Dec. 24, 2009.

**Haskell v. Brown (N.D. Cal. 2009)**

On December 23, 2009, Judge Breyer of the U.S. District Court for the Northern District of California decided another similar case: Haskell v. Brown. Breyer denied plaintiff Haskell’s motion to enjoin enforcement of the California arrestee DNA statute, finding the plaintiff unlikely to succeed in establishing that the statue violated the Fourth Amendment or Fourteenth Amendment. Judge Breyer also applied the totality of the circumstances test to uphold DNA collection from arrestees in California, because although “[a]rrestees undoubtedly have a greater privacy interest than convicted felons[,] . . . [p]laintiffs have not shown that that interest outweighs the government’s compelling interest in identifying arrestees, and its interest in using arrestees’ DNA to solve past crimes.” Haskell is distinguished from Pool in that Haskell does not explicitly tether sampling to the judicial finding of probable cause, but instead to the

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215 *Id.* at *8* (emphasis added, citation omitted, internal quotation marks omitted).
216 *Id.* at *8*.
219 *Id.*
220 *Id.* at 1202 (finding that permitting warrantless searches of pre-trial detainees “is proper under the totality of the circumstances test . . . .”).
221 *Id.* at 1201 (emphasis added).
diminished expectation of privacy among arrestees generally. Like *Pool, Haskell* is currently on appeal in the Ninth Circuit.\(^{222}\)

**Open Questions about DNA Collection Fourth Amendment**

**Jurisprudence**

**Constitutionality of DNA Collection from Arrestees**

DNA collection from arrestees is a recent development, and its ultimate status under the Fourth Amendment remains unclear.

Whereas the Ninth Circuit is trending toward upholding collection from arrestees and pre-trial detainees—per *Pool, Haskell*, and the plurality in *Kincade*—such an outcome is far from assured: The Ninth circuit also explicitly declined to extend its totality of the circumstances justification to arrestees in *Kriesel*, and moreover *Kincade* was decided *en banc*, 6-5, over vigorous dissent. In addition, the Third Circuit’s resolution of *Mitchell* could well create a circuit split more serious than the current disagreement, which simply concerns which rationale to employ when upholding DNA collection from convicts and those on supervised release. Finally, the Supreme Court has thus far declined to grant certiorari on a Fourth Amendment challenge to the federal DNA Act, or one of its many state counterparts. An opinion resolving the disagreements amongst circuits therefore has yet to issue.

**DNA Databases Require a Search—But When?**

Besides the constitutionality of DNA collection itself, DNA profiling raises another interesting question: When exactly does a protected search occur?

Courts seem generally to accept that the most relevant search is the initial taking of a biological sample.\(^{223}\) However, all biological samples are not equal: some are taken only for immediate use—to test sobriety, for instance\(^ {224}\)—whereas others, such as DNA samples, are informative as long as the subject lives. Moreover, stored DNA samples can reveal new information in future as scientists uncover new correlations and devise novel genetic assays.

Courts have also noted in dicta that “analyzing the DNA contained within [a] blood sample, or even from a cheek swab, must pass Fourth Amendment scrutiny,”\(^ {225}\) but to date no Fourth Amendment challenge to DNA profiling has turned on sample analysis.

The subsequent creation and storage of a DNA profile, as well as routine search queries against a database of such profiles, could also be considered protected searches in their own right. Dissenting in *Kincade*, Judge Kozinski argued that the true Fourth Amendment concern should be the inclusion of a DNA profile into a searchable database.\(^ {226}\) The *Mitchell* court recently adopted a similar view, stating that “even though the taking of a sample may not be unreasonably intrusive, the search of the sample is quite intrusive, severely affecting [an arrestee’s] expectation of privacy in his most intimate matters.”\(^ {227}\)

Problems with the “Search as Sampling” View

Attaching the search to a physical sampling—no matter how minimally intrusive—is problematic, because DNA can quite easily be gathered without direct

\(^{223}\) See, e.g., *Banks v. U.S.*, 490 F.3d at 1183 (“Government-forced compliance with a blood draw constitutes a search subject to the Fourth Amendment.”) (citing *Skinner*, 489 U.S. at 616).

\(^{224}\) See, e.g., *Schmerber v. California*, 384 U.S. 757 (1966) (concerning use a blood sample for sobriety testing).

\(^{225}\) *Banks v. U.S.*, 490 F.3d at 1183 (citing *Skinner*, 489 U.S. at 616) (emphasis added). See also *Schlicher v. Peters*, 103 F.3d 940, 942-43 (10th Cir. 1996) (stating that “the collection, analysis and storage of blood and saliva ... is a search and seizure within the meaning of the Fourth Amendment”).

\(^{226}\) *Kincade*, 379 F.3d at 873, (“[I]t is important to recognize that the Fourth Amendment intrusion here is not primarily the taking of the blood, but seizure of the DNA fingerprint and its inclusion in a searchable database.”) (Kozinski, J., dissenting).

\(^{227}\) 2009 WL 5551383, *10 (emphasis added).
physical contact. Consider for instance shed DNA samples. As discussed in Section I, humans shed DNA regularly—228 and sampling DNA taken from litter or stray hair follicles is unlikely to infringe on an individual’s reasonable expectation of privacy.229

Alternately, by using “blood already extracted for other purposes,” such as for routine blood tests or the heel-stick test already performed on newborns, the government could similarly avoid “the most serious negative factor—the piercing of the skin.”231 In either case, absent a reasonable expectation of privacy, no Fourth Amendment search exists at all.232

To close this apparent loophole, courts would need to distinguish those cases finding no reasonable expectation of privacy in discarded material,233 and instead identify the analysis of biological samples—however they are obtained—as a distinct invasion of privacy.234

The germ of this reasoning exists in Skinner, wherein the Supreme Court stated that chemical analysis of bodily tissues could constitute an invasion of privacy interests, though it declined to elevate it to the status of a search.235 Laboratory analysis of a

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228 See supra note 62, and accompanying text.
230 Newborns routinely receive the Guthrie test (or a modern evolution of the same), a test devised in the 1960s to assay for various diseases in infants. See, e.g., R. Guthrie & A. Susi, A simple Phenylalanine method for detecting Phenylketonuria in large populations of newborn infants, 32 PEDIATRICS 338 (1963).
231 Kincade, 379 F.3d at 872 (Kozinski, J., dissenting) (citing id. at 836-38.) Judge Kozinski goes on to state that “[a]rguably, we have no more reasonable expectation of privacy in blood turned over to third parties and abandoned than we do in our trash cans or bank records.” Id. at 872-73 (citing United States v. Miller, 425 U.S. 435, 442-43, (1976) (no reasonable expectation of privacy in material conveyed to third party, like bank records, even if conveyed in confidence and for a limited purpose)). Voluntary contribution of DNA samples may also serve to justify its collection. See, e.g., Smith v. Maryland, 442 U.S. 735 (1979) (holding that the installation and use of a telephone “pen register” to trap and store dialed numbers was not a search within the meaning of the Fourth Amendment because the subject voluntarily conveyed numerical information to the telephone company.)
233 See, e.g., Greenwood, 486 U.S. at 39-41.
234 This seems a reasonable boundary to draw. After all, dead skin cells or saliva samples reveal little absent laboratory analysis, and most people would likely distinguish their privacy interest in floor sweepings to be discarded from their privacy interest in sweepings to be chemically analyzed to explore their DNA.
235 See Skinner, 489 U.S. at 616 (“The ensuing chemical analysis of the sample to obtain physiological data is a further invasion of the tested employee’s privacy interests).
biological sample also could conceptually run afoul of the “plain view” doctrine,\textsuperscript{236} though it is not clear how this would apply to discarded or abandoned material.

Modern Fourth Amendment jurisprudence—which owes much to the “reasonable expectation of privacy” standard introduced in \textit{Katz v. United States}\textsuperscript{237}—simply did not contemplate the involuntary and ubiquitous scattering of deeply personal information in this manner.

Perhaps the most severe problem with “search as sampling” is that by subjecting only initial sample collection to Fourth Amendment scrutiny, law enforcement can “tag” an individual at a time when his privacy is diminished\textsuperscript{238}—say, during supervised release—and thereafter exploit this information forever.\textsuperscript{239}

\section*{The Unexamined Expansion: Familial DNA Search}

This subsection examines the effective inclusion of offenders’ family members via familial DNA search. This new technique, as yet unexamined by courts,\textsuperscript{240} either poses staggering Fourth Amendment concerns or none at all, depending chiefly upon whether or not an individual’s \textit{effective} inclusion in CODIS constitutes a protected search or seizure.

\section*{Does Familial DNA Search Involve a Protected Search?}

\begin{footnotesize}
\begin{itemize}
\item \textsuperscript{236} See, e.g., \textit{Arizona v. Hicks}, 480 U.S. 321, 324-325, (1987) (stating that moving stereo equipment to view serial numbers, as opposed to simply recording what was in plain view, constitutes a search).
\item \textsuperscript{237} 389 U.S. 347 (1967).
\item \textsuperscript{238} See \textit{Monteleoni, supra} note 159, at 270.
\item \textsuperscript{239} See \textit{Kincade}, 379 F.3d at 874 (Kozinski, J., dissenting) (Noting that government wished to obtain DNA sample from individual on supervised release not to ensure he complied with conditions of that release, but “precisely so his DNA will be available in the CODIS database for the rest of his life.”)
\item \textsuperscript{240} As of April 30, 2010, the only mention of “DNA” and “familial search” in the Westlaw “allcases” database is found in an employment action, decided April 2, 2010, wherein a Massachusetts crime lab employee is alleged to have, \textit{inter alia}, carried out improper familial searches. See \textit{Department of State Police v. Massachusetts Organization of State Engineers and Scientists}, 456 Mass. 450, 924 N.E.2d 248 (Mass., 2010).
\end{itemize}
\end{footnotesize}
Examining the issue in 2006, Professor Hank Greely of Stanford Law School identified “no general legal barrier to the use of family forensic DNA.” Greely reasoned that familial search might be permitted on the simple theory that, as far as the relatives are concerned, “nothing has been seized from them and they have not been searched.”

If true, this is so only because courts have heretofore focused on physical DNA sampling as the relevant search for Fourth Amendment purposes.

But as stated above, this analysis is incomplete for two reasons: first, DNA samples can readily be obtained without any new physical intrusion at all (e.g., from litter or repurposed blood samples), and second, several other landmark events in the DNA profiling process might also qualify as separate protected searches.

Setting aside physical DNA sample collection, a protected search could still attach to (1) DNA sample analysis and profile creation (as suggested under *Skinner*), (2) additional genetic analysis of stored DNA samples (again under *Skinner*), (3) inclusion of profiles in a searchable database, (per *Mitchell*, and Judge Kozinski’s dissent in *Kincade*), and (4) actual queries against the profile database.

In cases (1) and (2), considering sample analysis and DNA profile creation to be protected searches would not implicate the Fourth Amendment in familial search, since no sample has been taken, and no DNA profile created, from the offender. (Note that although a DNA profile of the offender has been generated from forensic evidence such as crime-scene DNA, courts have never held profiling of recovered DNA evidence to constitute a search of the individual who left it, and it would be absurd to do so.)

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242 *Id*. at 257.
243 See *supra* notes 223-227 and accompanying text.
244 See *Kincade*, 379 F.3 at 872 (Kozinski, J., dissenting) (asking “what if Congress were to require medical labs to submit the excess blood for DNA fingerprinting so it can be included in CODIS?” and reasoning that, under “the [*Kincade*] plurality’s balancing analysis, I'm hard pressed to see how this would violate anyone's Fourth Amendment rights.”)
245 See *supra* note 225 and accompanying text.
246 See *supra* notes 226-227 and accompanying text.
The only profiles in play are the one derived from the forensic evidence, and those of existing offenders profiled in CODIS—a group that, in a familial search, necessarily does not include the search target. (After all, the sole appeal of familial DNA search is that it may provide a means to “reach” those whose profiles are not included in the database.) Thus, anointing sample analysis and profile generation as protected searches subject to Fourth Amendment scrutiny would alter the constitutional calculus for DNA profiling generally, but would create no obstacle for familial search.

It is in cases (3) and (4)—DNA profile inclusion in a searchable database, and actual searches against such a database—that familial DNA could raise substantial Fourth Amendment concerns.

The reasonableness of inclusion of offenders’ DNA profiles in a searchable database—whether they be convicts, parolees or arrestees—has to date always hinged upon the diminished expectation of privacy assigned to these individuals. But if a diminished expectation of privacy is required for inclusion to pass Fourth Amendment muster, then the rote inclusion of an offender’s relatives is surely presumptively unjustifiable.

A wrinkle with this reasoning is that individuals potentially “reachable” through familial search—that is, close blood relatives of profiled offenders—are not actually included in the database, but are nonetheless effectively included. The biological reality of DNA and inheritance is that an individual’s genomic privacy can be invaded not only through her own DNA, but also through the DNA of her relatives. For this reason, including one family member in CODIS has the effect of partially including many others,

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247 Courts acknowledge that DNA sampling and analysis is done for the purposes of inclusion in searchable databases, whether or not they identify such inclusion as an independent search or seizure. For a full discussion, see Section III, supra.
an issue that courts—armed with traditional legal reasoning applied to discernible information states—may be ill-equipped to address.  

The most sensible reduction of this problem seems to be the following: An individual is either “reachable” through CODIS, or is not. The development of familial search protocols means that profiled offenders are no longer the only ones “reachable” through CODIS: That group has grown to include close relatives of profiled offenders. Therefore, to justify the use of this new technology, we must be able to justify the inclusion in CODIS—effective or actual—of all those it can reach.

If familial DNA search is to run afoul of Fourth Amendment protections, it will need to be ushered in on the grounds that effective inclusion of innocent relatives in a searchable database, absent the diminished expectation of privacy heretofore necessary for inclusion, constitutes a search.

Absent such finding, Professor Greely’s view is likely to prevail: Nothing has been seized from offenders’ relatives, and they have not been searched. With that, Fourth Amendment inquiry ends, and law enforcement is free to conduct familial DNA searches at will. Notwithstanding of the likelihood of this outcome, the following subsections will deal with the alternative: That a familial DNA query constitutes a Fourth Amendment search.

Neither Special Needs nor Totality of the Circumstances Tests Should Apply

Assuming that tracking an individual through partial CODIS matches to a relative is deemed a protected search or seizure of that individual subject to Fourth Amendment

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scrutiny, courts will need to decide which test to apply when evaluating its reasonableness.

Such a search would be warrantless, since if probable cause existed to single out a suspect for arrest, there would be no reason to troll blindly through CODIS for his identity; the suspect could be detained and (under arrestee DNA sampling laws) sampled immediately. On similar logic, family search cases would also lack individualized reasonable suspicion.

The totality of the circumstances test has to date been applied only where triggered by a diminished privacy interest in identity (for instance, in convicts, parolees, and most recently, arrestees). An individual does not have a diminished privacy interest merely by being related to a criminal. Thus, all else equal, an application of the totality test to a search of that individual is plainly improper.

The special needs rationale may at first seem a better fit, but it too suffers from problems in application. This test is limited to instances where special needs beyond the need for ordinary law enforcement make traditional warrant standards impracticable. This is difficult to envision how directed DNA profile searching responsive to specific crime-scene evidence is at all distinguishable from routine law enforcement activity. Where courts have applied the special needs rationale to DNA sampling, it has been on the theory that DNA collection aids in investigation of other crimes—namely past or future offenses. Something about the remoteness and abstract nature of these

249 For a full discussion, see supra notes 170-177 and accompanying text.
250 See Monteleoni, supra note 159, at 264.
251 See, e.g., Kincade, 347 F.3d at 839 (noting that DNA profiling “contributes to the solution of past crimes”).
offenses may suffice to distinguish DNA collection from routine law enforcement. But most courts have rejected even this rationale, and in the case of familial searches, the crime at issue is not some abstract past or future offense, but real and currently under investigation.

It is therefore pure confusion to portray pursuing a suspect—wanted for a discrete and actual crime—as somehow distinct from ordinary law enforcement.

In sum, neither test currently employed to uphold Fourth Amendment intrusions occasioned by DNA profiling is applicable to familial DNA search. Courts would need to adopt a simple balancing test without any trigger, which runs afoul of both the plain text of the Fourth Amendment and existing interpretive doctrine.

**If Either Test Does Apply, Familial Search Likely Passes Balancing Test**

Setting aside their applicability, the *outcome* of the two popular balancing tests for suspicionless searches of individuals—special needs, and totality of the circumstances—depend upon balancing the state’s interest in the protected action against the invasion of privacy upon the individual.

Applying the totality of the circumstances test, the *Kincade* court balanced the “monumental” state interest in preventing recidivism and solving unspecified past crimes

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252 See *supra* note 188 and accompanying text.

253 Cf. *Nicholas v. Goord*, 430 F.3d 652, 668-669 (2d. Cir., 2005) (“we find it crucial that the state, in collecting DNA samples, is not trying to determine that a particular individual has engaged in some specific wrongdoing. Although the DNA samples may eventually help law enforcement identify the perpetrator of a crime, at the time of collection, the samples in fact provide no evidence in and of themselves of criminal wrongdoing, and are not sought for the investigation of a specific crime.”) (emphasis added, citations and internal quotation marks omitted).
against the minimal intrusion occasioned by physical blood sampling to uphold DNA collection from offenders.254

In the case of familial DNA search, the balance should tip even further in the state’s favor: The crime in question is discrete, real, and unsolved, and the privacy intrusion is physically nonexistent. Indeed, an individual singled out through familial search has no way of knowing this search has ever occurred—he255 has been neither physically searched nor literally included in CODIS.

Nonetheless, this unknowing individual could then be singled out for highly individualized surveillance and investigation. In Colorado, for instance, “individuals identified through the familial DNA search as related to the CODIS offender” will be investigated using “surveillance data,” “DNA samples obtained surreptitiously,” “financial searches,” “motor vehicle records,” or other means.256 While no doubt carefully scripted to avoid wanton triggering of Fourth Amendment scrutiny, these follow-up searches are unquestionably individualized—and potentially politically unpalatable given the absence of articulable particularized suspicion.

**Summary of Legal Standards**

Compulsory DNA collection from convicts, parolees and supervised releasees stands on firm legal footing, upheld through either the special needs test, or more commonly, the totality of the circumstances test for suspicionless searches. Recent

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254 347 F.3d at 843 (characterizing state interests served by DNA collection as “undeniably compelling” and “monumental” and the privacy intrusion as “minimally invasive—both in terms of the bodily intrusion it occasions, and the information it lawfully produces.”)

255 And it would likely be a “he”—aside from the presumed overrepresentation of men in CODIS, Y-STR analysis (the standard follow up test performed to verify candidate matches returned by familial search) requires the presence of a Y-chromosome in both parties, and therefore works only on male-male relative pairs.

expansion of DNA databases to include arrestees has spurred new legal challenges—but so far, district courts have largely upheld such collection. Familial DNA search is as yet unexamined by courts, and its constitutionality likely hinges on whether or not effective inclusion in CODIS of offenders’ kin is identified as a protected search or seizure. If not, nothing prohibits law enforcement from performing familial searches; if so, neither the special needs test nor the totality of the circumstances test should apply. Nonetheless, if a new test is applied that triggers a traditional balancing test, familial search will be justifiable due to the strong state interest and de minimis privacy intrusion (if any).

The following two sections identify key problems with current CODIS policy, and propose reform.

IV. DNA Sample Retention: The True Privacy Threat

Current Federal policy—and that of most states—dictates that in addition to profiling 13 CODIS STR loci, biological DNA samples are retained by crime labs, often indefinitely. Sample retention adds very little to the effectiveness of DNA profiling, and unnecessarily aggravates privacy concerns. DNA samples from profiled individuals should be destroyed, making CODIS a sample-free database.

Easy Access, Controlled Use: A Realistic Approach to DNA Samples

Sound reasons exist to keep our genetic information private. Yet it is virtually impossible to prevent scattering stray copies of our complete genomic DNA as we

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257 See supra note 144 and accompanying text.
258 For a full discussion, see supra notes 56, 59-61, and accompanying text.
proceed through life, and current Fourth Amendment jurisprudence recognizes no right to privacy in publicly discarded material.

A solution to this conundrum is to accept that genetic material can be obtained easily, and to aim instead to limit its use. For instance, it may always be legal to sweep the street for litter, but legislators could enact a law prohibiting the sequencing of any DNA thusly recovered. GINA takes precisely this approach, accepting that DNA samples are likely to be broadly available, and identifying and prohibiting improper uses of genetic material against this backdrop.

With this in mind, this subsection begins by distinguishing the proper use of DNA to generate DNA profiles from an improper use—long-term sample preservation and additional analysis.

**DNA Profiles are a Proper Use**

The citizenry, acting through legislatures, has broad discretion to define proper and improper uses of DNA. If courts are called upon to assess any such definition, they are likely to apply a form of interest balancing, similar to the tests currently employed to evaluate DNA collection from offenders.

CODIS-style STR-based DNA profiles should, and do, pass such a balancing test. As previously stated, their tremendous forensic value outweighs their modest privacy implications: DNA profiles are useful chiefly for identification, and are unlikely

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259 Any serious attempt to avoid leaving genetic material strewn about in our wake would surely be prohibitive: The daily scrubbing and paranoia would cripple our lives. For an interesting dramatization of this process, see *Gattaca* (Columbia Pictures, 1997).

260 See supra note 229, and accompanying text.

261 See supra note 58, and accompanying text.

262 See Section III, supra, discussing judicial balancing and approval of DNA collection for profiling.
ever to reveal sensitive health-related information. They should properly be deemed an acceptable use of DNA.

**Sample Retention is Not a Proper Use**

Long-term storage and preservation of whole-genome biological samples, however, should not pass similar scrutiny. The benefits of stored samples are minor, limited to routine verification of stored DNA profiles and occasionally to follow up familial search testing. The privacy implications, however, are substantial.

As understanding of our genetic makeup continues to grow, each new advance permits re-examination of existing DNA with an eye to new features and correlations. And keeping samples on ice in secure crime labs makes it very hard to monitor how they are being used.

Imagine an individual who paid a princely sum to have her own genome sequenced in the early 2000s. At that time, she would have learned little from the billions of A, C, G and Ts that make up her genetic code. Today, that very same sequence—her genome sequence is hers for life, and does not change—reveals a good deal more, since scientists have identified new genes and correlations, and can re-examine her sequence with these in mind. A genome contains a vast wealth of data, only a small fraction of which we can currently decipher. Today’s innocuous sequence of letters will reveal very different things tomorrow.

The future will certainly bring further discoveries in genomic science. It is not unthinkable to posit that genetic correlations may one day be uncovered that suggest a
predisposition to violence, for instance, or other traits of interest to law enforcement.\footnote{See generally Rosen, supra note 31 (“As genetic research—led by private companies such as 23andMe—reveals increasing ties between genes and predisposition to violence and other antisocial behavior, there may be growing discomfort with the idea of giving the government access to DNA, which could lead to people being surveilled, detained, or suspected for their behavioral tendencies rather than their actions.”)} At such time, society will need to determine whether and how to use these findings, but a policy of DNA sample retention makes it far too easy for law enforcement to carry out such additional tests without public knowledge, and without explicit approval or oversight.

**Limiting New Use of Stored DNA Samples Has Proven Ineffective**

Despite statutory usage controls and stiff penalties for misuse of CODIS DNA profiles or samples,\footnote{See supra notes 153-154, and accompanying text.} “that firewall that the FBI said exists between the genetic sample and the edited profile is [already] being breached through familial searching.”\footnote{Rosen, supra note 31.} This is because California and Colorado now access stored samples for Y-STR profiling, to sort through candidate matches from familial searches. In both states, this is occurring absent any applicable statutory change. This perceived freedom to tap into stored DNA samples for further inquiry is precisely the sort of behavior that has privacy advocates worried about sample retention. After all, if Y-STR tests simply performed without statutory revision, “how long will it be before they say: let’s . . . see if someone is a sociopath?”\footnote{Id.}

**For Offender Profiles, Sample Retention is Unnecessary**

\footnote{Supervised Analytic Writing / THE PROBLEM CHILD / Seringhaus (YLS 2010)}
U.S. federal and state crime labs retain DNA samples on a quality-control rationale. Such reasoning is common among scientists, who tend in general to exhibit a pack-rat-like fastidiousness with respect to preserving biological sample material. Given that CODIS grew out of scientific and technical working groups and that many state CODIS policies exist only in laboratory manuals, it is perhaps unsurprising that DNA samples are retained.

They should not be. The value of samples for quality control is marginal—stored samples do nothing to cure sample mix-ups and labeling errors, and for true verification fresh samples must be taken from suspects anyway—and the concomitant privacy implications of storing full genomic DNA is simply too high.

Various scholars have argued for immediate destruction of DNA samples upon DNA profile creation; Professors Kaye and Smith even posited creating DNA profiling machinery to accomplish both in a single transaction. Others have noted that as a result of DNA dragnets, CODIS laboratories gather and retain samples from individuals never implicated in any crime.

Forensic scientists will protest that information may someday be needed from a DNA sample to supplement CODIS DNA profiles; for instance, Y-STR typing to follow

267 See supra note 145 and accompanying text.
268 The author spent a decade as a student and post-doctoral associate in biochemistry, bioinformatics and molecular biology research laboratories.
269 Academic research labs commonly contain several large freezers full of sample trays and miniature test tubes, each carefully labeled for potential future use. This is quite sensible. Many biological samples, such as carefully crafted plasmid DNA, can be considerably more work to prepare than to duplicate.
270 See supra note 90.
271 See supra notes 131, 133-134 and accompanying text.
272 See Wallace & Simoncelli, supra note 144 (stating that “re-testing the same sample clearly cannot correct for many sorts of errors, such as sample mix-ups. In fact, in both the UK and the US, testing of a fresh DNA sample from the suspect is always required before the DNA evidence is admissible. Thus the stored samples do nothing to prevent future miscarriages of justice”).
273 See Kaye, Let’s Bury the Junk, supra note 16, at n.27 (stating that “sample retention poses a scientifically real privacy risk . . . .”); Monteleoni, supra note 159, at 258 n.60.
up on familial DNA search. The straightforward answer is that this is simply too bad. Crime labs should take whatever information they require (and are authorized to take) from the DNA sample at the time of initial processing. If additional analysis is desired, they must secure appropriate authorization and resample the offender in question. This may be a hassle, but it represents a viable and less invasive alternative means to secure the same information in a targeted and individualized manner, perhaps along with a warrant requirement or other judicial oversight.

**For Forensic Profiles, Sample Retention is Necessary**

Whereas re-sampling is possible in the case of profiled offenders—especially if they become suspects in a new investigation—re-sampling is obviously not possible for most forensic DNA evidence, which captures a fleeting snapshot of a crime scene. Thus, if further analysis or re-processing of crime-scene DNA evidence is ever required, accessing a stored sample is the only way to comply. Since no viable and less invasive alternative exists, forensic sample storage is necessary.

Moreover, forensic samples do not trigger quite the same set of privacy concerns as offender samples; for instance, they should be associated with a crime scene, not with any individual’s record.

Good reasons exist to retain forensic samples in CODIS, subject to the same usage restrictions and privacy protections currently in place.
Summary: Offender DNA Samples Should Not Be Retained

Where courts have upheld DNA collection against Fourth Amendment challenges, it has largely been on the theory that DNA profiles are used only for identification. Where courts have rejected it, it has been because DNA can do much more than just identify.

In a sense, both positions are correct: The former correctly describes DNA profiles, and the latter DNA samples. Profiles are very different from samples in information content and potential for invasiveness, and they should be treated differently.

The *Kincade* court noted “weighty” concerns regarding sample retention, but dismissed them based on existing statutory protections against misuse and the fact that no such abuse was then at issue before the court.

But retention of DNA samples corresponding to offender DNA profiles is an unjustified and avoidable byproduct of an otherwise acceptable DNA profiling regime. Legislatures and courts should not wait to distinguish between the acceptable use of DNA to compute and store DNA profiles, and the unacceptable long-term storage of whole-genome DNA samples from profiled individuals.

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276 See, e.g., *Kincade*, 379 F.3d at 837, (“the DNA profile derived from the defendant's blood sample establishes only a record of the defendant's identity”).
277 As in *Mitchell*. See supra notes 214-215 and accompanying text.
278 *Kincade*, 379 F.3d at 837.
279 See 42 U.S.C. §§ 14132(b)(3) (limiting permissible uses of DNA profiles and samples) and 14135e (establishing criminal penalties improperly disclosure or receipt of DNA profiles or samples).
280 *Kincade*, 379 F.3d at 838 (“if . . . some future program permits the parade of horribles the DNA Act's opponents fear . . . we have every confidence that courts will respond appropriately.”)
V. RACIAL BIAS AND UNJUSTIFIED EXPANSION: CURBING FAMILIAL DNA SEARCH

Familial DNA search represents a *de facto* expansion of the U.S. DNA database system, one that stands poised to push CODIS well beyond its mandate. Using CODIS to reach offenders’ family members is unjustifiable under any current Fourth Amendment theory of DNA profiling—all of which condition inclusion on a diminished expectation of privacy due to arrest, imprisonment or supervised release—and correcting the harmful effects of familial search will require either radical statutory repair, or a fresh judicial take on DNA collection under the Fourth Amendment.

All else equal, increasing CODIS coverage will solve more crimes. But thought must be given to the means of this growth, since expansion to include offenders’ kin imposes externalities that may in practice prove unpalatable, such as overextending the CODIS database system, improperly subjecting innocent civilians to scrutiny and stigmatization, and grossly aggravating the racial bias already embodied in offender databases. This Section sets forth arguments why familial search, though occasionally useful, is unjustifiable.

**Arguments Against Familial DNA Search**

**Familial Search Overextends CODIS**

Professor Jeffrey Rosen of George Washington University Law School has argued that “[t]he strongest legal argument against familial searches is that they’re not what Congress intended when it set up the [DNA] database.”281 Rosen cites the two main reasons underlying the plurality decision in *Kincade*, namely the diminished expectation of privacy, and the state’s interest in ensuring reform over recidivism. “Familial searches

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can’t be justified by either rationale. The family members of offenders have done nothing to reduce their expectation of privacy, and the state is investigating new crimes, not stopping repeat offenders.”282 Thus, in a very real way, familial searching represents an improper overextension of CODIS’s statutory mandate, as interpreted by courts.

From a technical standpoint, CODIS software is not optimized for familial search, and does a poor job of sifting out false positive matches. To effectively perform familial searches, states must design and implement novel software platforms. That the FBI has to date declined to institute its own familial search program at least anecdotally suggests that the Bureau may consider familial search an improper expansion or overextension of its CODIS platform.

Familial search is also an overextension of the 13 CODIS STR loci. These 13 STRs are a powerful tool for exact matching of DNA profiles: They permit the association of a forensic DNA sample with a profiled offender to a very high degree of certainty. However, this set of 13 loci falls short when forced to resolve partial matches. The drop in resolving power and dramatic increase in false positives suggests that to properly conduct familial searches on a growing database, the core CODIS loci should be expanded.

The human genome contains tens of thousands of STR loci,283 a substantial number of which are just as well suited to profiling as any CODIS STR; family search based on 100 loci would be far more effective than that based on just 13—and moreover, could reliably identify more distant relatives. This is not intended to argue in favor of familial search, but rather to state that if familial search is to be sanctioned and conducted properly, an expansion of CODIS loci is in order.

282 Rosen, supra note 31.
283 See National Institutes of Science and Technology, STRbase, http://www.cstl.nist.gov/strbase/ (last visited July 2, 2009); some STRs have already been analyzed and recommended for forensic use. See http://www.cstl.nist.gov/strbase/newSTRs.htm
Denver District Attorney Morrissey has opined that the 13 CODIS markers are “an extremely powerful tool,” and that declining to employ them for familial DNA search would be like building “a Porsche [and driving it] like a Pinto.” The D.A. has it backwards: familial search is driving a Pinto like a Porsche, and if authorities are set upon doing so they should upgrade their motor pool.

In sum, familial search overextends CODIS, legally and technically.

**Singling Out Offenders’ Kin for Increased Scrutiny is Improper**

Frederick Bieber, co-author of a seminal *Science* article on familial DNA searching and a medical geneticist at Brigham and Women’s Hospital in Boston, has opined that familial searching of offender databases would be of little use “if close relatives didn’t commit crimes.” He points to a “familial clustering in crime,” citing a 1999 study that found “46% of prison inmates had at least one close relative who had been incarcerated.”

As such, one might argue, relatives of offenders are not just easy targets for database broadening because of their genetic relatedness to profiled individuals, but are actually properly subjected to increased scrutiny in future criminal investigations due solely to the actions of their relatives.

American constitutional law thankfully affords no opportunity to concoct reasonable suspicion or probable cause from such generalizations. It is one thing to note such statistics, and quite another to employ them to direct investigations. Any investigative technique that posits beginning with the relatives of convicts as first-order

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286 Dr. Frederick Bieber as quoted in Nakashima, *supra* note 113.
287 *Id.*
288 Even the idea of implicating families in investigations is likely to have a profound impact on the families involved. See Erica Haimes, *Social and Ethical Issues in the Use of Familial Searching in Forensic Investigations: Insights from Family and Kinship Studies*, 34 J.L. MED. & ETHICS 263 (2006).
suspects runs counter American ideals of civil liberty, and is properly aborted by constitutional protections against bills of attainder and “corruption of blood.”

A second argument—likely somewhat less offensive to civil libertarians—is that offenders’ family members are not specifically targeted on account of any arguably increased propensity to commit crime; instead, their susceptibility to familial search is biological happenstance, a by-product of the inheritance process underlying our genetic constitution. As such, offenders’ family members are simply low-hanging fruit for database operators, an easy expansion of CODIS coverage that can be exploited in cold cases without leads.

Thankfully however, courts have not promulgated a “low-hanging fruit” doctrine to justify warrantless searches and seizures in the name of simple convenience to law enforcement. Thus, familial search—a convenient repurposing of CODIS that achieves “virtual” expansion through a neat biological trick—is no more acceptable than routinely searching the next-door neighbors of arrestees, or erecting roadblocks adjacent to an existing traffic stop. Mere convenience is no substitute for probable cause or reasonable suspicion.

If family members of offenders are to be searched like offenders, there must be a justifiable reason. Familial search offers none.

**Familial DNA Search Aggravates Racial Bias in CODIS**

As several scholars have noted, familial DNA searching is particularly worrisome from a political standpoint because it will grossly aggravate the racial bias already embodied in CODIS.

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289 U.S. Const. Art. III. § 3, cl. 2 states that “The Congress shall have Power to declare the Punishment of Treason, but no Attainder of Treason shall work Corruption of Blood, or Forfeiture except during the Life of the Person attained.” Note, however, that this protects relatives from conviction on account of their familial relationships; it does not explicitly protect them from suspicion or even investigation on the same account.
The FBI does not release statistics concerning the racial composition of CODIS databases. However, because African Americans make up a disproportionately large fraction of felony arrests in the United States, Professor Greely reasons that they must account for a similarly large fraction of records in the CODIS database.\footnote{Greely, supra note 83 at 258.}

By applying familial DNA searches to this database, the fraction of the total African American population “reachable” through CODIS (either directly or indirectly) would be roughly four to five times larger than the corresponding fraction of Caucasians or Hispanics.\footnote{Roughly 17\% versus 4\%. Greely, supra note 83 at 258-259.} (A student note has argued that due to the commonness of large families among U.S. Hispanics, that population might also be overrepresented in databases extended by familial DNA searches.)\footnote{See Grimm, supra note 111.}

On average, 28.5\% of African American men, 16\% of Hispanic men and 4.4\% of Caucasian men are likely to be imprisoned on a felony charge at some point in life.\footnote{See Kaye & Smith, supra note 290, at 452.} Extending effective database coverage to include first-degree relatives of these people means a very substantial fraction of the African American population will eventually be “reachable” through CODIS, compared to a very small fraction of the Caucasian population. If all arrestees are included, as opposed to just felony arrestees, Kaye and Smith point out that the end result may be functionally indistinguishable from a universal DNA database for African Americans only.\footnote{Id. at 455-456.}

It is not clear what legal issues may arise from this disparate representation by race in CODIS databases; courts have not yet addressed the issue. Professor Greely has discounted equal protection arguments based on disparate impact, but nonetheless states

\footnote{See David H. Kaye and Michael E. Smith, DNA identification databases: Legality, legitimacy and the case for population-wide coverage, WISC. L. REV. 413 (2003); Greely, supra note 83; Murphy, supra note 72; Grimm, supra note 111.}
that this disparity “does seem fundamentally unfair.” He suggests that the issue may have more political than legal traction.

Whether political or legal in nature, problems are sure to arise if DNA database approach universal coverage for certain races and not others.

**Implementation: How to Prohibit Familial DNA Search**

If courts or legislatures decide to prohibit familial searches, they could do so readily either by restricting use of DNA profile databases to only CODIS software (which is ill-suited to family search), or more broadly by prohibiting reporting or pursuit of deliberately-sought partial profile matches. The latter approach is most easily achieved by classifying partial match searching as an improper use of stored DNA profiles.

Banning all use of partial matches would be overbroad, since partial match searching arose as a means to extract some value from degraded or incomplete forensic DNA samples, and from samples containing multi-source mixtures of DNA. Although such searches depend upon incomplete matches against stored profiles, they still seek to match to a single individual actually profiled in CODIS. Thus, these searches enhance the effectiveness of CODIS without effectively including anyone in the database who has not rightly been profiled.

To properly isolate familial search, courts or legislatures should address the use of both “fortuitous” and “deliberate” partial profile matches whose aim or effect is the identification of a profile in CODIS that, though it clearly does not match the forensic sample, may match a relative of the suspect—or more broadly, anyone not properly

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296 Greely, supra note 83, at 259.
297 Id. at 259-260.
profiled in their own right. An example of language prohibiting such searches (indeed, the sole statutory prohibition of familial search) exists in Maryland Code § 2-506(d).  

VI. MOOTING FAMILIAL SEARCH: TOWARD A UNIVERSAL DNA DATABASE

Familial search poses a vexing problem. It is likely politically untenable, and appears on its face to violate basic Fourth Amendment principles regarding suspicionless search, but due to technical sleight of hand—and the absence of any clearly identifiable search or seizure against offenders’ relatives—it may yet prove difficult for courts to prohibit.

This paper has argued that courts could identify a protected search based on the overall effect of being “reachable” through CODIS, but if this idea does not find traction, the public may be left with a problem that current Fourth Amendment jurisprudence is powerless to solve.

An ambitious alternative is a population-wide DNA database. Extending CODIS coverage to all U.S. citizens would at once moot concerns about incomplete coverage (such as racial bias, and stigma or suspicion attaching to unjustified inclusion), subject CODIS to greater privacy oversight (through the citizenry’s new stake in protection), and at the same time create a potent law enforcement tool.

A Universal DNA Database: Hotly Debated, Still On Hold

A universal DNA database is at once a bête noire for privacy advocates, and the obvious answer to the problems posed by familial DNA search.

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298 Supra note 132.
The proposal is not new. A liberal U.K. judge has suggested universal databasing in response to racial concerns. Former New York Mayor Giuliani publicly supported a proposal to sample DNA from all newborns and make records available to law enforcement.

The idea has also gained traction among scholars. In 2002, Professor Akhil Amar of Yale Law School argued publicly in support of a universal U.S. DNA database, which he termed “a godsend to innocent convicts.” The following year, Professors Kaye & Smith detailed a proposal for such a database. The proposal has appeared more recently in a thorough student note as well as opinion pieces by this author and others.

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299 Professor Rosen warns of this “unsettling future,” cautioning that governments might “shar[e] DNA profiles in law enforcement databases with insurance companies, employers, schools, and the private sector.” Rosen, supra note 31. See also generally Tania Simoncelli, Dangerous Excursions: The Case Against Expanding Forensic DNA Databases to Innocent Persons, 34 J. L. MED. & ETHICS 390 (2006); Rebecca Sasser Peterson, Note, DNA Databases: When Fear Goes too Far, 37 AM. CRIM. L. REV. 1219 (2000) (arguing that warrantless profiling of every citizen’s DNA is unconstitutional.)


301 See Larry Miller, The U.K.’s ‘Big Brother’ DNA Database, CBS NEWS (Sept. 8, 2007), available at http://wap.cbsnews.com/site?sid=cbsnews&pid=sections.detail&storyId=3242563&index=1 (last accessed May 5, 2010) (“[A] senior British judge suggested that every man, woman and child in the country, and those who come to visit, should have their genetic fingerprint, their DNA taken and held on a national police database. Lord Justice Sir Stephen Sedley . . . sits on the more liberal end of the bench [but is] angered that minorities disproportionately have their DNA taken.”).


304 See Kaye & Smith, supra note 290.

305 See Monteleoni, supra note 159.

The idea has also received a fair amount of criticism. Professor Rosen calls the idea “utopian,” arguing that sample retention, the lack of nuanced privacy regulations, and the inability to ensure that the government would access the database only to solve crimes makes this proposal unfeasible.\footnote{See Rosen, supra note 31.} Rosen and others also warn of ominous-sounding “genetic surveillance.” An early student note lamented that although a universal DNA database was likely constitutional under the Fourth Amendment,\footnote{Tania Simoncelli, ACLU Science Advisor, as quoted in Nakashima, supra note 113. Prof. Rosen also uses this term. See Rosen, supra note 31.} it should be prohibited due to “current procedural uncertainties” such as “rate of error of current testing procedures, the lack of industry standards and regulation, and juror tendency to overvalue scientific evidence.”\footnote{Jennifer Sue Deck, Note, Prelude To A Miss: A Cautionary Note Against Expanding DNA Databanks In The Face Of Scientific Uncertainty, 20 VT. L. REV. 1057, 1059 (1996) (“It is both feasible and conceivable that the United States Supreme Court would allow the creation of a national DNA databank.”)} Christine Rosen cautions that “there is a long way to go from academic speculation to political reality.”\footnote{Id. at 1060.} Some scholars recognize that more coverage in DNA databases is desirable, but stop short of advocating universal inclusion.\footnote{Christine Rosen, Liberty, Privacy, and DNA Databases, 1 NEW ATLANTIS 37 (2003), available at \url{http://www.thenewatlantis.com/publications/liberty-privacy-and-dna-databases} (discussing universal DNA databases)}

The following subsection presents arguments in favor of a universal DNA database that is responsive to the threat of familial search, and retains no DNA samples.
Arguments in Support of a Sample-Free, Universal DNA Profile

Database

DNA Profiles Offer Very Limited Possibility for Misuse

A sample-free database should mitigate most genetic privacy concerns. As previously stated, whereas DNA samples contain an individual’s full genomic material, DNA profiles are stripped-down numerical distillations of a very small subset of this information. Keeping profiles while discarding samples, as Kaye & Smith advocate, would limit the use of DNA databases to identification, with the only reasonable potential for abuse being possible mapping of paternity or other familial relationships. A universal DNA profile database would resemble a collection of Social Security numbers, not a medically useful genomic snapshot. So long as tissue samples are not retained, the opportunity for this data to disclose meaningful biological or health information is virtually nonexistent.

Genetic privacy advocates would do well to focus on the arguably far greater risk that surrounds us every day: Any classmate or coworker could swab your discarded soda can and mail the sample in for private genomic analysis, which can cost as little as $399 and will reveal ancestry information, as well as test results for hundreds of genetic diseases and other traits.

Universal Coverage Moots Expansion and Eliminates Problematic Partial Coverage

313 For a full discussion, see Section I, supra notes 58-66 and accompanying text.
314 See Kaye & Smith, supra note 290, at 437, 440 n. 96.
315 See generally Kaye, Let’s Bury the Junk, supra note 16.
A universal database moots in one fell swoop the inevitable incremental expansion\textsuperscript{317} of CODIS, a steady growth that continues to stretch Fourth Amendment justifications to the point of mere rationalizations.\textsuperscript{318} Driven by a pressing state interest to solve heinous crimes, the government will continue to sweep more and more individuals into DNA databanks. This will result in spotty and inconsistent coverage, just as has occurred with fingerprints.\textsuperscript{319}

In the 1930s, calls for universal fingerprinting essentially mirrored modern arguments in favor of a universal DNA database, but were rejected “on civil libertarian grounds.”\textsuperscript{320} As a result, fingerprint databases, like CODIS, were limited to offenders—but as Judge Kozinski points out in his \textit{Kincade} dissent, the subsequent expansion of fingerprint coverage offers a grim preview of the path CODIS may soon take.

First, in 1929, J. Edgar Hoover expanded offender-based fingerprint records by including all civil servants.\textsuperscript{321} The Alien Registration Act of 1940 “eventually delivered over a million prints to the FBI.”\textsuperscript{322} Judge Kozinski goes on to point out that now, “the FBI’s Integrated Automated Fingerprint Identification System contains the fingerprints of over 47 million people, \textit{including prints acquired related to a background check for employment, licensing, and other non-criminal justice purposes} and submitted voluntarily by state, local, and federal law enforcement agencies.”

\textsuperscript{317} Kincade, 379 F.3d at 845 (Reinhardt, J., dissenting) (“A brief examination of the origins and development of CODIS helps demonstrate why further \textit{limitless expansion of the scope and reach of this nationwide database is inevitable},”) (emphasis added); see also \textit{Id}. at 873 (Kozinski, J., dissenting) (referring to the “inevitable expansion” of CODIS).

\textsuperscript{318} See, e.g., Judge Reinhardt’s emphatic dissent in \textit{Kincade}, 347 F.3d at 842-871.

\textsuperscript{319} See, e.g., \textit{Banks v. U.S.}, 490 F.3d 1178, 1193 (10th Cir. 2007) (stating that the FBI CODIS database “operates much like an old-fashioned fingerprint database (albeit more efficiently).”); \textit{Nicholas v. Goord}, 430 F.3d 652, 671 (2nd Cir. 2005) (the intrusion of privacy effected by DNA sampling is similar to the intrusion and maintenance of fingerprint records).

\textsuperscript{320} Monteleoni, \textit{supra} note 159 at 254 n.40 (citing \textsc{Simon A. Cole}, \textsc{Suspect Identities: A History of Fingerprinting and Criminal Identification} 245-49 (2001)).

\textsuperscript{321} \textit{Kincade}, 379 F.3d at 873-4 (Kozinski, J., dissenting).

\textsuperscript{322} \textit{Id} at 874.
agencies. Several states require fingerprints of all drivers' license applicants.'”

It is reasonable to assume, as Judge Kozinski suggests, that a similar fate will befall CODIS. 324

And when it does? Aside from the fundamental inequity of including some people and not others, partial database coverage in a law enforcement context creates new problems. Professor Lior Strahilevitz has identified dangers of incomplete coverage with respect to criminal history. 325 Judge Reinhardt, separately dissenting in Kincade, notes the dangers of expanding qualifying offenses to include minor crimes:

“If placed in the hands of an administration that chooses to ‘exalt order at the cost of liberty,’ [a DNA database of offender profiles] could be used to repress dissent or, quite literally, to eliminate political opposition. Many of the qualifying offenses in the DNA Act are crimes that involve conduct closely related to the exercise of First Amendment rights to free speech and assembly, such as incitement, civil disorder, and the various forms of “interference” crimes . . . .”

The post-expansion result of an offender-based CODIS database—that is, one for which any arrest guarantees lifelong inclusion—is the creation of a stigmatized subpopulation, routinely subject to different searches than the rest of us, despite many having recovered the same reasonable expectation of privacy. It is one thing for this population to include only convicted violent offenders (as, it should be noted, CODIS was originally envisioned to encompass). It is another thing entirely for this population to be expanded to include minor crimes.

323 Id. (emphases added, citations and internal quotation marks omitted).
324 See Jones v. Murray, 962 F.2d 302, 307 (4th Cir. 1992) (“The governmental justification for this form of identification, therefore, relies on no argument different in kind from that traditionally advanced for taking fingerprints and photographs, but with additional force because of the potentially greater precision of DNA sampling and matching methods.”)
325 See Lior Strahilevitz, Privacy versus Antidiscrimination, 75 U. CHICAGO L. REV. 363 (2008) (arguing that full disclosure of criminal histories could benefit certain groups otherwise prone to employment discrimination by removing the need for generalizations, or so-called problematic proxies).
326 Kincade, 379 F.3d at 847-8 (Reinhardt, J., dissenting) (citations omitted).
include anyone who has at any point crossed paths with law enforcement—say, for refusal to move at a political demonstration.

Incomplete coverage also presents technical concerns. Assume a crime is committed, and DNA samples recovered from the scene contain three people’s DNA—three people smoked cigarettes at the scene. Only one of these individuals, a prior offender, is profiled in CODIS—but let us assume that one of the others is the true culprit. A CODIS search of all DNA evidence from the scene will turn up only one hit: The profiled offender. This individual now faces a very difficult situation, since “[a] DNA match is considered infallible proof of guilt or innocence in many crimes.”327 This situation highlights a crucial failing of incomplete coverage: It subtly biases results to focus attention on those included in the database, possibly to their detriment and to the benefit of those not profiled. This is a variation of a so-called “Golden Rule” of biochemistry: The result recovered is determined by the scope of the test, or in other words, “you get what you assay for.”328

Universal coverage effectively extinguishes the possibility that certain communities will draw an undue share of police interest on the grounds of their inclusion in the database alone. The current trend of quiet expansion will in the long term pose a more substantial threat to privacy than creating a carefully considered and narrowly tailored universal DNA database today.

**Universal Coverage Also Moots Familial Search, Corrects Undue Racial Bias**

The most troubling expansion currently taking place in CODIS is the adoption of familial DNA search, which by partially matching DNA profiles enables authorities to search offenders’ kin without actually including them in the database. As previously

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328 The author first encountered this quotation during an undergraduate class lecture by Professor Andrew Macmillan, CHM347H1 Organic Chemistry of Biological Compounds, at the University of Toronto in fall 1998.
stated, familial DNA search raises potentially serious Fourth Amendment concerns, is likely to be politically unpopular, and most disturbing, greatly aggravates the racial bias already embodied in the CODIS offender databases. Specifically, permitting familial DNA search on a growing database might one day approach universal coverage for certain races only.329

True universal DNA database coverage would immediately render familial DNA search unnecessary: After all, if everyone is searchable as an exact match, nothing is gained by extending this search to relatives. Thus, states could retire special software and end the massaging of data that are necessary to sift through the many false positives that arise when partially matching DNA profiles. Instead, a universal database would employ the 13 CODIS STR loci as they were intended: as a means for exact profile-to-profile matching, a task at which they are proven to excel.

Moreover, ending familial search will prevent CODIS coverage from spreading to include family members of criminals, greatly aggravating a racial skew which—owing to racial inequality in arrest and conviction rates—is already present in the database.

For this discussion, I assume that there is nothing inherently wrong with racial inequality in an offender database, so long as this inequality embodies the actual racial breakdown of its constituent offenders.330 However, such inequality is only constitutionally and politically acceptable because, as a feature of a stand-alone database, 

\textit{it is not grounds for inclusion of anyone similar}. However, it becomes unacceptable to use this skewed starting point to profile offenders’ family members. This is because such an expansion is deliberately crafted to search (as yet) innocent people on the grounds of blood relation (known or unknown) to a profiled offender. Moreover, in racial terms there is an obvious disparate impact of such profiling, even if the act of profiling offenders’

329 See \textit{supra} note 295, and accompanying text.

330 Obviously, there are arguments to be made concerning social causes of crime, and whether it is just that more members of a certain race run afoul of law enforcement than members of another, but that is beyond the scope of this paper.
family members is facially neutral—and unlike in the case of profiling offenders, any balancing of interests to justify this intrusion should run afoul of the innocents’ unencumbered Fourth Amendment rights.

**Including All Citizens Properly Subjects CODIS to Increased Political Oversight**

Including every voting citizen in CODIS would thrust the issue of appropriate use of genetic material into the public spotlight, where it belongs. Giving every citizen a direct and immediate stake in CODIS policies will enhance legislative oversight.\(^{331}\)

Under the current system, wherein only criminals are profiled, it is relatively easy for government to justify invasive use of DNA in excess of profiling—such as revisiting stored samples for Y-STR analysis as a follow-up to familial DNA search—and for the public to accept such transgressions as applying only to a dangerous underclass of criminals. But in reality CODIS retains DNA profiles and samples for offenders of many types, long after their release and concomitant return to full Fourth Amendment rights.

If samples are being improperly retained or misused, the best way to combat this may be to increase every individual’s stake in proper privacy regulation of the database.

**Universal Database is a Potent Tool for Law Enforcement**

Perhaps the chief argument in support of a universal database is the same argument that currently undergirds the continued expansion of CODIS: namely, better database coverage translates to better success in solving crimes. The value of this should not be understated: if society benefits when criminals are caught, then a universal database should be a boon indeed. A universal database will increase apprehension rates,

\(^{331}\) *See* Amar, *supra* note 303 (“Building a universal database would encourage the creation of a broad political coalition with incentives to protect privacy interests from being eroded over time.”)
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decrease repeat offenses and deter crime more effectively than either the original or the current CODIS model.

A universal database would be an effective deterrent against first-time offenders, and would also permit police to more quickly apprehend criminals who typically offend many times before first getting caught (such as burglars).

Current DNA database coverage positions forensic DNA as a tool for deterring and investigating primarily repeat offenses, but with universal coverage there is no reason this need be so. Universal coverage would dispense with the questionable notion that when a crime is committed, the only meaningful suspects are prior offenders. As Kaye and Smith point out, “a convicted-felon database is of no help in deterring or investigating felonies committed by persons not previously convicted of a felony”\(^{332}\) and similarly, an arrestee database is of no use deterring those who have not yet been arrested. But even a database including all arrestees—which CODIS is on track to become—will nonetheless exclude those responsible for a “major proportion” of all felony offenses: 44% of people arrested and prosecuted for a serious felony have never before been arrested on felony charges, and roughly one third have no arrest record at all.\(^{333}\) Thus, by limiting coverage to offenders, CODIS forecloses the possibility of using powerful DNA evidence techniques to catch first offenders: Those responsible for over a third of all serious felonies.

As Professor Amar points out, expanding the database will also eliminate innocents from suspect lists\(^{334}\)—a compelling government interest that should weigh on the side of greater coverage.\(^{335}\)

\(^{332}\) See Kaye & Smith, supra note 290 at 451.

\(^{333}\) Id. at 451 n.134.

\(^{334}\) See Amar, supra note 303.

\(^{335}\) See U.S. v. Szubilek, 402 F.3d 175, 185 (3rd Cir. 2005) (“A DNA database promotes increased accuracy in the investigation and prosecution of criminal cases. It will aid in solving crimes when they occur in the future. Equally important, the DNA samples will help to exculpate individuals who are serving sentences of imprisonment for crimes they did not commit and will help to eliminate individuals from suspect lists when crimes occur . . . . The interest in accurate criminal investigations and...\)
Constitutionality of a Universal DNA Database

Just as the constitutionality of familial DNA search will turn upon whether courts are able to localize a protected search to family members’ effective inclusion in CODIS, determining whether or not a protected search exists is central to the constitutionality of a universal DNA database.

Physical DNA sampling has been deemed a search protected by the Fourth Amendment.336 Absent judicial reconsideration, therefore, deliberate DNA collection for profiling must pass similar judicial scrutiny. However, the dissenters in Kincade point out that under the plurality decision in that case, there is no reason why DNA could not be collected from a broad swath of citizens already—the minimal intrusion balanced against legitimate state interests would continue to tip the balance in favor of collection.337 Given the state’s “monumental” interest in solving crimes and preventing recidivism,338 upholding an expansion to population-wide coverage may be as simple as applying the existing totality of the circumstances test to a broader population.

California district courts have already blessed DNA collection from arrestees,339 and the only federal judicial opposition to this broadening (in Mitchell) did so by focusing on the fact that DNA does more than identify, due to the private health information contained in DNA samples.340 With this concern addressed—as it would be, in a sample-free, profile-only universal database—courts would lose a main avenue of argument opposing expansion.

prosecution is a compelling [government] interest that the DNA Act can reasonably said to advance.”). Moreover, this is an area where the government could use some prodding. See Shaila Dewan, Prosecutors Block Access to DNA Testing for Inmates, THE NEW YORK TIMES (May 17, 2009).

336 See supra notes 162-163, and accompanying text.
337 Judge Reinhardt suggests that expanding CODIS coverage to the whole population is too easy under Kincade because the plurality’s holding that the government interest is “monumental” and the infringement on privacy rights is “minimal” could be applied to a wide array of government information-seeking, including a universal DNA database. 379 F.3d at 849 (Reinhardt, J., dissenting). But see Green, 354 F.3d at 679-81 (Easterbrook, J., concurring) (“What is ‘reasonable’ under the fourth amendment for a person on conditional release, or a felon, may be unreasonable for the general population.”).
338 Kincade, 379 F.3d at 839.
339 For a full discussion, see supra notes 199-222 and accompanying text.
340 See supra notes 214-215, and accompanying text.
The Supreme Court has permitted regular searches where justified by a routine, administrative purpose.\(^{341}\) Instead of compelling sample collection from individuals with a diminished expectation of privacy, sample collection (say, via cheek swab) might someday become a required step for any number of societal hurdles: obtaining a driver’s license, for instance, or a Social Security Number.\(^{342}\) This idea is not far-fetched; DNA is already taken from military recruits and from newborns.\(^{343}\)

Even if direct DNA sampling of civilians does not pass constitutional muster, there are currently no relevant Fourth Amendment limitations on the collection or analysis of DNA from litter, shed skin cells, saliva and so forth; Judge Kozinski has also suggested that no Fourth Amendment prohibition should attach to the extraction of CODIS DNA profiles from repurposed blood samples, which would presumably include the “Guthrie cards” taken from all newborns.\(^{344}\)

In sum, if DNA sampling continues to be considered a protected search, applying this search to the population at large may well be justified as reasonable under existing Fourth Amendment jurisprudence, especially if tied to particular government hurdles such as obtaining a driver’s license—to which articulable state interests in identification attach.

If such searches are not justified as reasonable, the government may still be able to achieve broad coverage by repurposing Guthrie cards, or sampling from other discarded material. Current Fourth Amendment jurisprudence does not extend privacy interests to discarded material, even though that material often contains genomic DNA.

\(^{341}\) See Griffin, 483 U.S. at 873, supra note 170.

\(^{342}\) Compelling government interests in identification can be envisioned beyond those for law enforcement: For instance, state Department of Motor Vehicles offices might have an interest in identifying remains from road accidents; the Social Security Administration has an obvious interest in identification, which could extend to missing persons, disoriented or mentally challenged individuals, and so forth. These ideas arose during the author’s discussion with Prof. Hank Greely, Stanford Law School (Friday June 19, 2009).

\(^{343}\) See Rosen, supra note 311.

\(^{344}\) For a full discussion, see supra notes 223-237, and accompanying text.
CONCLUSION

CODIS has grown rapidly since its creation. The database system now profiles convicts, parolees, foreign detainees, and in many cases arrestees. While courts have largely upheld such expansion, two states have already pushed the bounds further: California and Colorado have implemented familial search regimes to extend effective coverage to include innocent relatives of profiled offenders.

This paper has presented a scientific, statutory and jurisprudential analysis of DNA collection, and on the basis of this analysis, argued for two key reforms.

First, DNA samples should not be retained. The benefits stored DNA samples provide—which are limited to quality control of DNA profiles, and the ability to conduct further follow-up tests—are minimal and achievable by less invasive means, such as re-sampling of offenders when needed. By contrast, the risk of storing such samples is great: whereas DNA profiles are merely 52-character numerical strings without meaningful phenotypic correlation, DNA samples include 3 billion-nucleotide data strings replete with sensitive genetic and health information.

Second, familial DNA search is unjustifiable and should not be permitted. It overextends CODIS both legally and technically, and subjects offenders’ family to special scrutiny entirely unjustifiable under any accepted Fourth Amendment theory. More troubling still, it threatens to amplify existing racial inequality embodied in the CODIS offender database. Even if such bias is ultimately found to be legally permissible, it should still prove politically unpalatable.

If possible, courts or legislatures should prohibit familial DNA search directly. However, if federal legislators are unwilling to unify the bricolage of state laws, courts may be unable to help: Due to peculiarities of existing Fourth Amendment jurisprudence—specifically, in localizing when a protected search occurs—courts might be unable to prohibit familial search.
If familial DNA search is allowed to continue, this paper proposes an immediate expansion to a sample-free, population-wide universal DNA database. Universal coverage may already be possible under existing Fourth Amendment jurisprudence in *Kincade*, and if not can be justified on other theories, including administrative search, or DNA profiling from abandoned or pre-existing samples. From a genetic privacy standpoint, DNA profiles are useful chiefly for identification, are incapable of disclosing sensitive health information, and present very minimal opportunity for misuse—much less than the biological samples currently retained by CODIS.

Universal coverage would provide a potent tool for law enforcement capable of identifying (and deterring) first-time offenders. It would remove the stigma associated with improper inclusion in a partial-coverage system, and would also solve problems associated with familial DNA searching; most notably its gross aggravation of racial inequality in the searchable population.

A universal DNA database will require careful regulation and oversight to ensure compliance with valid privacy concerns. The alternative—failing the prohibition of family search—is the steady expansion of CODIS, with incremental blessing by courts, to include a greater and greater fraction of our population: Arrestee misdemeanants alongside convicted violent felons, and some—like offenders’ families—included only by biological happenstance. That—not carefully tailored universal coverage—is the true privacy threat posed by forensic DNA databases.