Race and Genetics

Controversies in Biomedical, Behavioral, and Forensic Sciences

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Among biomedical scientists, there is a great deal of controversy over the nature of race, the relevance of racial categories for research, and the proper methods of using racial variables. This article argues that researchers and scholars should avoid a binary-type argument, in which the question is whether to use race always or never. Researchers should instead focus on developing standards for when and how to use racial variables. The article then discusses 1 context, criminology, in which the use of racial variables in behavioral genetics research could be particularly problematic. If genetic studies of criminalized behavior use forensic DNA databanks or forensic genetic profiles, they will be confounded by the many racial biases of the law enforcement and penal system.

Over the last three centuries, scientific and "folk" conceptions of race have been inextricably intertwined. Because of this interweaving, scientists tend to look back over the history of their respective fields and conclude that previous generations erred by being caught up in the social maelstrom of their times (slavery, eugenics, evolutionary or theologically based theories of the origins of separate races, etc.). Although quite willing to acknowledge these past errors, scientists attribute them to a research agenda mired in the social realities of bygone times. Each succeeding generation of researchers believes that contemporary scientific views of race transcend the current social milieu. Each generation believes that it has achieved a heretofore unrealized level of scientific objectivity, free from ideology or the pressures of politics, funding sources, and administrative requirements.

In this context, it is notable that the last decade has produced a remarkable fracture of the scientific consensus about race. The literature in several fields is replete with language about "the end of race" as a legitimate concept in scientific discourse, practice, and application (Katz, 1995). This no-race argument has elicited a strong countering position, with proponents vociferously arguing for the continued meaningful use of the biology of race (Burchard et al., 2003; Risch, Burchard, Ziv, & Tang, 2002). In this article, we examine the implications of this debate in different realms of inquiry and practical action. The first section addresses what we call the *binary trap in contemporary science discourse*, a dead-end debate that has generated more heat than light. We offer an alternative approach for analyzing the relationship between race and biology, one that may prove more productive for those studying health and behavior.

In the second section of the article, we examine forensic (law enforcement) and behavioral uses of genetics. Technologies originally developed for biomedical purposes can have multiple uses, including law enforcement applications. Forensic and behavioral genetics may operate in conjunction with or in opposition to biomedical genetics to reify existing racial categories or produce new permutations and understandings of race. Furthermore, when biomedical or behavioral scientists use biological samples collected for forensic purposes, they may not be aware of the sampling biases introduced through law enforcement processes. Such biases may create misleading correlations of race, genetics, and behavior.

Race in Science—A Way Out of the Binary Trap

The Race-in-Science Debate

Recent population genetics studies and related media reports have produced confusion and a contentious debate within the natural sciences regarding the nature of human races and the role of race in biomedical research and clinical practice. Some prominent scientists have argued that race is not biologically real, that it is such a flawed, imprecise concept that it should not be used in research or medicine (Bhopal, 1997; Chaturvedi, 2001; Schwartz, 2001). Other equally prominent leaders in the fields of population genetics and clinical medicine have argued that retaining racial categories is important because (a) they can serve as useful proxies for ancestry and (b) using racial categories will improve research quality or decrease cost by reducing irrelevant background variability between cases and controls (Burchard et al., 2003; Risch et al., 2002).

In the late 1990s, pharmaceutical companies and the biotechnology industry focused their attention on between-group genetic differences. Such differences might permit firms to market drugs to particular racial or ethnic groups whose collective genetic constitution indicates a statisti-

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cally greater-than-average likelihood of positive drug responses or a lower risk of side effects (Kahn, 2003; Winslow, 2001). In March 2001, the pharmaceutical company Nitromed received a green letter of approval from the Food and Drug Administration for the first clinical trials purposefully aimed at detecting drug efficacy in one racial group-African Americans. The drug under study, BiDil, is a heart failure drug and has been touted as the "first ethnic drug." Nitromed's chief executive officer, Michael Loberg, explicitly stated that the African American population would be the marketing target for the drug, because meta-analyses of early studies indicated that "BiDil reduced mortality in 66% of African Americans, but proved of very little benefit to Whites" (Winslow, 2001, p. B6). The BiDil trial in African Americans was stopped in the summer of 2004.[1]

The racialized nature of the BiDil trial and marketing is highly contested terrain, and the fields of pharmacogenomics and pharmacotoxicology are engaged in fierce internal battles as to the appropriate role of race in diagnostics and treatment (Braun, 2002; Frank, 2001; Kahn, 2003; Lee, Mountain, & Koenig, 2001; Xie, Kim, Wood, & Stein, 2001). This article will not present details of the BiDil debate. Rather, it notes this debate as an example of the possibility that antiquated folk notions of race as a set of deep, mutually exclusive biological (genetic) categories may reenter the scientific and medical discourse through DNA analysis. While attempting to provide medical benefit, or market products, scientists and the pharmaceutical industry may reinvigorate the very notions of biological difference that have resulted in racially disparate treatment and racially disparate health.

Whether or not race should be used in scientific research and medicine is a binary trap; the question has generated a fruitless debate in which proponents and opponents line up on one or the other side of a great divide without illuminating the complex interplay between biological and social aspects of human taxonomies. This dichotomous, categorical framing precludes nuanced discussions of the meaning of data on so-called racial differences and of the interplay between the social and biological in generating medical outcomes.

The trap incorporates two important assumptions: (a) that the reality of race can be determined by genetic data and (b) that the answer to whether researchers should use race in science and medicine turns on whether race can be defined or described genetically. We suggest a third way of thinking about the relationship between race and health—race and racial categories can best be understood as a set of social processes that can create biological consequences; race is a set of social processes with biological feedbacks that require empirical investigation. Researchers ought to be discussing when and how best to use race as a variable rather than arguing about the categorical exclusion or inclusion of race in science. Researchers ought to interrogate the meaning of observed racial differences. In doing so, they must recognize that race may be a consequence of differential treatment and experiences rather than an independent cause of differential outcomes.

The Science of Human Variation

Scientists and nonscientists frequently refer to four or five racial groups, each of which encompasses millions of people. Folk beliefs about race incorporate the assumption that racial categories reflect dramatic, underlying, essential differences among racial groups. To many observers, individuals of different races look and act very differently from each other, and these observable differences must reflect some fundamental, underlying causal mechanism—genetics.

From its origins in the scientific literature, race was conceptualized as an intrinsic feature of persons who share distinctive physical characteristics; racial groups have represented natural boundaries within which people are essentially similar and between which people are essentially different. Human races are often analogized to families, implying a fundamental affinity and close, shared descent among all members of any one race (Marks, 2002). A recent article in *Demography* described races as "genetic entities" that arose because "generations of reproductive isolation have led to differences in gene frequency across racial groups" (Van Den Oord & Rowe, 2000, p. 286). Another recent article noted that "Race distinguishes major groups of people according to their ancestry and a more or less distinctive combination of physical characteristics. Race is most often used to differentiate a population related by blood, common descent, or heredity" (Edwards, Fillingim, & Keefe, 2001, p. 134).

The preceding definitions imply that races are coherent, genetically structured collectives that exist in nature independent of human choices about how and why researchers categorize people. They imply a simplistic model of human migration and expansion throughout the world, a model in which small groups of humans traveled to each continent at about the same time, became reproductively isolated and then expanded rapidly to fill the continent in the absence of subsequent events that would create significant within-race patterns of human genetic variation—a nice "just so story" that is largely consistent with folk beliefs about race, but a story that is contradicted by data from anthropology and human genetics.

Assumptions about natural, essential boundaries among races are contradicted by the findings that allele frequency comparisons among human populations rarely show discontinuities that map onto racial boundaries (Marks, 2002; Molnar, 1998). Anthropologists long ago discovered that humans' physical traits vary gradually, with groups that are close geographic neighbors being more similar than groups that are geographically separated. This pattern of variation, known as *clinal variation*, is also observed for many alleles that vary from one human group to another. Another observation is that traits or alleles that vary from one group to another do not vary at the same

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[1] In July 2004, Nitromed abruptly ended the clinical trials, which had only been conducted on African Americans, claiming that the drug had been so effective that it would now be made available to all patients (Pollack, 2004).

rate. This pattern is referred to as *nonconcordant variation*. Because the variation of physical traits is clinal and non-concordant, anthropologists of the late 19th and early 20th centuries discovered that the more traits and the more human groups they measured, the fewer discrete differences they observed among races and the more categories they had to create to classify human beings. The number of races observed expanded to the 30s and 50s, and eventually anthropologists concluded that there were no discrete races (Marks, 2002). Twentieth and 21st century biomedical researchers have discovered this same feature when evaluating human variation at the level of alleles and allele frequencies. Nature has not created four or five distinct, nonoverlapping genetic groups of people.

The human species possesses remarkably little genetic variation when compared with other organisms. Chimpanzees (Pan troglodytes), close primate relatives to humans, possess approximately four times as much within-species genetic variation as do humans (Bamshad, Wooding, Salisbury, & Stephens, 2004; Kittles & Weiss, 2003). The relative lack of variability among humans can be observed when researchers measure genetic variation between two individuals or genetic variation between two human groups. Any two unrelated persons, chosen at random from across the globe, are 99.9% identical in their nucleotide sequences (nucleotides are the four famous DNA building blocks—cytosine, guanine, adenine, and thymine). That is, their genomes are 99.9% the same. Humans' comparative genetic similarity can be explained by the fact that they are a young species, one that migrated out of Africa relatively recently in evolutionary terms and expanded rapidly to populate the globe (Kittles & Weiss, 2003; Olson, 2002). In the first decade of the Human Genome Project (circa 1988–1998), humans' incredible genetic homogeneity was the basis of the claim that any one person's genome could be used to create the reference human genome sequence.

Although the first decade of the Human Genome Project emphasized human genetic similarities, once the draft genome sequence was completed and scientists were ready to undertake the next stages of research, their focus shifted and they began to emphasize human genetic differences. Humans are all 99.9% genetically alike, but this means that there is approximately 0.1% genetic difference between any two people. The human genome contains approximately three billion DNA building blocks, which means that, between any two people, there are at least three million points of difference in the DNA. That 0.1% difference translates into quite a lot of genetic variability for scientists to study.

Researchers are interested not only in the genetic variation between any two individuals but also in the variation between any two human groups. Lurking in the corridors of computer-generated correlations and patterns is a previously unimagined mathematical and statistical power to formulate and reformulate groups, to compare large numbers of people at many different positions in their DNA. Scientists' interest in identifying patterns of group difference has been fueled by the belief among some members of the biomedical research community that knowing more about group-based allele frequency variation will improve the efficiency with which they can identify medically important correlations between genes and diseases in studies with very large sample sizes, such as thousands or tens of thousands of people (Bamshad et al., 2004).

Most human genetic variation—approximately 85%—can be found between any two individuals from the same group (racial, ethnic, religious, etc.). Thus, the vast majority of variation is within-group variation. Unrelated people of the same racial, ethnic, or religious group are not particularly similar to each other. This means that people of the same race, ethnicity, or religious background do not necessarily have a great deal of shared or common ancestry; they are not necessarily closely related.

The maximum variation observed between human groups is a statistically significant difference in allele frequencies at about 15% of genetic locations (discrete positions on the DNA strand are referred to as *loci*). Of that 15% of genetic variation, approximately 10% can be measured as different genetic marker frequencies between two groups from the same continent (Marks, 2002; Molnar, 1998). For instance, when a group of White people from Norway is compared with a group of White people from Italy, about 10% of the time a researcher will find a genetic variant that is relatively frequent in one group and infrequent in the other. Because the majority of between-group variation is found within any race, researchers cannot assume that people of the same race are genetically similar in ways that matter for medicine or other between-group comparisons.

Approximately 5% of human genetic variation can be observed only when comparing two groups of people from different continents, such as a group of White people from Norway and a group of Asian people from Japan.[2] Comparison of people from different continents is often taken as a rough proxy for comparisons between racial groups. Intergroup comparisons are often made using regions of humans' DNA that have a large number of short repeated sequences all in a row. Such genetic markers may have many, many possible variants. If researchers observe genetic variation at a particular marker between, for instance, a group of Norwegians and a group of Japanese, it does not mean that all Norwegians will have one version of the marker and all Japanese will have another. It just means that there is a statistically significant difference in the frequency with which particular numbers of DNA repeats are found in each group. The Japanese may have a preponderance of the five-repeat version of the marker, whereas the Norwegians have a preponderance of the eight-repeat version.

Suppose that a researcher was studying human hair color and comparing people in Los Angeles to people in New York City. In Los Angeles, the researcher observed a

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[2] The precise amount of between-group variation observed depends on several factors, including the manner in which the groups are constituted, the number of genetic markers studied, and the kinds of genetic markers studied. This is true regardless of whether the groups being compared are from the same continent or from different continents.

hair color distribution of 5% red, 10% black, 15% brown, 60% blond, 5% green, and 5% purple. In New York, she observed a hair color distribution of 8% red, 20% black, 40% brown, 30% blond, 1% green, and 1% purple. She would find statistically significant differences in hair color between people in New York and people in Los Angeles, but it would not mean that all New Yorkers have brown hair and all Angelinos have blond hair. Similarly, an observation of between-group differences at a particular genetic locus should not be taken to imply that within each group all people are genetically similar at that genetic marker.

Taken together, the empirical observations discussed above contradict the assumption that races reflect fundamental within-group similarity and between-group difference.

Africans show the greatest degree of within-group and between-group genetic variation, suggesting that Black is a particularly incoherent human category from a genetic standpoint (Marks, 2002). There are more DNA variants among people of Africa than there are among peoples with recent ancestry from other continents, so two unrelated Black Africans or African Americans are less likely to possess genetic similarity than are two people of other races. Yet, outside of Africa, Blacks are frequently treated as a homogeneous group in a broad variety of social and scientific contexts. Here lurks an undertheorized fundamental truth, the understanding of which would go far in reducing researchers' current confusion about race. This truth bears repeating: Around the globe, Blacks have the most internal genetic variation of any racialized population group yet are most likely to be treated as if they were genetically homogeneous.

Although not genetically homogeneous, Black people are often placed at the bottom of the social hierarchy, and this fact has practical, biomedical consequences. Similar social treatment and similar relations to the material world can produce patterned similarities among Blacks and differences between Blacks and other racial groups. Many observers have wrongly assumed that such patterned between-group differences reflect genetic similarity among Blacks and differences between Blacks and others. Researchers should avoid inferring genetic causation of racial differences; they should only make such claims if the data truly support them.

Some argue that the comparatively high rate of several rare genetic diseases in people of Ashkenazi Jewish descent (or in people of other ancestries such as Norwegian or sub-Saharan African) justifies using race as a variable in science and medicine (Burchard et al., 2003; Risch et al., 2002). When the example of Ashkenazi Jewish people is used, the argument wrongly conflates race with a religious/cultural group whose Ashkenazi Jewish ancestors were a population in the narrow sense of that term—a group living within a relatively small geographical area and in which reproduction was largely restricted to pairings within the group. People of Ashkenazi Jewish descent have been routinely classified as members of the White race for most of the 20th century. Rather than providing an argument for

the salience of race in research or medicine, this example suggests that historical events affecting small groups of people produced medically important patterns of genetic variation within races and that small populations within races will often be the more relevant units of interest.

Genetics, race, and ancestry. Recently, a cottage industry that purports to conduct ancestry tracing through genetic testing has emerged. Given a cheek swab that contains nucleated cells, companies will provide information regarding the proportion of a person's ancestry that derived from the continents of Africa, Europe, Asia, or the Americas. At least one U.S. company claims to have "race-determining genetic markers" (Gaskin, 2003). Ancestry-tracing technology developed out of biomedical and forensic genetic research, and some proponents of the use of race in biomedical science point to genetic ancestry tracing to argue that race is real and relevant for biomedical sciences. These proponents believe that race is real because they believe that it is genetically discernable.

To make claims about a person's continent(s) of recent origin, geneticists evaluate the approximately 5.0% of the 0.1% of locations in the human genome at which alleles vary in frequency among groups from different continents. Most of these ancestry informative markers are in regions of the genome that do not code for functional molecules such as proteins. When geneticists evaluate a single individual at many of these markers, each of which will provide an answer with a small statistical probability that associates the testee's ancestors with one region of the world or another, then geneticists can make statistical predictions about where in the world a person's recent ancestors were located (Rosenberg et al., 2002).

Setting aside the fact that such analyses may give surprising results, results that contradict a person's lived experience of race and knowledge of her ancestors, we ought also to realize that views about ancestry are only one component of race as the concept is commonly understood. Empirically, scholars observe that racial categorization turns on numerous characteristics including continent of origin, nationality, skin color and other morphological features, and behaviors such as language spoken or religion practiced (Lopez, 1996). Furthermore, ancestry does not always correlate with other indicia of race. People whose skin color is perceived as white can have genetic profiles indicating that 80% of their recent ancestry is West African, and people whose skin color is perceived as black can have genetic profiles indicative of predominately European ancestry (Parra et al., 2003; Shriver et al., 2003). A person with substantial, recent African ancestry may pass as White and may have medically and psychologically consequential social advantages of whiteness. On the other hand, a person may pass as White but possess medically relevant alleles more commonly associated with Blacks or with African ancestry.

Although a tiny fraction of human genetic variation can be used to make statistical claims about a person's recent ancestral origins, most genetic markers will not distinguish continent of ancestry at all (Kittles & Weiss, 2003). Some markers that do vary between or among

human groups can be used to assign people's ancestry to subcontinental regions, such as different parts of Europe, Asia, or Africa. There is no reason to believe that the fraction of human genetic variation that is useful in assigning continental ancestry is more defining of human individual or group identity or characteristics than is the vast majority of human genetic variation. Ancestry informative genetic markers do not carry racial essences, because people of the same race and quite similar geographic ancestry can have different variants at any particular ancestry informative site in the DNA. Genetic differences between human groups and individuals exist, but these genetic differences do not sort the human species into a small, discrete set of racial groups. Human genetic variation is far more complex.

Contemporary race scholarship and the relevance of race for science. After sifting through decades of data on cranial shapes, skin color, hair texture, and now allelic variation, contemporary race scholars have concluded that no combination of physical characteristics can be used to define race because human biological traits vary continuously and nonconcordantly. But if races are not distinct genetic categories of humans, then what is race and why might it matter to those studying human health or behavior? Race is a complex but empirically demonstrable stratifying practice that creates identity and hierarchy through social interaction. People often interact with each other on the basis of their beliefs that race reflects physical, intellectual, moral, or spiritual superiority or inferiority (American Sociological Association, 2003). By acting on their beliefs about race, people create a society in which individuals of one group have greater access to the goods of society—such as high-status jobs, good schooling, good housing, and good medical care—than do individuals of another group.

The social fact of racial stratification has biological consequences, which is why race is a relevant, appropriate variable in some biomedical research. The sheer volume of data on racial disparities in health and treatment outcomes highlights the point that in the United States race correlates with many facts about people that are of concern to clinicians and biomedical scientists (Cruickshank & Beevers, 1989; Massey, 2004; Smedley, Stith, & Nelson, 2002). For example, the fact that African Americans have a 60% higher incidence of prostate cancer than European Americans (Stanford et al., 1999) is deserving of investigation.

Some complain that race is too indefinite a concept around which to conduct valid scientific research. Racial identities may change with the economic, historical, geographic, or political context—the same person can be Black in one state and White in another, can be Black in one decade and not in another, can be racialized as Mexican or Chicano/a in one region of the United States and not in another (American Sociological Association, 2003; Lopez, 1996; Mays, Ponce, Washington, & Cochran, 2003). That race can be situationally fluid and also be at the root of enduring practices is one of its mysteries. Despite the fluidity with which particular individuals are assigned to one race or another, the practice of creating social hierar-

chies based on perceived race has deep and pervasive historical roots; racial stratification has been a significant aspect of the U.S. social and political landscape since this country's inception.

The malleability of racial classification creates difficulties for retrospective and meta studies, but it does not preclude all valid research using race as a variable. After all, population biologists conduct experiments even though populations change over time and their boundaries at any particular time are indeterminate. Elegant biomedical research has been conducted using such culturally malleable concepts as the family. And commonly used variables, such as socioeconomic status variables, are electively defined but often help produce illuminating analyses.

Because many aspects of social life in the United States are racially patterned, many demographic variables are potential confounders for racial comparisons (Kaufman, Cooper, & McGee, 1997). Why include race if it can be decomposed into other variables? There are several reasons. First, race effects are not always reducible. The lifetime accumulated effect of numerous racially patterned experiences and exposures may yield racially distinct physiological responses that are not dictated by allele frequency differences among racial groups nor reducible to currently measurable demographic variables (Freeman, 1998). For instance, many studies show racial differences in people's experiences of and responses to pain (Edwards et al., 2001). Although the explanation for these differences is not yet clear, it could lie in the cumulative physical, cultural, and psychological effects of living as a member of a particular racialized group (Zola, 1966). Second, including race, in addition to a variety of other demographic variables, may help identify the effects of racism on health and treatment outcomes. Third, although researchers should not use race as a proxy for other measurable factors known to affect health, such as income and education, they often do not know which demographic factors play an etiologic role in the outcome under investigation. By including race as a variable, researchers may capture important residual influences. And finally, by collecting information about race, they may gain a more complete understanding of how race is created and maintained, how social stratification creates racialized bodies.

When race variables are used in research, they should be used with attention to interactions between the social and the biological, and therefore, researchers should refrain from leaping to the conclusion that any observed interracial difference reflects allele frequency variation between races (Cooper & Kaufman, 1998). As responsible scientists, colleagues, and reviewers, researchers should carefully examine their own and other's research design and data interpretation for the influence of unsupported assumptions about race and unwarranted inferences of genetic causation. Given that over 90% of genetic variation occurs within rather than between racial groups, researchers and scholars should apply a rebuttable presumption that genetic differences are the least likely explanation for observed interracial differences (King, 1998). Rather than jettison race altogether, researchers and scholars should be design-

ing innovative protocols that allow us to examine complex interactions among many possible etiological factors that may lead to interracial differences.

Race, Genetics, Forensics, and Behavior[3]

As biomedical scientists debate whether race is real or genetically discernable, scientists using genetic techniques and knowledge generated through biomedical research have forged on to develop methods for genetic profiling of crime suspects. Such profiles may uniquely identify individuals, but they may also involve a genetic version of racial profiling (Evett, Gill, Scrange, & Wier, 1996; Evett et al., 1997; Lowe, Urquhart, Foreman, & Evett, 2001). Why should an article about genetics, race, and behavioral research discuss law enforcement uses of genetics? Because behaviors considered socially aberrant are a common subject of scientific inquiry. As genetics moves into law enforcement and into behavioral research, the search for "criminal genes" will be tempting. This section discusses some reasons why genetic research on criminal behavior will be fraught with racial confounders. Such research runs a high probability of reinforcing racial stereotypes and antiquated folk notions of race.

Three Examples of Law Enforcement Genetics

Genetic technologies and discoveries that hold out the promise of producing safer and more effective medical treatments can also be useful in law enforcement. For instance, by testing 13 highly variable regions of the human genome, scientists can create a genetic profile that uniquely identifies an individual (unless the person has an identical twin). The markers tested to create identifying profiles are not in genes; rather, they are in regions of the DNA termed *noncoding* regions. Noncoding regions are segments of DNA that do not encode information that tells cells how to make useful molecules, such as proteins or RNA. Identifying DNA profiles can be stored in computers as bar codes or as a series of numbers that describe a unique pattern of DNA variants.

Forensic DNA profiling has been used to free more than 140 wrongly convicted prisoners, some of whom were on death row, and others of whom served decades for rapes they did not commit (Dwyer, Neufeld, & Scheck, 2000).[4] Similarly, law enforcement occasionally can score a cold hit and catch a rapist or other perpetrator who leaves biological material at the scene of a crime, because officials can match DNA from the crime scene to a DNA profile already in a database. The use of this technology in highly visible cases has led to arguments for widening the net of the DNA database by increasing the number of samples. This expansion would be achieved by increasing the range of persons from whom samples would be collected. Policy analysts have proposed that law enforcement authorities should obtain samples from all convicted felons, from arrestees, or even from suspects (Puri, 2001; Stevens, 2001). At the extreme, two authors propose that the entire population of the United States should have DNA profiles

in a forensic database (Kaye & Smith, 2003). In early 2002, the attorney general of the United States ordered the FBI to generate a plan that is supposed to expand the federal DNA database to 50 million profiles.

What more objective way could there be of exculpating the innocent and convicting the guilty? What could be harmful or unfair about expanding forensic DNA databases? Unfortunately, arguments in favor of expanding these databases conflate three quite distinct practices of the criminal justice system, practices that need to be separated and analyzed for their disparate impact on different racial and ethnic populations.

The first practice is the use of DNA in postconviction situations to determine whether there was a wrongful conviction, a practice that can help to free the innocent. This practice does not require that DNA profiles be saved in any database, nor does it require that biological samples be stored in a tissue bank. So long as evidence from a crime scene is properly preserved and stored, then at some later date DNA could be extracted from the evidence and compared with that of a person actually convicted of the crime.

The second practice is the collection of DNA to form a DNA profile database that can be used for identification purposes. Currently, states collect DNA from people convicted of a variety of crimes. Some even collect DNA from suspects or arrestees in pretrial circumstances.

Forensic DNA databases create a net with which to catch the guilty. To identify a suspect, law enforcement personnel search for a match between a profile from DNA left at the scene of an unsolved crime and the profile of any person in the database. These databases can be used to match persons already convicted of one crime with material left at the scene of another previously unsolved crime. Law enforcement personnel can also use forensic DNA databases to determine whether a person who is stopped and arrested has DNA that matches material left at a crime scene unrelated to the present detainment. This would be similar to the current practice in which police stop a driver and determine whether there are outstanding warrants that can be used as the basis for an arrest.

The examples above are not just hypothetical. In early 2000, the New York City Police Department began a pilot project experimenting with portable DNA laboratories (Flynn, 2000). The police take a buccal swab—some saliva from inside the cheek of the person stopped—and place it on a chip the size of a credit card. They then put this card through a machine no larger than a hand-held compact disk player, where the relevant bits of DNA sequence are read in two minutes. Thirteen DNA markers are assessed to create a profile of the person stopped. When this task is completed, the police can then transmit the profile to a central database, where it currently requires about 12 minutes to

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[3] The following section is based on an adaptation of Duster (in press, 2004).

[4] At the time of Dwyer's report, the number was less than 100, but in the last two years there have been a number of additions.

determine whether the stopped person's profile matches with any sample from a crime scene.

A third law enforcement use of genetics involves testing crime scene material for information that could be used to create a physical or behavioral profile of a suspect. In contrast to the traditional fingerprint, which provides only an identifying mark, a person's DNA contains information about many other aspects of her or his life and health. Although the traditional DNA-identification profile tests noncoding regions of DNA, coding regions could also be tested. DNA left at a crime scene could be tested for ancestry informative markers and for genetic markers of observable physical traits (such as hair or eye color). It could be tested for the possibility that the source of the DNA has an inherited disease, such as sickle cell disease or Huntington's disease. Genes that correlate with behaviors or psychological traits could also be tested. Such testing could produce a physical and psychological profile of a suspect and some estimates of other relevant characteristics, such as where the person might be found (in a sickle cell clinic, for instance). Furthermore, by using the traditional individual-identification genetic markers but asking the computer for a partial match rather than a perfect match to a profile in a database, police may be able to identify siblings or parents of persons who leave material at crime scenes.

In 1993, a British forensic scientist published what is perhaps the first DNA test that claimed to provide "intelligence information" along ethnic lines for "investigators of unsolved crimes" (Evett, Buckleton, Raymond, & Roberts, 1993, p. 243). Ian Evett, of the Home Office's forensic science laboratory in Birmingham, England, and his colleagues in the Metropolitan Police claimed that their DNA test can distinguish between Caucasians and Afro-Caribbeans in nearly 85% of the cases (Evett et al., 1993, 1996). Recently, a U.S. biotech company worked with Louisiana police to develop a racial profile of a suspect in a rape case. Police had been searching for a White suspect on the basis of psychological profiles, but geneticists told police that on the basis of ancestry the perpetrator was not likely to appear White (Gaskin, 2003). The case was solved using other evidence; however, because the arrested suspect did not appear White, some commentators viewed this as proof of the principle that DNA testing could (or should) be used to produce racial profiles of suspects.

Although the FBI and local and state law enforcement officials state that they are only looking at genetic markers in noncoding regions of the DNA, 29 states now require that tissue samples be retained in their DNA databanks after profiling is complete (Kimmelman, 2000). Only one state, Wisconsin, requires the destruction of tissue samples once profiling is complete.

The degree to which the third approach—racial and other nonidentifying profiling—is adopted by the law enforcement community will probably depend on its cost effectiveness. Although human races cannot be categorically distinguished using genetic technology, there are some alleles that are more likely to be found in people whose ancestors are from one geographic region of the world rather than another (discussed above). If a U.S. locality is populated by two or three groups of individuals whose recent ancestors are from geographically distant parts of the world, then ancestry information from crime scene samples might prove of some use in suspect profiling. Law enforcement agencies in such localities might find it efficient to adopt this genetic approach. In other U.S. localities, the nature of the populous will make genetic racial profiling inefficient. This could happen if the population is fairly homogenous with respect to ancestry, perhaps in places such as rural Wisconsin or Minnesota. In other localities, the populace will contain many people of recently mixed ancestry and many people whose phenotypic characteristics make them racially ambiguous. Localities with large populations of Latin American, Middle Eastern, or South Asian descent, or parts of Louisiana, might be regions of the country in which attempts to draw inferences about a person's race on the basis of her or his ancestry would not prove useful.

Law enforcement officials would also do well to remember that genetic information about ancestry can be at odds with a person's self-identified or attributed race. As discussed above, some percentage of people who look White will possess genetic markers indicating that a significant majority of their recent ancestors were African. Some percentage of people will who look Black will possess genetic markers indicating that the majority of their recent ancestors were European. Native Americans may be genetically indistinguishable from Hispanics (Mexican Americans) or African Americans. Inferring race from genetic ancestry may mislead police rather than illuminate their search for a suspect.

Aside from questions about utility and cost effectiveness, how could anyone possibly be opposed to the use of genetic technologies for valorous crime-fighting purposes? How could anyone oppose the use of forensic DNA databases for biomedical and behavioral research? The answer is a bit complex, but it has to do with (a) some hidden social forces that create a patterned bias determining that certain racial and ethnic groups will be more likely subjected to DNA profiling and (b) the resuscitation of some old and dangerously regressive ideas about how to explain criminal behavior.

Race, Crime, and Behavioral Research

It is now commonplace to deride the science of phrenology, a once widely respected and popular research program in the late 19th century that attempted to explain crime by measuring the shapes of the heads and faces of criminals. Yet the idea that researchers begin with a population that is incarcerated and then use correlational data from their bodies in an attempt to explain their behavior is very much alive and well as a theoretical and methodological strategy. When researchers deploy computer-generated DNA profiles or markers and correlate them with the crimes of those caught in the grip of the criminal justice system, the findings take on the authority of human molecular genetics (Nelkin & Lindee, 1995). Even though there is a mantra that correlation does not imply causation, the volatile social

and political context of these correlations will require persistent vigilance and close monitoring if society is to avoid the mistakes of the past.

As biomedical researchers turn to the study of between-group genetic differences, it is little wonder that similar concerns have also captured the imaginations and the research agendas of psychologists, psychiatrists, and behavioral geneticists. It was inevitable that some among them would attempt to deploy genetic technologies in the hope that DNA differences might explain different behaviors. Those who study behavior have rushed to find genetic markers (and sometimes even genes) that they can associate with complex behaviors. In the last five years, readers of popular magazines and newspapers have seen claims linking DNA regions to cognitive ability in children (Chorney et al., 1998), crime (Jensen, Fenger, Bolwig, & Sorensen, 1998), violence (Caspi et al., 2002), and attention-deficit/hyperactivity disorder (Smalley et al., 2002). If leading figures in the field of pharmacogenomics could publish, in *Science*, the claim that "All pharmacogenetic polymorphisms studied to date differ in frequency among ethnic and racial groups" (Evans & Relling, 1999, p. 488) and that this "marked racial and ethnic diversity . . . dictates that race be considered in studies aimed at discovering whether specific genotypes or phenotypes are associated with disease risk or drug toxicity" (Evans & Relling, 1999, p. 488), then it would only be a matter of time before behavioral geneticists would attempt to link genes to behaviors such as violence, impulsivity, and crime, with beliefs and concerns about race lurking in the background. It took less than 30 months.

The MAOA gene and predictions of violent behavior. In the last half of 2002, *Science* published an article that cemented the new engagement between behavioral genetics and molecular genetics, with a promissory note of an impending marriage. This was a report of research in which the authors claimed that their "findings provide initial evidence that a functional polymorphism in the MAOA gene moderates the impact of early childhood maltreatment on the development of antisocial behavior in males" (Caspi et al., 2002, p. 853).

The following quotation is from the last two sentences of this article and is pregnant with policy implications that will regenerate a somewhat dormant social and ethical debate about the advisability of early identification of young people at risk for becoming violent and/or antisocial, as measured by their interactions with the criminal justice system: "Moreover, 85% of cohort males having a low activity MAOA genotype who were severely maltreated developed some form of antisocial behavior. Both attributable risk and predictive sensitivity indicate that these findings could inform the development of future pharmacological treatments" (Caspi et al., 2002, p. 853). The notion that one can intercept, and then treat with pharmaceuticals, presumes that the observed correlation reflects a causal connection between the observed alleles and the relevant behaviors.

Isolating, identifying, and treating subjects has its own social dynamic. There is a remarkable slippage here, between individual DNA and the operationalization of the concept of antisocial. Although the DNA is a property of the individual study subjects, the conceptualizations and measures of both antisocial and maltreatment are interactional, depending on relationships between the study subjects and parents, school authorities and law enforcement authorities. Some substantially greater attention to the interactional dynamics should be a part of any discussion of early identification and, even more significantly, of breaking down the components of antisocial behavior and attempting to identify genetic determinates. Getting in trouble with the criminal justice system is partly about individuals, but it is substantially about individuals with membership in particular social groups on which the legal lens and enforcement apparatus is disproportionately focused. For example, the U.S. war on drugs, which accounts for more than half of all those incarcerated in U.S. jails and prisons, has been tightly aimed at African Americans and Latinos (Cole, 1999; Miller, 1992; Reinarman & Levine, 1997).

The Racially Selective Aim of Law Enforcement Artillery

In the last three decades, the racial composition of the U.S. prison population has transformed to a remarkable degree. If an observer turned the clock back just about 60 years, Whites constituted approximately 77% of all prisoners in the United States, whereas African Americans constituted only 22% (Hacker, 1992). This information provides the context for reviewing Table 1. Notice how in the last half century, the incarceration rate of African Americans in relation to Whites has gone up in such a striking manner. In 1933, Blacks were incarcerated at a rate approximately three times that of Whites. In 1950, the ratio had increased to approximately four times; in 1970, it was six times; and in 1989, it was seven times that of Whites.

However dramatic these figures are, incarceration is but one end of the long continuum of the criminal justice system, a continuum that begins when police stop a suspect and continues with arrest, trial, conviction, and sentencing. Racial disparities are suffused throughout the entire system. One form of racial profiling that occurs at the beginning of the continuum involves "DNA dragnets"—rounding up of hundreds of individuals and asking them to "voluntarily" provide DNA samples to be matched with those from a crime scene. DNA dragnets originated in England and are most advanced in Europe and Great Britain.

Although the United States has only had about a dozen DNA dragnets, what is most notable about them is their racialized character. San Diego, CA, was among the first jurisdictions to conduct the practice, when, in the early 1990s, a serial killer murdered six persons in their homes. On the basis of eyewitness reports, the police suspected an African American male, so more than 750 African American men were rounded up and genetically tested. In 1994, Ann Arbor, MI, police obtained nearly 200 samples from African Americans in the hunt for yet another serial rapist and murderer. In both the San Diego and Ann Arbor cases,

Table 1

Incarceration Rates by Race

Year	Population[a]			Incarceration[b]			Rate (%) of incarceration per population			Approximate ratio (Black to White)
	Total	Black	White	Total	Black	White	Total	Black	White	
1933	125,579	112,815	12,764	137,997	102,118	31,739	11	9	25	2.5:1
1950	151,684	135,814	15,870	178,065	115,742	60,542	12	9	38	4:1
1960	180,671	160,023	19,006	226,065	138,070	83,747	13	9	44	5:1
1970	204,879	179,491	22,787	198,831	115,322	81,520	10	6	36	6:1
1989	248,240	208,961	30,660	712,563	343,550	334,952	29	16	109	7:1
1995	263,168	218,149	33,095	1,126,287	454,961	546,005	43	21	165	8:1

[a] Total population of the United States by ethnicity (in thousands). Data are from U.S. Department of Commerce, Bureau of the Census (1975, 1976, 1997).
[b] Total number of prison population by ethnicity. Data are from U.S. Department of Justice, Bureau of Justice Statistics (1986, Table 3–31; 1997).

a suspect was apprehended and convicted, but not as a result of the dragnet. In 2004, Charlottesville, VA, had a racialized dragnet that generated such an outraged response from civil liberties groups that the police temporarily abandoned the dragnet strategy. If samples from dragnets are not destroyed, they may later become available for research purposes. Researchers should be aware of the racially targeted manner in which these samples were collected.

Racial profiling at the beginning of the law enforcement continuum occurs at the stop and arrest stages and is exemplified by the notorious offense of DWB—"driving while Black." Some commentators question whether this type of racial profiling actually occurs, so it is instructive to present data on the topic (see Figures 1 and 2). Figures 2 and 3 show data on drivers stopped by the Maryland State Police along the I-95 corridor, from January 1995 to September 1996. Note that although drivers in all racial categories have a high percentage of violations that could justify stops (e.g., lane changing without signaling or speeding), racial and ethnic minority drivers were stopped at a higher rate than Whites. From these data, one could reasonably infer that the Maryland State Police engaged in racial profiling.[5]

The war on drugs has played the dominant role in the disproportionate focus by law enforcement on U.S. minorities. Although racial profiling is often characterized as a local police practice, the phenomenon of young minority men being "just stopped by the police" was actually a national strategy first deployed by the Reagan administration and promulgated by the Drug Enforcement Administration.[6] According to the federal government's own best statistics, during the height of the drug war, African Americans constituted only 15%–20% of the nation's drug users (Flanagan & Maguire, 1990), but in most urban areas, they constituted approximately half to two thirds of those arrested for drug offenses. Indeed, in New York City, African Americans and Latinos constituted 92% of all those arrested for drug offenses (McConnell, 1992).

The drug war also affected the races quite differently with regard to incarceration rates. The most striking figure showing this is the shift in the racial composition of prisoners in the State of Virginia: In 1983, approximately 63% of the new prison commitments for drugs were White, whereas the rest, 37%, were minority. Just six years later, in 1989, the situation had reversed; only 34% of the new drug commitments were White and 65% were minority. The nation gasped at statistics reported by the Sentencing Project in 1990, citing the figure that nearly one fourth of all young African American men in the United States, between 20 and 29 years of age, were either in prison, in
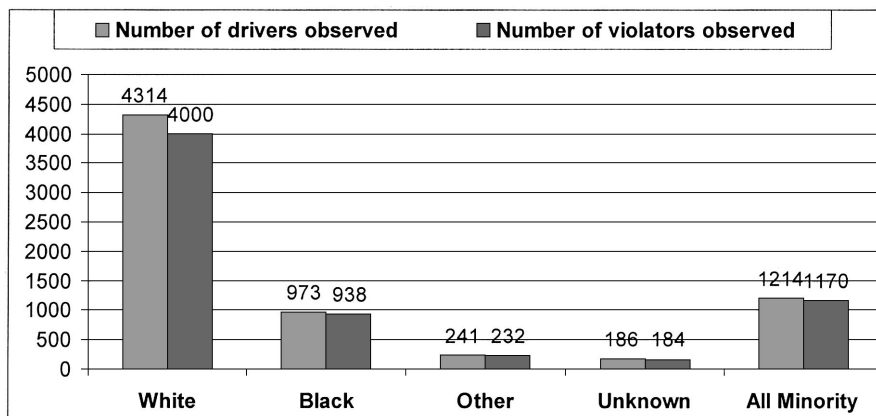
Figure 1

Incarceration Rates by Race, 1933–1995
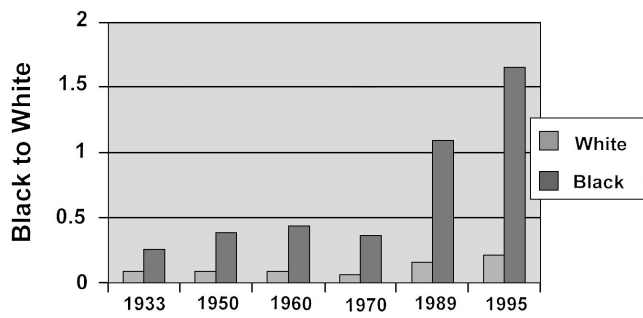
[5] For a full account of the methodology, see http//www/aclu.profiling/report/index/html

[6] In 1986, the Drug Enforcement Administration initiated Operation Pipeline, a program designed in Washington, DC that ultimately trained 27,000 law enforcement officers in 48 participating states over the ensuing decade. The project was designed to alert police and other law enforcement officials of likely profiles of those who should be stopped and searched for possible drug violations. High on the list was young, male African Americans and Latinos driving in cars that signaled that something might be amiss. For example, a 19-year-old African American driving a new Lexus would be an obvious alert, because the assumption was that his family could not have afforded such a car and the driver must therefore be into drugs.

Figure 2
Maryland State Police Data, January 1994 to September 1996: Drivers Stopped by Race on the I-95 Corridor

jail, on probation, or on parole on a given day in the summer of 1989 (Flanagan & Maguire, 1990). This figure has been recited so often that many have become inured, so that there was (relatively) a collective yawn in mid-1992 when a study revealed that 56% of Baltimore's young African American men were under some form of criminal justice sanction on any given day in 1991 (Miller, 1992). Indeed, of the nearly 13,000 individuals arrested on drug charges in Baltimore during 1991, more than 11,000 were African Americans.

African Americans are not only incarcerated at a higher rate but are also disproportionately affected by sentencing policies that keep them in prison longer. A study by the Federal Judicial Center revealed that mandatory minimum sentencing has had a dramatically greater impact on African Americans than on Whites (Meierhoefer, 1992). For example, powder cocaine is most likely to be sold and consumed by Whites, whereas African Americans are more likely to sell and consume crack (Flanagan & Maguire, 1990), and the mandatory sentences for powder cocaine are substantially shorter than those for crack.[7] Although the figures are most shocking for cocaine, the shift toward longer sentences for African Americans also includes other drugs. From 1986 to 1990, the average sentence length for African Americans convicted of drug-related crimes, compared with Whites, increased from 11% greater to 49% greater, respectively (Meierhoefer, 1992).

Given that racial minorities, especially African Americans, are disproportionately targeted by the law enforcement and the criminal justice system at every step, DNA samples taken from those who are arrested or convicted will include a disproportionate amount of DNA from racial minorities. DNA profiles created from those who are arrested or convicted will include a disproportionate number of profiles from racial minorities. This biased inclusion could result in a vicious cycle if the databases are used to generate suspects in unsolved crimes. Minorities will more likely be identified as suspects on the basis of cold hits, because their DNA is more likely to be in the database. This is true even though minorities are no more likely to commit crimes and in some cases are actually less likely to do so. Furthermore, if those studying violence or crime use DNA from populations of individuals stopped, of individuals arrested, or of individuals incarcerated, they will start with a racially biased sample.

***The proliferation of forensic DNA databases and databanks: Implications for behavioral research.*** States are the primary venues for the prosecution of violations of the criminal law, and their autonomy has generated considerable variation in the use of DNA databases and DNA repositories (a database contains information, such as a numerical representation of a DNA profile, whereas a repository contains biological material that can be genetically tested and retested over time). Even as late as the mid-1980s, most states were only collecting DNA samples from sexual offenders. However, in 1994 Congress passed a law authorizing the FBI to establish a national DNA database.[8] That became the Combined DNA Index System (CODIS), which permits DNA profiles to be shared and compared within and between states (Simoncelli, 2004). All 50 states now contribute to the CODIS system. Thirty states now collect DNA from all felons, and 23 states collect DNA from those who commit misdemeanors. Louisiana, Texas, and Virginia now authorize the collection of DNA from arrestees, and a new ballot

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[7] Those who defend disparate sentencing policies for crack and cocaine argue that crack produced a more violent environment. For a full discussion of these issues, Reinarman and Levine (1997).

[8] In 1994, the United States Congress passed the Violent Crime Control and Law Enforcement Act of 1994, which established a federal DNA database. The act has been amended several times, most recently by the Justice for All Act of 2004 and by the DNA Analysis Backlog Elimination Act of 2000.

Figure 3
Maryland State Police Files, January 1995 to September 1996: Percentage of Drivers Observed, Percentage of Drivers in Violation, and Percentage of Drivers Stopped by Police
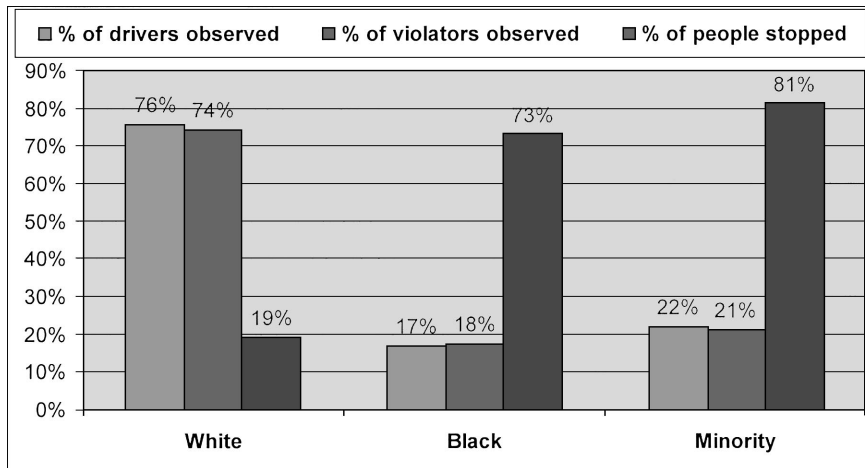
initiative in California in the fall of 2004 proposed to follow this strategy for the most populous state in the union.

Moreover, there has been rapid change in the inter-linking of state databases. In just two years, the national database went from a total of nine states cross-linking "a little over 100,000 offender profiles and 5,000 forensic profiles" to 32 states, the FBI, and the U.S. Army now linking "nearly 400,000 offender profiles, and close to 20,000 forensic profiles" (Brown, 2000). States are now uploading an average of 3,000 offender profiles every month. Information technology is increasingly efficient, and it now takes only 500 microseconds to search 100,000 genetic profiles in a database.

As law enforcement authorities increase the numbers of profiles in the forensic databases and biological material in repositories, these collections of information and samples will become an irresistible lure for forensic researchers who want to conduct genetic research, for instance, on particular types of offenders. Twenty-four states allow biological samples collected by law enforcement agencies to be used for a variety of purposes that go beyond individual identification (Simoncelli, 2004), and 20 states authorize the use of forensic tissue repositories for research on forensic techniques. In several of those states, the statutory language is general enough to cover research into genetics markers that purport to predict antisocial or criminalized behaviors. Tom Callaghan, program manager of the FBI's Federal Convicted Offender Program, refused to rule out such uses (Kimmelman, 2000). This is a wedge that can expand, via "function creep" (the tendency for a policy aimed at a specific problem to diffuse into other arenas) to genetic research on all manner of crimes and misdemeanors. Today, nearly half the states include profiles of some misdemeanants in their DNA databases. Once a person's

profile is in a database, or her biological material is in a repository, it may never come out.

If a DNA database is primarily composed of those who have been touched by the criminal justice system and that system engages in practices that routinely and disproportionately target minority groups, there will be an obvious skew or bias in the databases and repositories. Some propose to address this racial bias by sampling and profiling everyone in the U.S. population (Kaye & Smith, 2003). Even if this approach were politically feasible, it would not fully ameliorate racial bias in law enforcement or in the accompanying research that might be done using law enforcement databases or repositories.

Bias would still exist because law enforcement's lens does not focus equally on all types of crimes. Some kinds of activity, such as drug-related street crime, receive far more attention from police than parallel kinds of crime, such as cocaine sales at predominately White college fraternities. For this reason, even if the fraternity members' DNA profiles are in a databank, they will not be subject to the same level of matching or of subsequent allele frequency profiling research to "help explain" their behavior. The behavior of fraternity members will not have been recorded. That is, if the police are not stopping or arresting fraternity members, it matters far less whether their DNA is in a database; they are far less likely to be criminalized by the selective aim of the artillery of the legal system.

Even if a universal database or forensic repository resulted in less racial or ethnic bias in stops and arrests, racial minorities would still be the more likely targets of genetic research on criminalized behavior. It is certainly true that if a fraternity member committed a crime and left some tissue at the scene, the police could nab him if his DNA profile were in a database. However, because (a) Whites are less likely to be convicted than are racial and

ethnic minorities, (b) Whites are less likely to be incarcerated if convicted, and (c) Whites receive shorter sentences if incarcerated, it is less likely that a White fraternity member would become the object of behavioral research related to his crime. The selective criminalization of racial minorities is not likely to be altered by the existence of a population-wide DNA database. However, the surface fiction of objectivity could lead to research that unintentionally produces racially biased results.

The seeming objectivity of a population-wide database or sample repository masks a serious threat in the deployment of genetic technologies. The threat is that population-based or genetic epidemiology attempts to associate particular genetic markers with offender or criminal behaviors could reinforce stereotypes about racial propensities toward criminality. One could do a genetic study of rapists and sex offenders and find some markers that offenders putatively possess at a higher rate than members of the nonoffender population. If the offender population is more likely to have some ancestries than others, then spurious or noncausal correlations may be found; markers that are more common in the minority prison population may be associated with socially disfavored behaviors. If molecular genetics and the emergence of group-based research agendas fractured the public health and biomedical consensus regarding the utility or nonutility of racial classifications, researchers can expect an even more dramatic parallel development when it comes to discussions of the public safety.

Conclusion

Biomedical scientists are currently engaged in cataloging, lumping, and splitting human genetic variation. In addition to comparing individuals, scientists make genetic comparisons between groups of people. When genetic markers vary between human groups, the variation tends to be gradual and continuous, rather than discontinuous. Between-group variation is generally a matter of statistically significant differences in allele or marker frequencies, rather than an allele or marker that is present in one group and absent in another.

The recent focus on between-group genetic comparisons has raised inevitable questions about race. Contemporary molecular genetic data show that humans are not naturally divided into four or five discrete racial categories. Most genetic variation is within any racial category. Only a tiny percentage of the genetic variation can be found between groups that could be described as different races, and this variation is no more significant in defining human groups than is other, within-race genetic variation. Genetics can provide some information about ancestry, but ancestry may or may not correlate well with a person's race.

Although genetic variation is complex, humans' social interactions tend to separate people into four or five racial categories. Social stratification on the basis of race may have significant impacts on people's health, including their mental health. Racial health disparities may result from living in a racially stratified society.

Many recent criticisms of the use of race in science are well founded. Racial categories may be used in research without consideration as to whether race is the most effective means of categorizing people for any particular study. However, rather than categorically rejecting the use of race in science, or mandating its use for all data analysis, the scientific community should engage in a more nuanced discussion of when and how to use race variables in research.

One area in which the use of race will be particularly inflammatory is behavioral genetics research. Criminal behavior is an attractive problem to study, because of social anxiety about public safety. In the abstract, there is a public consensus about the desirability of reducing crime. However, when it comes to the routine practices of the criminal justice system, a demonstration of systematic racial bias has eroded (and will further erode) any societal consensus on how public safety is best achieved. This fracture will be exacerbated by the search for genetic markers among incarcerated people and the seductive slide into genetic explanations of crime. To the extent that researchers are looking for genetic explanations among incarcerated people, they will be looking at a flammable triumvirate of associations among genes, crime, and race.

Like the phrenology of the 19th century, findings of genetic markers that correlate with criminalized behavior will likely be only that—correlations and not explanations of the causes of violence or crime. The many causes of crime (or any human behavior) involve a wide range of forces, including genes that encode particular proteins and prenatal development. However, genes do not act in a vacuum; they are expressed in particular environments. The full range of relevant explanatory variables for criminal behavior and incarceration also includes the many ways in which law enforcement and the penal system focus on one part of the town and one group of people rather than another.

The new generation computers can make 7.5 trillion calculations per second in analyses that associate genetic markers with outcomes of various sorts, be they medical or behavioral. These are sirens beckoning researchers who wish to do correlational studies of population-based allele frequencies with ethnic estimations and groupings of felons. The seduction of a false technological precision, and the authority associated with molecular biology, will make even statistical associations into front page news. A higher and more determined vigilance of these developments is necessary if society is to avoid repeating the mistakes of the late 19th century.

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